

81 Sequence 178091,
c 82 Sequence 178562,
83 Sequence 517, App
c 84 Sequence 518, App
85 Sequence 537, App
c 86 Sequence 538, App
87 Sequence 45, Appli
c 88 Sequence 2, Appli
c 89 Sequence 3, Appli
c 90 Sequence 2, Appli
91 Sequence 42, Appl
c 92 Sequence 2, Appli
c 93 Sequence 19, Appl
94 Sequence 38, Appl
95 Sequence 40, Appl
96 Sequence 53, Appl
c 97 Sequence 65, Appl
98 Sequence 118, App
99 Sequence 119, App
c 100 Sequence 120, App

; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor ARNT
; NAME/KEY: misc_difference
; LOCATION: (0)...(0)
; OTHER INFORMATION: 3' -half site
US-09-816-763-10

Query Match 100.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
|||
Db 1 GTG 3

ALIGNMENTS

RESULT 1
US-09-735-363A-8
; Sequence 8, Application US/09735363A
; Patent No. US20010041691A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillips, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735.363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-735-363A-8

Query Match 100.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
|||
Db 1 GTG 3

RESULT 2
US-09-816-763-10
; Sequence 10, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816.763
; CURRENT FILING DATE: 2001-03-23

RESULT 4
US-10-264-280-4
; Sequence 4, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleot
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264.280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

Query Match 100.0%; Score 3; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
|||
Db 1 GTG 3


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; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-264-280-4
Query Match      100.0%; Score 3; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
    |||
Db 1 GTG 3

RESULT 5
US-10-264-280-8
; Sequence 8, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gavol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotides
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc feature
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide
US-10-264-280-8
Query Match      100.0%; Score 3; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
    |||
Db 1 GTG 3

RESULT 6
US-10-686-317-13/c
; Sequence 13, Application US/10686317
; Publication No. US20040115716A1
; GENERAL INFORMATION:
; APPLICANT: Freier, Susan M.
; APPLICANT: Matveeva, Olga
; APPLICANT: Tsodikov, Alexander
; APPLICANT: Giddings, Michael C.
; APPLICANT: Wyatt, Jacqueline R.
; TITLE OF INVENTION: Methods of Obtaining Active Antisense Compounds
; FILE REFERENCE: ISPH-0457
; CURRENT APPLICATION NUMBER: US/10/686,317
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US/09/568,165
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-686-317-13
Query Match      100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
    |||
Db 3 GTG 1

RESULT 7
US-10-686-317-48
; Sequence 48, Application US/10686317
; Publication No. US20040115716A1
; GENERAL INFORMATION:
; APPLICANT: Freier, Susan M.
; APPLICANT: Matveeva, Olga
; APPLICANT: Tsodikov, Alexander
; APPLICANT: Giddings, Michael C.
; APPLICANT: Wyatt, Jacqueline R.
; TITLE OF INVENTION: Methods of Obtaining Active Antisense Compounds
; FILE REFERENCE: ISPH-0457
; CURRENT APPLICATION NUMBER: US/10/686,317
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US/09/568,165
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-686-317-48
Query Match      100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
    |||
Db 1 GTG 3

RESULT 8
US-10-821-568-10
; Sequence 10, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: DETECTION AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor ARNT
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: (0)...(0)
; OTHER INFORMATION: 3'-half site
US-10-821-568-10

Query Match      100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTG 3
Db      1 GTG 3

RESULT 9
US-09-735-363A-50
; Sequence 50, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-50

Query Match      66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GT 2
Db      1 GT 2

RESULT 10
US-09-735-363A-51
; Sequence 51, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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;
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-51

Query Match      66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TG 3
Db      1 TG 2

RESULT 11
US-09-971-894-19
; Sequence 19, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kaahi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Eitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerman, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; FILE REFERENCE: 01/22569
; CURRENT APPLICATION NUMBER: US/09/971,894
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-971-894-19

Query Match      66.7%; Score 2; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GT 2
Db      1 GT 2

RESULT 12
US-09-852-903C-20/c
; Sequence 20, Application US/09852903C
; Publication No. US20030104376A1
; GENERAL INFORMATION:
; APPLICANT: Diattech Pty. Ltd.
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2414918/EJH
; CURRENT APPLICATION NUMBER: US/09/852,903C
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 60/202,771
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/202,559
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 2
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ( )..(?)
; OTHER INFORMATION: CA-1
US-09-852-903C-20
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Query Match 66.7%; Score 2; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09; Indels 0;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 2 TG 3
||
Db 2 TG 1

RESULT 13
US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09; Indels 0;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GT 2
||
Db 2 GT 1

RESULT 14
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09; Indels 0;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 15
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09; Indels 0;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 16
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175403
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175403

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 17

US-10-027-632-175415
;; Sequence 175415, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175415
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175415

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 18

US-10-027-632-175419
;; Sequence 175419, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175419
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175419

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 19

US-10-027-632-175426
;; Sequence 175426, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175426
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175426

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

US-10-027-632-175426

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 20

US-10-027-632-175433
; Sequence 175433, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 21

US-10-027-632-178617
; Sequence 178617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
||
Db 1 TG 2

RESULT 22

US-10-027-632-178640
; Sequence 178640, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
||
Db 1 TG 2

RESULT 23

US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

RESULT 24
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280

Query Match 66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 2 GT 1

RESULT 25
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

Query Match 66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 26
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

Query Match 66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

```
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
   ||
Db 1 GT 2

RESULT 27
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
   ||
Db 1 GT 2

RESULT 28
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
   ||
Db 1 GT 2

RESULT 29
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
   ||
Db 1 GT 2

RESULT 30
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433

```

```

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred.No. 3.le+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 GT 2
        ||
Db      1 GT 2

```

Search completed: July 20, 2005, 22:43:05
Job time : 394 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 20:31:28 ; Search time 98 Seconds
(without alignments)
50.090 Million cell u

Title: US-09-735-363A-8

Perfect score; 3

Sequence: 1 gtg 3

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 112

Minimum DB seq length: 0

Maximum DB seq length:	3
------------------------	---

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:*

- ```
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTrus_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query |       |        | DB | ID                | Description       |
|------------|-------|-------|--------|----|-------------------|-------------------|
|            | Score | Match | Length |    |                   |                   |
| 1          | 2     | 66.7  | 2      | 3  | US-09-472-035A-19 | Sequence 19, Appl |
| 2          | 2     | 66.7  | 3      | 1  | US-07-791-213D-46 | Sequence 46, Appl |
| 3          | 2     | 66.7  | 3      | 1  | US-07-791-213D-62 | Sequence 62, Appl |
| 4          | 2     | 66.7  | 3      | 1  | US-08-602-036A-2  | Sequence 2, Appl  |
| 5          | 2     | 66.7  | 3      | 1  | US-08-293-150A-46 | Sequence 46, Appl |
| 6          | 2     | 66.7  | 3      | 1  | US-08-293-150A-62 | Sequence 62, Appl |
| 7          | 2     | 66.7  | 3      | 1  | US-08-502-374A-2  | Sequence 2, Appl  |
| 8          | 2     | 66.7  | 3      | 2  | US-08-642-407A-2  | Sequence 2, Appl  |
| 9          | 2     | 66.7  | 3      | 3  | US-08-793-634B-12 | Sequence 12, Appl |
| 10         | 2     | 66.7  | 3      | 3  | US-09-472-035A-22 | Sequence 22, Appl |
| 11         | 2     | 66.7  | 3      | 4  | US-09-307-106-45  | Sequence 45, Appl |
| 12         | 1.4   | 46.7  | 3      | 3  | US-08-873-709-9   | Sequence 9, Appl  |
| 13         | 1.4   | 46.7  | 3      | 3  | US-09-032-365A-36 | Sequence 36, Appl |
| 14         | 1.4   | 40.0  | 3      | 3  | US-09-411-862A-10 | Sequence 10, Appl |
| 15         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-10 | Sequence 10, Appl |
| 16         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-11 | Sequence 11, Appl |
| 17         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-11 | Sequence 11, Appl |
| 18         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-12 | Sequence 12, Appl |
| 19         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-12 | Sequence 12, Appl |
| 20         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-13 | Sequence 13, Appl |
| 21         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-13 | Sequence 13, Appl |
| 22         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-14 | Sequence 14, Appl |
| 23         | 1.2   | 40.0  | 3      | 3  | US-09-411-862A-14 | Sequence 14, Appl |
| 24         | 1     | 33.3  | 2      | 1  | US-08-268-679B-8  | Sequence 8, Appl  |
| 25         | 1     | 33.3  | 2      | 1  | US-08-457-274A-16 | Sequence 16, Appl |
| 26         | 1     | 33.3  | 2      | 1  | US-08-484-192-16  | Sequence 16, Appl |
| 27         | 1     | 33.3  | 2      | 3  | US-09-016-520-35  | Sequence 35, Appl |

## ALIGNMENTS

RESULT 1  
US-09-472-035A-19  
; Sequence 19, Application US/09472035A  
; Patent No. 6322985  
; GENERAL INFORMATION:  
; APPLICANT: Yecheskel Kashi et al.  
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING  
; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
; STREET: 2001 Jefferson Davis Highway, Suite 207  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
; COMPUTER: Twinhead\* Slimnote-890TX  
; OPERATING SYSTEM: MS DOS version 6.2,  
; OPERATING SYSTEM: Windows version 3.11  
; SOFTWARE: Word for Windows version 2.0 converted to  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/472,035A

; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Friedmam, Mark M.  
; REGISTRATION NUMBER: 33,883  
; REFERENCE/DOCKET NUMBER: 74/77  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 972-3-5625553  
; TELEFAX: 972-3-5625554  
; TELEX:

; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

US-09-472-035A-19  
Query Match 66.7%; Score 2; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 8e+08;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
||  
DB 1 GT 2

RESULT 2  
US-07-791-213D-46  
; Sequence 46, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match 66.7%; Score 2; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 5.3e+08;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3  
||  
DB 1 TG 2

RESULT 3  
US-07-791-213D-62  
; Sequence 62, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,213D

```
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-791-213D-62

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 1 TG 2

RESULT 4
US-08-602-036A-2
; Sequence 2, Application US/08602036A
; Patent No. 5789248
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602.036A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-039CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA

; FILING DATE: 13-NOV-1991
; ANTI-SENSE: NO
; US-08-602-036A-2

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 5.3e+08;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 1 GU 2

RESULT 5
US-08-293-150A-46
; Sequence 46, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-293-150A-46

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 1 TG 2
```

```
RESULT 6
US-08-293-150A-62
; Sequence 62, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshihiro
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62
Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
Db 1 TG 2

RESULT 7
US-08-502-374A-2
; Sequence 2, Application US/08502374A
; Patent No. 5872007
; GENERAL INFORMATION:
; APPLICANT: Fodstad, Oeystein
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 21
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,374A
; FILING DATE: 14-Jul-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HVZ-039DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6000
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-502-374A-2
Query Match 66.7%; Score 2; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 5.3e+08;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
Db 1 GU 2

RESULT 8
US-08-642-407A-2
; Sequence 2, Application US/08642407A
; Patent No. 5877308
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,407A
; FILING DATE: 03-May-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-039CPDV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; US-08-642-407A-2

Query Match 66.7%; Score 2; DB 2; Length 3;  
Best Local Similarity 50.0%; Pred. No. 5.3e+08;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
Db 1 GU 2

RESULT 9  
US-08-793-634B-12  
; Sequence 12, Application US/08793634B  
; Patent No. 6211431  
; GENERAL INFORMATION:  
; APPLICANT: Boevink, Petra C.  
; APPLICANT: Surin, Brian P.  
; APPLICANT: Keese, Paul K.  
; APPLICANT: Chu, Paul W.G.  
; APPLICANT: Waterhouse, Peter M.  
; APPLICANT: Khan, Rafiqul I.  
; APPLICANT: Larkin, Philip J.  
; APPLICANT: Taylor, William C.  
; APPLICANT: Marchall, Jerry S.  
; TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,634B  
; FILING DATE: June 9, 1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10530  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-793-634B-12

Query Match 66.7%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 5.3e+08;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TG 3  
Db 1 TG 2

RESULT 10  
US-09-472-035A-22  
; Sequence 22, Application US/09472035A  
; Patent No. 6322985  
; GENERAL INFORMATION:  
; APPLICANT: Yechezkel Kashi et al.  
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
; STREET: 2001 Jefferson Davis Highway, Suite 207  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
; COMPUTER: Twinhead\* Slimnote-890TX  
; OPERATING SYSTEM: MS DOS version 6.2,  
; OPERATING SYSTEM: Windows version 3.11  
; SOFTWARE: Word for Windows version 2.0 converted to  
; SOFTWARE: an ASCII file  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/472,035A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Friedman, Mark M.  
; REGISTRATION NUMBER: 33,883  
; REFERENCE/DOCKET NUMBER: 74/77  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 972-3-5625553  
; TELEFAX: 972-3-5625554  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-09-472-035A-22

Query Match 66.7%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 5.3e+08;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
Db 2 GT 3

RESULT 11  
US-09-307-106-45  
; Sequence 45, Application US/09307106  
; Patent No. 6603063  
; GENERAL INFORMATION:  
; APPLICANT: Feltelson, Jerald S.

APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schneits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Finstad-Lee, Stacey  
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide  
TITLE OF INVENTION: Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/307,106  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 05-MAY-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-307-106-45  
Query Match 66.7%; Score 2; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 5.3e+08;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TG 3  
DB 2 TG 3  
RESULT 12  
US-08-873-709-9  
Sequence 9, Application US/08873709  
Patent No. 6037126  
GENERAL INFORMATION:  
APPLICANT: Grossman, Abraham  
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND  
TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF  
TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME  
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:  
ADDRESSER: Abraham Grossman  
STREET: 666 Washington Avenue  
CITY: Pleasantville  
STATE: NY  
COUNTRY: USA  
ZIP: 10570  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/873,709  
FILING DATE: 12-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: Q001/002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-747-9108  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-873-709-9  
Query Match 46.7%; Score 1.4; DB 3; Length 3;  
Best Local Similarity 66.7%; Pred. No. 5.3e+08;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GTG 3  
DB 1 GGG 3  
RESULT 13  
US-09-032-365A-36  
Sequence 36, Application US/09032365A  
Patent No. 6114502  
GENERAL INFORMATION:  
APPLICANT: No. 6114502th, Michael  
APPLICANT: Nishina, Patsy  
APPLICANT: Naggart, Juergen  
APPLICANT: No. 6114502en-Trauth, Konrad  
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
TITLE OF INVENTION: NEUROSENSORY DEFECTS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Avenue, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,365A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-2CIP2  
TELEPHONE: 650-327-3400  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-09-032-365A-36

Query Match 46.7%; Score 1.4; DB 3; Length 3;  
Best Local Similarity 66.7%; Pred. No. 5.3e+08;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTG 3  
DB 1 GGG 3

RESULT 14  
US-09-411-862A-10  
; Sequence 10, Application US/09411862A  
; Patent No. 6348583  
; GENERAL INFORMATION:  
; APPLICANT: David Segev  
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC  
; ACIDS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina  
; STREET: 2001 Jefferson Davis Highway, Suite 207  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
; COMPUTER: Twinhead\* Slimnote-890TX  
; OPERATING SYSTEM: MS DOS version 6.2,  
; Windows version 3.11  
; SOFTWARE: Word for Windows version 2.0 converted to  
; an ASCII file  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/411.862A  
; FILING DATE: 04-Oct-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/384,995  
; FILING DATE: 20 AUG 1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sol Sheinbein  
; REGISTRATION NUMBER: 25,457  
; REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 972-3-6127676  
; TELEFAX: 972-3-6127575  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-411-862A-10

Query Match 40.0%; Score 1.2; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 5.3e+08;  
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
DB 2 SW 1

RESULT 16  
US-09-411-862A-11  
; Sequence 11, Application US/09411862A  
; Patent No. 6348583  
; GENERAL INFORMATION:  
; APPLICANT: David Segev  
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC  
; ACIDS

```
/
/ ACIDS
/
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
/ STREET: 2001 Jefferson Davis Highway, Suite 207
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: United States of America
/ ZIP: 22202
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
/ COMPUTER: Twinhead* Slimnote-890TX
/ OPERATING SYSTEM: MS DOS version 6.2,
/ Windows version 3.11
/ SOFTWARE: Word for Windows version 2.0 converted to
/ an ASCII file
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/411,862A
/ FILING DATE: 04-Oct-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/384,995
/ FILING DATE: 20 AUG 1999
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sol Sheinbein
/ REGISTRATION NUMBER: 25,457
/ REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 972-3-6127676
/ TELEFAX: 972-3-6127575
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-411-862A-11

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 2 SW 3

RESULT 17
US-09-411-862A-11/c
/ Sequence 11, Application US/09411862A
/ Patent No. 6348583
/ GENERAL INFORMATION:
/ APPLICANT: David Segev
/ TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-
/ SULFOXIDE) AND POLY(ETHER-SULFONE) NUCLEIC
/ ACIDS
/
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
/ STREET: 2001 Jefferson Davis Highway, Suite 207
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: United States of America
/ ZIP: 22202
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
/ COMPUTER: Twinhead* Slimnote-890TX
/ OPERATING SYSTEM: MS DOS version 6.2,
/ Windows version 3.11
/ SOFTWARE: Word for Windows version 2.0 converted to
/ an ASCII file
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/411,862A
/ FILING DATE: 04-Oct-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/384,995
/ FILING DATE: 20 AUG 1999
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sol Sheinbein
/ REGISTRATION NUMBER: 25,457
/ REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 972-3-6127676
/ TELEFAX: 972-3-6127575
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 12:
INFORMATION FOR SEQ ID NO: 12:
```

```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/411,862A
/ FILING DATE: 04-Oct-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/384,995
/ FILING DATE: 20 AUG 1999
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sol Sheinbein
/ REGISTRATION NUMBER: 25,457
/ REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 972-3-6127676
/ TELEFAX: 972-3-6127575
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-411-862A-11

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 2 SW 1

RESULT 18
US-09-411-862A-12
/ Sequence 12, Application US/09411862A
/ Patent No. 6348583
/ GENERAL INFORMATION:
/ APPLICANT: David Segev
/ TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-
/ SULFOXIDE) AND POLY(ETHER-SULFONE) NUCLEIC
/ ACIDS
/
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
/ STREET: 2001 Jefferson Davis Highway, Suite 207
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: United States of America
/ ZIP: 22202
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
/ COMPUTER: Twinhead* Slimnote-890TX
/ OPERATING SYSTEM: MS DOS version 6.2,
/ Windows version 3.11
/ SOFTWARE: Word for Windows version 2.0 converted to
/ an ASCII file
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/411,862A
/ FILING DATE: 04-Oct-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/384,995
/ FILING DATE: 20 AUG 1999
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sol Sheinbein
/ REGISTRATION NUMBER: 25,457
/ REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 972-3-6127676
/ TELEFAX: 972-3-6127575
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 12:
INFORMATION FOR SEQ ID NO: 12:
```



## ; SEQUENCE CHARACTERISTICS:

LENGTH: 3  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-411-862A-12

Query Match 40.0%; Score 1.2; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 5.3e+08;  
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2

Db ::  
2 SW 3

## RESULT 19

US-09-411-862A-12/c  
; Sequence 12, Application US/09411862A

; Patent No. 6348583

; GENERAL INFORMATION:

; APPLICANT: David Segev

; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC  
ACIDS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina

; STREET: 2001 Jefferson Davis Highway, Suite 207

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

; COMPUTER: Twinhead\* Slimnote-890TX

; OPERATING SYSTEM: MS DOS version 6.2,

; Windows version 3.11

; SOFTWARE: Word for Windows version 2.0 converted to

; an ASCII file

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/411.862A

; FILING DATE: 04-Oct-1999

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/384,995

; FILING DATE: 20 AUG 1999

; ATTORNEY/AGENT INFORMATION:

; NAME: Sol Sheinbein

; REGISTRATION NUMBER: 25,457

; REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 972-3-6127676

; TELEFAX: 972-3-6127575

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-411-862A-12

Query Match 40.0%; Score 1.2; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 5.3e+08;  
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2

Db ::  
2 SW 1

## RESULT 20

US-09-411-862A-13

; Sequence 13, Application US/09411862A

; Patent No. 6348583

; GENERAL INFORMATION:

; APPLICANT: David Segev

; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC  
ACIDS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina

; STREET: 2001 Jefferson Davis Highway, Suite 207

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

; COMPUTER: Twinhead\* Slimnote-890TX

; OPERATING SYSTEM: MS DOS version 6.2,

; Windows version 3.11

; SOFTWARE: Word for Windows version 2.0 converted to

; an ASCII file

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/411.862A

; FILING DATE: 04-Oct-1999

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/384,995

; FILING DATE: 20 AUG 1999

; ATTORNEY/AGENT INFORMATION:

; NAME: Sol Sheinbein

; REGISTRATION NUMBER: 25,457

; REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 972-3-6127676

; TELEFAX: 972-3-6127575

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-411-862A-13

Query Match

Best Local Similarity 40.0%; Score 1.2; DB 3; Length 3;

Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2

Db ::

2 SW 3

## RESULT 21

US-09-411-862A-13/c

; Sequence 13, Application US/09411862A

; Patent No. 6348583

; GENERAL INFORMATION:

; APPLICANT: David Segev

; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC  
ACIDS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina

; STREET: 2001 Jefferson Davis Highway, Suite 207

; CITY: Arlington

; STATE: Virginia

```
/
/ COUNTRY: United States of America
/ ZIP: 22202
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
/ COMPUTER: Twinhead* Slimnote-890TX
/ OPERATING SYSTEM: MS DOS version 6.2,
/ Windows version 3.11
/
/ SOFTWARE: Word for Windows version 2.0 converted to
/ an ASCII file
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/411,862A
/ FILING DATE: 04-Oct-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/384,995
/ FILING DATE: 20 AUG 1999
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sol Sheinbein
/ REGISTRATION NUMBER: 25,457
/ REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 972-3-6127676
/ TELEFAX: 972-3-6127575
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-411-862A-13

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred.No.5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db ::
2 SW 1

RESULT 22
US-09-411-862A-14
; Sequence 14, Application US/09411862A
; Patent No. 6348583
; GENERAL INFORMATION:
; APPLICANT: David Segev
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-
; SULFOXIDE) AND POLY(ETHER-SULFONE) NUCLEIC
; ACIDS
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sol Sheinbein c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
;
; SOFTWARE: Word for Windows version 2.0 converted to
; an ASCII file
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,862A
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/384,995
; FILING DATE: 20 AUG 1999
```

```
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sol Sheinbein
/ REGISTRATION NUMBER: 25,457
/ REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 972-3-6127676
/ TELEFAX: 972-3-6127575
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-411-862A-14

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred.No.5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db ::
2 SW 3

RESULT 23
US-09-411-862A-14/c
; Sequence 14, Application US/09411862A
; Patent No. 6348583
; GENERAL INFORMATION:
; APPLICANT: David Segev
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-
; SULFOXIDE) AND POLY(ETHER-SULFONE) NUCLEIC
; ACIDS
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sol Sheinbein c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
;
; SOFTWARE: Word for Windows version 2.0 converted to
; an ASCII file
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,862A
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/384,995
; FILING DATE: 20 AUG 1999
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Sol Sheinbein
; REGISTRATION NUMBER: 25,457
; REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-6127676
; TELEFAX: 972-3-6127575
; TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-411-862A-14
```

Query Match 40.0%; Score 1.2; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 5.3e+08;  
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
Db 2 SW 1

## RESULT 24

US-08-268-679B-8  
; Sequence 8, Application US/08268679B  
; Patent No. 5674729  
; GENERAL INFORMATION:  
; APPLICANT: WIMMER, ECKARD; MOLL, ANIKO V.  
; TITLE OF INVENTION: DE NOVO CELL-FREE  
; SYNTHESIS OF PICORNAVIRUS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVE.  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT # 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/268,679B  
; FILING DATE: 30-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/846,914  
; FILING DATE: 06-MAR-1992  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 07/719,761  
; FILING DATE: 24-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MARIA C.H. LIN  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 0887-4095 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: UNKNOWN  
; MOLECULE TYPE:  
; DESCRIPTION: OLIGONUCLEOTIDE  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE: N.A.  
; POSITION IN GENOME: N.A.

## US-08-268-679B-8

Query Match 33.3%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 8e+08;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1  
Db 1 G 1

## RESULT 25

US-08-457-274A-16/C  
; Sequence 16, Application US/08457274A  
; Patent No. 5734086  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Jeffrey G.  
; APPLICANT: Tomita, Takashi  
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: P.O. Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,274A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-263-1304  
; TELEFAX: 716-263-1600  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Musca domestica  
; STRAIN: Learn-Pyr  
; DEVELOPMENTAL STAGE: Adult  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: Chromosome 1

## US-08-457-274A-16

Query Match 33.3%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 8e+08;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2  
Db 2 T 2

## RESULT 26

US-08-484-192-16  
; Sequence 16, Application US/08484192  
; Patent No. 5756291  
; GENERAL INFORMATION:  
; APPLICANT: GRIFFIN, LINDA C.  
; APPLICANT: ALBRECHT, GLENN  
; APPLICANT: LATHAM, JOHN  
; APPLICANT: LEUNG, LAWRENCE  
; APPLICANT: VERMAAS, ERIC  
; APPLICANT: TOOLE, JOHN J.  
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
; METHODS OF MAKING  
; NUMBER OF SEQUENCES: 181  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER

```

; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: replace(1,"")
; OTHER INFORMATION: /note= "this is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 33.3%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08; 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
Db 2 G 2

RESULT 27
US-09-016-520-35
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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```

; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-35

Query Match 33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08; 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
Db 1 T 1

RESULT 28
US-09-130-973-35
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
; OTHER INFORMATION: Sequence
US-09-130-973-35

Query Match 33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08; 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
Db 1 T 1

RESULT 29
US-09-477-902-35
; Sequence 35, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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Search completed: July 20, 2005, 21:47:41  
Job time : 100 secs

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; OTHER INFORMATION: Sequence
; NAME/KEY: misc_feature
; LOCATION: (1).(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
US-09-477-902-35

Query Match 33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
Db 1 T 1

RESULT 30
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; Sequence 3, Application US/08361024
; Patent No. 6207368
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; TITLE OF INVENTION: Method, Reagent and Kit
; TITLE OF INVENTION: for Detection and
; TITLE OF INVENTION: Amplification of
; TITLE OF INVENTION: Nucleic Acid Sequence
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 Mb
; COMPUTER: IBM
; OPERATING SYSTEM: MS.DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,024
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/925,059
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Burgoon, Richard P.
; REGISTRATION NUMBER: 34,787
; REFERENCE/DOCKET NUMBER: 128D-126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-7610
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: yes
; ANTI-SENSE: no
US-08-361-024-3
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Query Match 33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
Db 1 G 1
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 20:09:32 ; Search time 1842 Seconds  
(without alignments)  
61.994 Million cell updates/sec

Title: US-09-735-363A-8  
Perfect score: 3  
Sequence: 1 gtc 3

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 882

Minimum DB seq length: 0  
Maximum DB seq length: 3

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| C 1        | 3     | 100.0       | 3      | 9     | CL423861 01S0750-0 |
| C 2        | 2     | 66.7        | 2      | 7     | CF301411 7LEAF--06 |
| C 3        | 2     | 66.7        | 2      | 7     | CF306288 HDAL--03  |
| C 4        | 2     | 66.7        | 2      | 7     | CF331310 NACL--07  |
| C 5        | 2     | 66.7        | 2      | 7     | CF333014 JMT--01-L |
| C 6        | 2     | 66.7        | 2      | 7     | CO792627 NT015C-D1 |
| C 7        | 2     | 66.7        | 2      | 9     | CL661289 PRI0139B  |
| C 8        | 2     | 66.7        | 2      | 9     | CL670560 PRI0162b  |
| C 9        | 2     | 66.7        | 2      | 9     | CL682684 PRI0134C  |
| C 10       | 2     | 66.7        | 2      | 9     | CL688205 PRI0148d  |
| C 11       | 2     | 66.7        | 2      | 9     | CL872635 abe83g10- |
| C 12       | 2     | 66.7        | 2      | 9     | CL874640 abe96h02. |
| C 13       | 2     | 66.7        | 2      | 9     | CL876415 abf13c11. |
| C 14       | 2     | 66.7        | 2      | 9     | CL883717 abf63c08. |
| C 15       | 2     | 66.7        | 2      | 3     | CA850938 D08D06_H1 |
| C 16       | 2     | 66.7        | 2      | 3     | CA851961 D19E06_I1 |
| C 17       | 2     | 66.7        | 2      | 3     | CF305942 HDAL--02  |
| C 18       | 2     | 66.7        | 2      | 3     | CF308858 ABF--02-N |
| C 19       | 2     | 66.7        | 2      | 3     | CF310006 ABF--04-H |
| C 20       | 2     | 66.7        | 2      | 3     | CF311628 ABF--06-O |
| C 21       | 2     | 66.7        | 2      | 3     | CF313258 HD--01-FO |
| C 22       | 2     | 66.7        | 2      | 3     | CF315632 HD--04-KO |
| C 23       | 2     | 66.7        | 2      | 3     | CF317717 HD--07-IO |
| C 24       | 2     | 66.7        | 2      | 3     | CF338538 RCL1--01- |

|          |           |      |     |      |   |   |          |
|----------|-----------|------|-----|------|---|---|----------|
| CF339357 | RCL1--04- | 25   | 2   | 66.7 | 3 | 7 | CF339357 |
| CF339421 | RCL1--04- | 26   | 2   | 66.7 | 3 | 7 | CF339421 |
| CF339646 | RCL1--05- | 27   | 2   | 66.7 | 3 | 7 | CF339646 |
| CF340077 | RCL1--06- | C 28 | 2   | 66.7 | 3 | 7 | CF340077 |
| CF372478 | CSECS052H | C 29 | 2   | 66.7 | 3 | 7 | CF372478 |
| CK575874 | IST_WT5_9 | C 30 | 2   | 66.7 | 3 | 7 | CK575874 |
| CK632435 | AM1-AP000 | C 31 | 2   | 66.7 | 3 | 7 | CK632435 |
| CO793948 | NT019B_A0 | C 32 | 2   | 66.7 | 3 | 7 | CO793948 |
| CO819398 | CSECS153H | C 33 | 2   | 66.7 | 3 | 7 | CO819398 |
| CV179297 | CSECS016C | C 34 | 2   | 66.7 | 3 | 7 | CV179297 |
| CL656746 | PRI0127b  | C 35 | 2   | 66.7 | 3 | 9 | CL656746 |
| CL664603 | PRI0147c  | C 36 | 2   | 66.7 | 3 | 9 | CL664603 |
| CL668376 | PRI0157c  | C 37 | 2   | 66.7 | 3 | 9 | CL668376 |
| CL689749 | PRI0160b  | C 38 | 2   | 66.7 | 3 | 9 | CL689749 |
| CL679295 | PRI0125c  | C 39 | 2   | 66.7 | 3 | 9 | CL679295 |
| CL884066 | abf65h10. | C 40 | 2   | 66.7 | 3 | 9 | CL884066 |
| CF315089 | HD--03-N2 | 41   | 1.4 | 46.7 | 3 | 7 | CF315089 |
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| CK449137 | nsgepl1E4 | C 43 | 1.4 | 46.7 | 3 | 7 | CK449137 |
| AL039341 | DKFZp434F | C 44 | 1   | 33.3 | 2 | 1 | AL039341 |
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| AL039455 | DKFZp434N | C 46 | 1   | 33.3 | 2 | 1 | AL039455 |
| AL039455 | DKFZp434N | C 47 | 1   | 33.3 | 2 | 1 | AL039455 |
| AL042337 | DKFZp434O | C 48 | 1   | 33.3 | 2 | 1 | AL042337 |
| AL042337 | DKFZp434O | C 49 | 1   | 33.3 | 2 | 1 | AL042337 |
| AL043859 | DKFZp434B | C 50 | 1   | 33.3 | 2 | 1 | AL043859 |
| AL043859 | DKFZp434B | C 51 | 1   | 33.3 | 2 | 1 | AL043859 |
| AL047069 | DKFZp586P | C 52 | 1   | 33.3 | 2 | 1 | AL047069 |
| AL047069 | DKFZp586P | C 53 | 1   | 33.3 | 2 | 1 | AL047069 |
| BX266185 | BX266185  | C 54 | 1   | 33.3 | 2 | 5 | BX266185 |
| BX266563 | BX266563  | C 55 | 1   | 33.3 | 2 | 5 | BX266563 |
| BX267110 | BX267110  | C 56 | 1   | 33.3 | 2 | 5 | BX267110 |
| BX267110 | BX267110  | C 57 | 1   | 33.3 | 2 | 5 | BX267110 |
| BX267118 | BX267118  | C 58 | 1   | 33.3 | 2 | 5 | BX267118 |
| CA850819 | D06H04_H0 | C 59 | 1   | 33.3 | 2 | 6 | CA850819 |
| CA850842 | D07B06_C1 | C 60 | 1   | 33.3 | 2 | 6 | CA850842 |
| CA850864 | D07D08_G2 | C 61 | 1   | 33.3 | 2 | 6 | CA850864 |
| CA850952 | D08B09_J2 | C 62 | 1   | 33.3 | 2 | 6 | CA850952 |
| CA851273 | D12A01_B1 | C 63 | 1   | 33.3 | 2 | 6 | CA851273 |
| CF280384 | 14ETL--07 | C 64 | 1   | 33.3 | 2 | 7 | CF280384 |
| CF280384 | 14ETL--07 | C 65 | 1   | 33.3 | 2 | 7 | CF280384 |
| CF280511 | 14ETL--07 | C 66 | 1   | 33.3 | 2 | 7 | CF280511 |
| CF280511 | 14ETL--07 | C 67 | 1   | 33.3 | 2 | 7 | CF280511 |
| CF281505 | 14ETL--08 | C 68 | 1   | 33.3 | 2 | 7 | CF281505 |
| CF281609 | 14ETL--08 | C 69 | 1   | 33.3 | 2 | 7 | CF281609 |
| CF282353 | 14ETL--09 | C 70 | 1   | 33.3 | 2 | 7 | CF282353 |
| CF291112 | 14ROOT--0 | C 71 | 1   | 33.3 | 2 | 7 | CF291112 |
| CF292081 | 14ROOT--0 | C 72 | 1   | 33.3 | 2 | 7 | CF292081 |
| CF295832 | 30DGS--05 | C 73 | 1   | 33.3 | 2 | 7 | CF295832 |
| CF296698 | 30DGS--07 | C 74 | 1   | 33.3 | 2 | 7 | CF296698 |
| CF299103 | 7LEAF--02 | C 75 | 1   | 33.3 | 2 | 7 | CF299103 |
| CF299550 | 7LEAF--03 | C 76 | 1   | 33.3 | 2 | 7 | CF299550 |
| CF299550 | 7LEAF--03 | C 77 | 1   | 33.3 | 2 | 7 | CF299550 |
| CF299571 | 7LEAF--03 | C 78 | 1   | 33.3 | 2 | 7 | CF299571 |
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| CF299728 | 7LEAF--03 | C 80 | 1   | 33.3 | 2 | 7 | CF299728 |
| CF299820 | 7LEAF--05 | C 81 | 1   | 33.3 | 2 | 7 | CF299820 |
| CF300639 | 7LEAF--05 | C 82 | 1   | 33.3 | 2 | 7 | CF300639 |
| CF301112 | 7LEAF--07 | C 83 | 1   | 33.3 | 2 | 7 | CF301112 |
| CF302235 | 7LEAF--07 | C 84 | 1   | 33.3 | 2 | 7 | CF302235 |
| CF302259 | 7LEAF--07 | C 85 | 1   | 33.3 | 2 | 7 | CF302259 |
| CF307078 | HDAL--05- | C 86 | 1   | 33.3 | 2 | 7 | CF307078 |
| CF307078 | HDAL--05- | C 87 | 1   | 33.3 | 2 | 7 | CF307078 |
| CF307123 | HDAL--05- | C 88 | 1   | 33.3 | 2 | 7 | CF307123 |
| CF307878 | ABF--01-H | C 89 | 1   | 33.3 | 2 | 7 | CF307878 |
| CF307878 | ABF--01-H | C 90 | 1   | 33.3 | 2 | 7 | CF307878 |
| CF311389 | ABF--06-J | C 91 | 1   | 33.3 | 2 | 7 | CF311389 |
| CF311389 | ABF--06-J | C 92 | 1   | 33.3 | 2 | 7 | CF311389 |
| CF311851 | ABF--07-E | C 93 | 1   | 33.3 | 2 | 7 | CF311851 |
| CF312294 | ABF--07-O | C 94 | 1   | 33.3 | 2 | 7 | CF312294 |
| CF312294 | ABF--07-O | C 95 | 1   | 33.3 | 2 | 7 | CF312294 |
| CF315237 | HD--04-B0 | C 96 | 1   | 33.3 | 2 | 7 | CF315237 |
| CF348132 | NACL--02- | C 97 | 1   | 33.3 | 2 | 7 | CF348132 |

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c 99 1 33.3 2 7 CF329006 CF329006 NACL--04-
c 100 1 33.3 2 7 CF329006 CF329006 NACL--04-

ALIGNMENTS

RESULT 1
CL423861/c
LOCUS 01S0750-04C1-C02 UniformMu MutAIL Library Zea mays genomic clone
DEFINITION
ACCESSION CL423861
VERSION 01S0750-04C1-C02, genomic survey sequence.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 3)
AUTHORS Lathaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize
 population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
 Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA
 Tel: 352-392-1928 x322
 Email: drmc@ufl.edu
 Sequence flanking probable Mu insertion site in UniformMu
 line: 01S0750-04, primer set: C
 Class: transposon insertion site.

FEATURES source
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 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="01S0750-04C1-C02"
 /clone_lib="UniformMu MutAIL Library"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match 100.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
 |||
 3 GTG 1

Db

RESULT 2
CF301411/c
LOCUS 7LEAF--06-E07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--06-E07, mRNA
 sequence.
ACCESSION CF301411
VERSION CF301411.1 GI:33673172
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 2)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..2
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-E07"
/tissue_type="leaf"
/dev stages="7 days after germination"
/lab host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 66.7%; Score 2; DB 7; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
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 2 GT 1

Db

RESULT 3
CF306288/c
LOCUS HDAL--03-E23.g1 OshDACL-overexpressing transgenic rice lambda phage
DEFINITION cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
 clone HDAL--03-E23, mRNA sequence.
ACCESSION CF306288
VERSION CF306288.1 GI:33678049
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaeae; Oryza.
 1 (bases 1 to 2)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HDAL--03-E23"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 2)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..2
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAL--03-E23"

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/tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice lambda  
 phage cDNA library I (HDA1)"  
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
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 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+10;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3  
 ||  
 Db 2 TG 1

## RESULT 4

CF331310/c

LOCUS  
 DEFINITION NACL--07-G04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-G04, mRNA sequence.

ACCESSION

VERSION

CF331310.1 GI:33810838

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .2

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="NACL--07-G04"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 66.7%; Score 2; DB 7; Length 2;

Best Local Similarity 100.0%; Pred. No. 1.9e+10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2

||

Db 2 GT 1

## RESULT 5

CF333014/c

LOCUS

DEFINITION

JMT--01-L21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--01-L21, mRNA sequence.

CF333014

ACCESSION

VERSION

CF333014.1 GI:33814278

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .2

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="JMT--01-L21"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 66.7%; Score 2; DB 7; Length 2;

Best Local Similarity 100.0%; Pred. No. 1.9e+10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2

||

Db 2 GT 1

## RESULT 6

CF392627

LOCUS

DEFINITION

NT015C.D12 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'

similar to hypothetical protein, mRNA sequence.

CF392627

ACCESSION

VERSION

CF392627.1 GI:51008598

KEYWORDS

EST.

SOURCE

ORGANISM

Ambystoma mexicanum (axolotl)

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

1 (bases 1 to 2)

Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,

Fehlke,K., Sperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.

An Ambystoma mexicanum EST sequencing project: Analysis of 17,352

expressed sequence tags from embryonic and regenerating blastema

cDNA libraries

Genome Biol. (2004) In press

Contact: Eilly M. Tanaka

CF333014 2 bp mRNA linear EST 18-AUG-2003  
 JMT--01-L21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
 JMT--01-L21, mRNA sequence.

CF333014

ACCESSION

VERSION

CF333014.1 GI:33814278

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .2

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="JMT--01-L21"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 66.7%; Score 2; DB 7; Length 2;

Best Local Similarity 100.0%; Pred. No. 1.9e+10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2

||

Db 2 GT 1

CF392627 2 bp mRNA linear EST 05-AUG-2004  
 NT015C.D12 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'  
 similar to hypothetical protein, mRNA sequence.

CF392627

ACCESSION

VERSION

CF392627.1 GI:51008598

KEYWORDS

EST.

SOURCE

ORGANISM

Ambystoma mexicanum (axolotl)

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

1 (bases 1 to 2)

Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,

Fehlke,K., Sperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.

An Ambystoma mexicanum EST sequencing project: Analysis of 17,352

expressed sequence tags from embryonic and regenerating blastema

cDNA libraries

Genome Biol. (2004) In press

Contact: Eilly M. Tanaka

```

Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pforstenhauerstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT015C row: 12 column: D
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES
 source
 1..2
 /organism="Ambystoma mexicanum"
 /mol_type="mRNA"
 /db_xref="taxon:8296"
 /tissue_type="Neural Tube, Notochord, Somites"
 /cell_type="Includes Neural tube, notochord, somites"
 /dev_stage="Stage 18-22"
 /clone_lib="St18-22 Neural tube (NT)"
 /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
 Unnormalized cDNA plasmid library prepared by Invitrogen.
 Size fractionated mRNA was polydT primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.5 KB.
 TAG_LIB=NT"

ORIGIN
 Query Match 66.7%; Score 2; DB 7; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1.9e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
 ||
Db 1 GT 2

RESULT 7
CL661289
LOCUS
DEFINITION
 CL661289_G10 - PRI0139b.B21 (2) Mixed stage fosmid library of P.
 pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
 GSS.
 CL661289.1 GI:50147615
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
 AppADB: an AcedB database for the nematode satellite organism
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES
 source
 1..2
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
 Query Match 66.7%; Score 2; DB 9; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1.9e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 |||
Db 2 TG 1

RESULT 9
CL682684/c
LOCUS
DEFINITION
 CL682684 - PRI0134c.BR (2) Mixed stage fosmid library of P.
 pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
 GSS.
 CL682684.1 GI:50190105
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
 AppADB: an AcedB database for the nematode satellite organism
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES
 source
 1..2
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

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ORIGIN
 Query Match 66.7%; Score 2; DB 9; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1.9e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
 ||
Db 1 GT 2

RESULT 8
CL670560/c
LOCUS
DEFINITION
 CL670560 - PRI0162b.B21 (2) Mixed stage fosmid library of P.
 pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
 GSS.
 CL670560.1 GI:50168602
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
 AppADB: an AcedB database for the nematode satellite organism
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES
 source
 1..2
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
 Query Match 66.7%; Score 2; DB 9; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1.9e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 |||
Db 2 TG 1

RESULT 9
CL682684/c
LOCUS
DEFINITION
 CL682684 - PRI0134c.BR (2) Mixed stage fosmid library of P.
 pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
 GSS.
 CL682684.1 GI:50190105
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.

```

1 (bases 1 to 2)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppaDB: an AcedB database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..2  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="vector: pEpifos-5 Fosmid vector"

Query Match 66.7%; Score 2; DB 9; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.9e+10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3  
||  
2 TG 1

RESULT 10  
CL688205/c  
LOCUS  
DEFINITION  
CL688205 2 bp DNA linear GSS 09-JUL-2004  
PRI0148d.E06.2 - PRI0148d.BR (2) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
CL688205  
CL688205.1 GI:50197283  
GSS.  
SOURCE  
ORGANISM  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 2)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppaDB: an AcedB database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..2  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 2)

Number, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H. and Stacey, G.

Methylation filtered genomic sequences from Glycine max

Unpublished (2004)

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-1267

Fax: 573-882-0588

Email: stacey@missouri.edu

LibID: 227

Class: shotgun.

Location/Qualifiers

1..2

/organism="Glycine max"

/mol\_type="genomic DNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/tissue\_type="Young leaves"

/clone\_lib="Soybean methylation filtered genomic library"  
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 227"

#### ORIGIN

Query Match 66.7%; Score 2; DB 9; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.9e+10; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 2 TG 3

||

1 TG 2

#### RESULT 13

CL876415/c

LOCUS

DEFINITION abf13c11.y1 Soybean methylation filtered genomic library Glycine max genomic, genomic survey sequence.

CL876415

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 2)

Number, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H. and Stacey, G.

Methylation filtered genomic sequences from Glycine max

Unpublished (2004)

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-1267

Fax: 573-882-0588

Email: stacey@missouri.edu

LibID: 227

Class: shotgun.

Location/Qualifiers

1..2

/organism="Glycine max"

/mol\_type="genomic DNA"

#### FEATURES

source

#### ORIGIN

Query Match 66.7%; Score 2; DB 9; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.9e+10; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 1 GT 2

||

2 GT 1

#### RESULT 14

CL883717

LOCUS

DEFINITION

abf63c08.y1 Soybean random, unfiltered genomic library Glycine max genomic, genomic survey sequence.

CL883717

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 2)

Number, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H. and Stacey, G.

Methylation filtered genomic sequences from Glycine max

Unpublished (2004)

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-1267

Fax: 573-882-0588

Email: stacey@missouri.edu

LibID: 230

Class: shotgun.

Location/Qualifiers

1..2

/organism="Glycine max"

/mol\_type="genomic DNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/tissue\_type="Young leaves"

/clone\_lib="Soybean random, unfiltered genomic library"

/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 230"

FEATURES

source

#### ORIGIN

Query Match 66.7%; Score 2; DB 9; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.9e+10; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 2 TG 3

||

1 TG 2

#### FEATURES

source

RESULT 15  
CA850938  
LOCUS

3 bp mRNA linear EST 01-AUG-2003

```

DEFINITION D08D06 H18_07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08D06 5', mRNA sequence.
ACCESSION CA850938
VERSION CA850938.1 GI:33387731
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES source
 1..3
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Peking"
 /db_xref="taxon:3847"
 /clone="D08D06"
 /tissue_type="Roots"
 /dev_stage="Seedlings"
 /clone_lib="cDNA Peking library 2, 4 day SCN3"
 /notes="Vector: pBluescript SK-; cDNA clones from mRNA
 extracted from Peking roots 2 and 4 days past invasion."

REFERENCE
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
 infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
 USA
 Tel: 301 504 5750
 Fax: 301 504 5728

Query Match 66.7%; Score 2; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 |||
Db 1 TG 2

RESULT 16
LOCUS CA851961
DEFINITION D19E06 H18_09.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D19E06 5', mRNA sequence.
ACCESSION CA851961
VERSION CA851961.1 GI:33388754
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728

Query Match 66.7%; Score 2; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 |||
Db 1 TG 2

RESULT 17
LOCUS CF305942
DEFINITION HDAL--02-D03.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--02-D03, mRNA sequence.
ACCESSION CF305942
VERSION CF305942.1 GI:33677703
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 3)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm, B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
 1..3
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HDAL--02-D03"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E. coli SOLR"
 /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
 phage cDNA library I (HDAL)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
 was inserted into lambda Uni-ZAP XR vector at 5' end with
 EcoRI and 3' end with XhoI site. mRNA was derived from
 rice Histone Deacetylase overexpression line."

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm, B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

```

```

QY 2 TG 3
 ||
Db 2 TG 3

RESULT 18
CF308858/c
LOCUS ABF--02-N09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
ABF--02-N09.g1 ABF3-overexpressing transgenic rice plasmid cDNA clone
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CF308858
VERSION ABF--02-N09, mRNA sequence.
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 3)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Contact: Nahm B.H.
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--04-H03"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

FEATURES
 source
 ORIGIN
 Query Match 66.7%; Score 2; DB 7; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
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Db 2 TG 3

RESULT 20
CF311628/c
LOCUS CF311628
DEFINITION
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library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-O16, mRNA sequence.
ACCESSION
CF311628
VERSION CF311628.1 GI:33683389
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 3)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--02-N09"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

FEATURES
 source
 ORIGIN
 Query Match 66.7%; Score 2; DB 7; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
 ||
 3 GT 2

RESULT 19
CF310006
LOCUS CF310006
DEFINITION
ABF--04-H03.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-H03, mRNA sequence.
ACCESSION
CF310006
VERSION CF310006.1 GI:33681767
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

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/tissue\_type="leaf"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3  
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 Db 2 TG 1

## RESULT 21

CF313258/c  
 LOCUS  
 DEFINITION HD--01-P06.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--01-P06, mRNA sequence.

## ACCESSION

CF313258

## VERSION

CF313258.1 GI:33685019

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 3)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..3

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="HD--01-P06"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDACL1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
 ||  
 Db 2 GT 1

## RESULT 22

## CF315632/c

## LOCUS

## DEFINITION

HD--04-K01.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--04-K01, mRNA sequence.

## ACCESSION

CF315632

## VERSION

CF315632.1 GI:33687393

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 3)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..3

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone="HD--04-K01"

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/lab\_host="E.coli DH10B"

/clone\_lib="OshDACL1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
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 Db 3 GT 2

## RESULT 23

## CF317717/c

## LOCUS

## DEFINITION

HD--07-I05.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--07-I05, mRNA sequence.

## ACCESSION

CF317717

## VERSION

CF317717.1 GI:33689478

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 3)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| TITLE                 | Large-scale Sequencing Analysis of Rice ESTs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| JOURNAL               | Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| COMMENT               | Contact: Nahm B.H.<br>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University<br>Yongin, Kyeonggi, Korea<br>Tel: 82 31 330 6193<br>Fax: 82 31 321 6355<br>Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.                                                                                                                                                                                                                                                                                                                               |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| source                | 1..3<br>/organism="Oryza sativa (japonica cultivar-group)"<br>/mol_type="mRNA"<br>/cultivar="Nackdong"<br>/db_xref="taxon:39947"<br>/clone="HD--07-105"<br>/tissue_type="callus"<br>/dev_stage="proliferated callus on 2N6 media for 2 weeks"<br>/lab_host="E.coli DH10B"<br>/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"<br>/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."                 |
| ORIGIN                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Query Match           | 66.7%; Score 2; DB 7; Length 3;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Best Local Similarity | 100.0%; Pred. No. 1.3e+10;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Matches               | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| QY                    | 1 GT 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DB                    | 2 GT 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| RESULT 24             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| CF338538              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| LOCUS                 | CF338538 3 bp mRNA linear EST 18-AUG-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| DEFINITION            | Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P24, mRNA sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| ACCESSION             | CF338538                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| VERSION               | CF338538.1 GI:33825464                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| SOURCE                | Oryza sativa (japonica cultivar-group)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ORGANISM              | Oryza sativa (japonica cultivar-group)<br>Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.                                                                                                                                                                                                                                                                                                                                                                                                             |
| REFERENCE             | 1 (bases 1 to 3)<br>Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.<br>Large-scale Sequencing Analysis of Rice ESTs<br>Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                  |
| TITLE                 | Large-scale Sequencing Analysis of Rice ESTs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| JOURNAL               | Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| COMMENT               | Contact: Nahm B.H.<br>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University<br>Yongin, Kyeonggi, Korea<br>Tel: 82 31 330 6193<br>Fax: 82 31 321 6355<br>Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.                                                                                                                                                                                                                                                                                                                               |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| source                | 1..3<br>/organism="Oryza sativa (japonica cultivar-group)"<br>/mol_type="mRNA"<br>/cultivar="Nackdong"<br>/db_xref="taxon:39947"<br>/clone="RCL1--01-P24"<br>/tissue_type="callus"<br>/dev_stage="proliferated callus on 2N6 media for 30 days"<br>/lab_host="E.coli SOLR"<br>/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"<br>/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media" |
| ORIGIN                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Query Match           | 66.7%; Score 2; DB 7; Length 3;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Best Local Similarity | 100.0%; Pred. No. 1.3e+10;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Matches               | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| QY                    | 2 TG 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DB                    | 1 TG 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| RESULT 25             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| CF339357              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| LOCUS                 | CF339357 3 bp mRNA linear EST 18-AUG-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| DEFINITION            | Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-K02, mRNA sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| ACCESSION             | CF339357                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| VERSION               | CF339357.1 GI:33827102                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| SOURCE                | Oryza sativa (japonica cultivar-group)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ORGANISM              | Oryza sativa (japonica cultivar-group)<br>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.                                                                                                                                                                                                                                                                                                                                                                                                |
| REFERENCE             | 1 (bases 1 to 3)<br>Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.<br>Large-scale Sequencing Analysis of Rice ESTs<br>Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                  |
| TITLE                 | Large-scale Sequencing Analysis of Rice ESTs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| JOURNAL               | Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| COMMENT               | Contact: Nahm B.H.<br>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University<br>Yongin, Kyeonggi, Korea<br>Tel: 82 31 330 6193<br>Fax: 82 31 321 6355<br>Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.                                                                                                                                                                                                                                                                                                                               |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| source                | 1..3<br>/organism="Oryza sativa (japonica cultivar-group)"<br>/mol_type="mRNA"<br>/cultivar="Nackdong"<br>/db_xref="taxon:39947"<br>/clone="RCL1--04-K02"<br>/tissue_type="callus"<br>/dev_stage="proliferated callus on 2N6 media for 30 days"<br>/lab_host="E.coli SOLR"<br>/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"<br>/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media" |
| ORIGIN                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Query Match           | 66.7%; Score 2; DB 7; Length 3;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Best Local Similarity | 100.0%; Pred. No. 1.3e+10;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Matches               | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| QY                    | 2 TG 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DB                    | 1 TG 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| RESULT 26             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| CF338538              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| LOCUS                 | CF338538 3 bp mRNA linear EST 18-AUG-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| DEFINITION            | Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P24, mRNA sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| ACCESSION             | CF338538                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| VERSION               | CF338538.1 GI:33825464                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| SOURCE                | Oryza sativa (japonica cultivar-group)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ORGANISM              | Oryza sativa (japonica cultivar-group)<br>Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.                                                                                                                                                                                                                                                                                                                                                                                                             |
| REFERENCE             | 1 (bases 1 to 3)<br>Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.<br>Large-scale Sequencing Analysis of Rice ESTs<br>Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                  |
| TITLE                 | Large-scale Sequencing Analysis of Rice ESTs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| JOURNAL               | Unpublished (2003)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| COMMENT               | Contact: Nahm B.H.<br>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University<br>Yongin, Kyeonggi, Korea<br>Tel: 82 31 330 6193<br>Fax: 82 31 321 6355<br>Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.                                                                                                                                                                                                                                                                                                                               |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| source                | 1..3<br>/organism="Oryza sativa (japonica cultivar-group)"<br>/mol_type="mRNA"<br>/cultivar="Nackdong"<br>/db_xref="taxon:39947"<br>/clone="RCL1--01-P24"<br>/tissue_type="callus"<br>/dev_stage="proliferated callus on 2N6 media for 30 days"<br>/lab_host="E.coli SOLR"                                                                                                                                                                                                                                                                                                                              |



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CF339421
LOCUS CF339421 3 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--04-N02.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-N02,
 mRNA sequence.
ACCESSION CF339421
VERSION CF339421.1 GI:33827229
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--04-N02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
Db 1 TG 2

RESULT 28
CF340077/c
LOCUS CF340077 3 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--06-001.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-001,
 mRNA sequence.
ACCESSION CF340077
VERSION CF340077.1 GI:33828517
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--04-N02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
Db 1 TG 2

RESULT 27
CF339646
LOCUS CF339646 3 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--05-I07.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-I07,
 mRNA sequence.
ACCESSION CF339646
VERSION CF339646.1 GI:33827664
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source
 Location/Qualifiers
 1..3
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
Db 1 TG 2

RESULT 28
CF340077/c
LOCUS CF340077 3 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--06-001.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-001,
 mRNA sequence.
ACCESSION CF340077
VERSION CF340077.1 GI:33828517
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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COMMENT Contact: Nahm B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source
 Location/Qualifiers
 1..3
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--06-001"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:

```

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
||  
3 GT 2

## RESULT 29

CF372478/c

LOCUS

DEFINITION CSECS052H02 FLON0012 CabSau Normalised Flower Stage 12 (FLON0012)  
Vitis vinifera cDNA clone CSECS052H02 3', mRNA sequence.

ACCESSION CF372478  
VERSION  
KEYWORDS  
SOURCE

EST.

CF372478.1

GT:34319724

Vitis vinifera

Vitis vinifera

ORGANISM

Eukaryota; Vitis

Rosids; Vitaceae; Vitis.

1 (bases 1 to 3)

Iocco, P., Hua, C., Davies, C. and Thomas, M.R.

Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon

Unpublished (2003)

Contact: Mark R. Thomas

CSIRO Plant Industry

CSIRO

PO Box 350, Glen Osmond, SA, 5064, Australia

Tel: 61 8 83038600

Fax: 61 8 83038601

Email: Mark.R.Thomas@csiro.au

Seq primer: CCCAGTCACGACGTTGTAACG (M13 Forward)

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..3

/organism="Vitis vinifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clone="CSECS052H02"

/sex="Hermaphrodite"

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/clone\_lib="CabSau Normalised Flower Stage 12 (FLON0012)"

/note="Organ: Inflorescence including flowers; Vector: pZL; Normalised cDNA library from immature inflorescences at stage 12 of the modified E-L system. Tissue collected from field grown plants. A description of the modified E-L system can be found in the paper by B. G. Coombe 'Adoption of a system for identifying grapevine growth stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
||  
2 GT 1

## RESULT 30

CK575874

LOCUS

DEFINITION CSECS052H02 FLON0012 CabSau Normalised Flower Stage 12 (FLON0012)  
Vitis vinifera cDNA clone CSECS052H02 3', mRNA sequence.

ACCESSION CK575874  
VERSION  
KEYWORDS  
SOURCE

EST.

CK575874.1

GT:40959542

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 3)

Li, S., Armstrong, C.M., Bertin, N., Ge, H., Milstein, S., Boxem, M., Vidalain, P.O., Han, J.D., Chesneau, A., Hao, T., Goldberg, D.S., Li, N., Martinez, M., Rual, J.F., Lamesch, P., Xu, L., Tewari, M., Wong, S.L., Zhang, L.V., Berriz, G.F., Jacotot, L., Vaglio, P., Reboul, J., Hirozane-Kishikawa, T., Li, O., Gabel, H.W., Elewa, A., Baumgartner, B., Rose, D.J., Yu, H., Bosak, S., Sequerra, R., Fraser, A., Mango, S.E., Saxton, W.M., Strome, S., Van Den Heuvel, S., Piano, F., Vandenhaute, J., Sardet, C., Gerstein, M., Doucette-Stamm, L., Gunsalus, K.C., Harper, J.W., Cusick, M.E., Roth, F.P., Hill, D.E. and Vidal, M.

A Map of the Interactome Network of the Metazoan C. elegans

Science (2004) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. cDNAs were generated and cloned into the two hybrid vector pPC86 This interacting Sequence Tag IST\_WIS\_9516 (ZK858.4) interacts as a prey with the bait F10C5.1

PCR Primers

FORWARD: CGCGTTTGGAAATCACTACAGG

BACKWARD: GGAGACTTGACCAACCTCTGGCG

Insert Length: 3 Std Error: 2.00

Plate: 115 row: 10 column: B

Seq primer: CGCGTTTGGAAATCACTACAGG

High quality sequence stop: 2

POLYA=No.

FEATURES

Location/Qualifiers

1..3

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/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/sex="male, hermaphrodite"

/dev\_stage="embryos, L1, L2, L3, L4, adult, dauer"

/clone\_lib="AD-wrmcDNA library"

/note="Vector: pPC86; For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. This library was made with poly(A)+ RNA isolated from mated populations of wild-type (N2 strain) animals of all stages of development including embryonic, larval (L1 to L4 stages), adults and dauer. Approximately equal quantities of RNA from different populations were acquired. cDNAs were generated and cloned into the two hybrid vector pPC86. The library contains ~3\*10e7 clones. Reference - GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFeomes - Walhout AJ, Temple GF, Brasch MA, Hartley JL, Liorson MA, van den Heuvel S, Vidal M - Methods Enzymol. 2000;328:575-92"

## ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEFINITION IST\_WIS\_9516 AD-wrmcDNA library Caenorhabditis elegans cDNA 5' similar to ZK858.4, mRNA sequence.

ACCESSION CK575874

VERSION CK575874.1

SOURCE

GT:40959542

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 3)

Li, S., Armstrong, C.M., Bertin, N., Ge, H., Milstein, S., Boxem, M., Vidalain, P.O., Han, J.D., Chesneau, A., Hao, T., Goldberg, D.S., Li, N., Martinez, M., Rual, J.F., Lamesch, P., Xu, L., Tewari, M., Wong, S.L., Zhang, L.V., Berriz, G.F., Jacotot, L., Vaglio, P., Reboul, J., Hirozane-Kishikawa, T., Li, O., Gabel, H.W., Elewa, A., Baumgartner, B., Rose, D.J., Yu, H., Bosak, S., Sequerra, R., Fraser, A., Mango, S.E., Saxton, W.M., Strome, S., Van Den Heuvel, S., Piano, F., Vandenhaute, J., Sardet, C., Gerstein, M., Doucette-Stamm, L., Gunsalus, K.C., Harper, J.W., Cusick, M.E., Roth, F.P., Hill, D.E. and Vidal, M.

A Map of the Interactome Network of the Metazoan C. elegans

Science (2004) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. cDNAs were generated and cloned into the two hybrid vector pPC86 This interacting Sequence Tag IST\_WIS\_9516 (ZK858.4) interacts as a prey with the bait F10C5.1

PCR Primers

FORWARD: CGCGTTTGGAAATCACTACAGG

BACKWARD: GGAGACTTGACCAACCTCTGGCG

Insert Length: 3 Std Error: 2.00

Plate: 115 row: 10 column: B

Seq primer: CGCGTTTGGAAATCACTACAGG

High quality sequence stop: 2

POLYA=No.

FEATURES

Location/Qualifiers

1..3

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/sex="male, hermaphrodite"

/dev\_stage="embryos, L1, L2, L3, L4, adult, dauer"

/clone\_lib="AD-wrmcDNA library"

/note="Vector: pPC86; For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. This library was made with poly(A)+ RNA isolated from mated populations of wild-type (N2 strain) animals of all stages of development including embryonic, larval (L1 to L4 stages), adults and dauer. Approximately equal quantities of RNA from different populations were acquired. cDNAs were generated and cloned into the two hybrid vector pPC86. The library contains ~3\*10e7 clones. Reference - GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFeomes - Walhout AJ, Temple GF, Brasch MA, Hartley JL, Liorson MA, van den Heuvel S, Vidal M - Methods Enzymol. 2000;328:575-92"

Qy 2 TG 3  
Db 2 TG 3

Search completed: July 20, 2005, 21:46:02  
Job time : 1851 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:56:37 ; Search time 277 Seconds  
(without alignments)  
64.113 Million cell updates/sec

Title: US-09-735-363A-8

Perfect score: 3

Sequence: 1 gtc 3

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
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| C 2        | 2     | 66.7        | 3      | 2     | AAT33326 CAPL trin |
| C 3        | 2     | 66.7        | 3      | 4     | AAL20244 Human bre |
| 4          | 1.4   | 46.7        | 3      | 3     | AAA94655 Human TUB |
| 5          | 1     | 33.3        | 2      | 6     | ABK94446 Human BRC |
| C 6        | 1     | 33.3        | 2      | 6     | ABK94446 Human BRC |
| C 7        | 1     | 33.3        | 3      | 2     | AAT33326 CAPL trin |
| 8          | 1     | 33.3        | 3      | 4     | AAL20244 Human bre |
| 9          | 1     | 33.3        | 3      | 6     | ABN73392 Bovine em |
| C 10       | 1     | 33.3        | 3      | 6     | ABN73392 Bovine em |
| C 11       | 1     | 33.3        | 3      | 6     | ABN73302 Bovine em |
| C 12       | 1     | 33.3        | 3      | 6     | ABN73302 Bovine em |
| C 13       | 1     | 33.3        | 3      | 10    | ADES8066 Human gen |
| C 14       | 1     | 33.3        | 3      | 10    | ADES8066 Human gen |
| C 15       | 1     | 33.3        | 3      | 12    | ADG28481 Modified  |
| C 16       | 1     | 33.3        | 3      | 12    | ADOI4091 Part of r |
| C 17       | 1     | 33.3        | 3      | 12    | ADOI4091 Part of r |
| C 18       | 0.2   | 6.7         | 3      | 1     | AAN80743 Sequence  |
| C 19       | 0.2   | 6.7         | 3      | 1     | AAN80743 Sequence  |
| C 20       | 0     | 0.0         | 1      | 2     | AAX57131 Human mut |

|   |    |   |     |   |    |          |                    |
|---|----|---|-----|---|----|----------|--------------------|
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| C | 22 | 0 | 0.0 | 1 | 6  | ABK94535 | Abk94535 Human BRC |
| C | 23 | 0 | 0.0 | 1 | 6  | ABK94535 | Abk94535 Human BRC |
| C | 24 | 0 | 0.0 | 1 | 12 | ACH82100 | Ach82100 Human gen |
| C | 25 | 0 | 0.0 | 1 | 12 | ACH82100 | Ach82100 Human gen |
| C | 26 | 0 | 0.0 | 1 | 12 | ACH81204 | Ach81204 Human gen |
| C | 27 | 0 | 0.0 | 1 | 12 | ACH81204 | Ach81204 Human gen |
| C | 28 | 0 | 0.0 | 2 | 6  | ABK24295 | Abk24295 Human mic |
| C | 29 | 0 | 0.0 | 3 | 2  | AAQ85491 | Aaq85491 Plasmid p |
| C | 30 | 0 | 0.0 | 3 | 2  | AAQ85491 | Aaq85491 Plasmid p |
| C | 31 | 0 | 0.0 | 3 | 3  | AAA94655 | Aaa94655 Human TUB |
| C | 32 | 0 | 0.0 | 3 | 10 | ADD25606 | Add25606 Binding d |
| C | 33 | 0 | 0.0 | 3 | 10 | ADD25606 | Add25606 Binding d |
| C | 34 | 0 | 0.0 | 3 | 12 | ADG28481 | Adg28481 Modified  |

## ALIGNMENTS

RESULT 1  
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ID ABK24295 standard; DNA; 2 BP.  
XX AC ABK24295;  
XX DT 09-APR-2002 (first entry)  
XX DE Human microsatellite DIS191 detection PCR primer #3.  
XX KW Microsatellite; ligase-assisted spacer addition assay; LASA; cancer;  
KW nucleotide length polymorphism detection; neurodegenerative disease;  
KW fragile X syndrome; Huntington's disease; muscular dystrophy; forensic;  
KW gene mapping; population study; human; primer; ss.  
XX OS Homo sapiens.  
XX PN WO200185987-A1.  
XX PD 15-NOV-2001.  
XX PF 09-MAY-2001; 2001WO-AU000526.  
XX PR 09-MAY-2000; 2000US-0202771P.  
XX PR 10-MAY-2000; 2000US-0202559P.  
XX PA (DIAT-) DIATECH PTY LTD.  
XX PI Brockhurst V, Timms P, Wolter L, Barnard R, Giffard PM;  
XX WPI; 2002-121948/16.

Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-assisted spacer addition assay.

Example 10; Page 55; 89pp; English.

The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, Huntington's disease, or muscular dystrophy. Furthermore, the method may be used for identifying and/or typing microorganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic microorganisms; and for genotyping subjects including humans. The method is also useful for detecting certain cancers and other malignancies. Moreover, the method can be used to provide markers for use in identification of human and non-human individuals, plants and

CC microorganisms, to ascertain parentage of human or non-human individual,  
 CC and to monitor responses to therapies including the possibility of  
 CC nucleic acid damage. The nucleotide polymorphisms may be used in forensic  
 CC science to identify a particular victim or an alleged perpetrator of a  
 CC crime, in gene mapping and population studies. IASA may also be used in  
 CC the manufacture of a kit for detecting and/or identifying nucleotide  
 CC repeat regions such as a nucleotide length polymorphism in a eukaryotic  
 CC genome. The IASA method avoids the time and cost required by prior art  
 CC methods using gel electrophoresis and Southern transfer analysis. In  
 CC particular, current diagnosis of Huntington's disease relies heavily upon  
 CC the use of gel electrophoresis, a process that has proved difficult to  
 CC automate or miniaturize. The IASA method allows total avoidance of this  
 CC limiting step, making it a strong candidate for future use in clinical  
 CC and laboratory procedures. ABK24276-ABK24313 represent primers used to  
 CC detect polymorphisms or microsatellites as described in the method of the  
 CC invention  
 XX  
 SQ Sequence 2 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 2; DB 6; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+09; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

QY 2 TG 3  
 ||  
 Db 2 TG 1

RESULT 2  
 AAT33326  
 ID AAT33326 standard; RNA; 3 BP.

XX  
 AC AAT33326;

DT 12-NOV-1996 (first entry)

XX CAPL trinucleotide.

XX CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;  
 KW osteosarcoma; therapy; ss.

XX Synthetic.

PN WO9625499-A1.

XX 22-AUG-1996.

XX 16-FEB-1996; 96WO-US002108.

XX 17-FEB-1995; 95US-00391375.

XX (HYBR-) HYBRIDON INC.

XX (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.

PI Fodstad O, Hovig E, Engebraaten O, Maelandsmo GJ, Agrawal S;  
 PI Von Hofe E;

XX WPI; 1996-393400/39.

XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression - useful to  
 PT inhibit metastatic cancer, partic. osteo:sarcoma.

XX Claim 2; Page 56; 70pp; English.

XX Novel antisense oligonucleotides capable of inhibiting CAPL gene  
 CC expression may include the trinucleotide GUC (AAT33326, given in 5' to 3'  
 CC direction) found in codon 14 of CAPL mRNA. These and other antisense  
 CC oligonucleotides (AAT33327-36) complementary to specific regions of the  
 CC CAPL gene (see also AAT33345), as well as CAPL-specific ribozymes  
 CC (AAT33337-40) can be administered to a patient as a means of inhibiting  
 CC metastatic cancer

XX Sequence 3 BP; 0 A; 1 C; 1 G; 0 T; 1 U; 0 Other;

Query Match 66.7%; Score 2; DB 2; Length 3;  
 Best Local Similarity 50.0%; Pred. No. 2e+09; Indels 0; Gaps 0;  
 Matches 1; Conservative 1; Mismatches 0;

QY 2 TG 3  
 ||  
 Db 2 UG 3

RESULT 3  
 AAL20244/c  
 ID AAL20244 standard; cDNA; 3 BP.

XX AAL20244;

XX 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 12701.

KW Human; breast cancer; cell marker; cytostatic; ss.

XX Homo sapiens.

XX WO200151628-A2.

PD 19-JUL-2001.

XX 10-JAN-2001; 2001WO-US000798.

XX 14-JAN-2000; 2000US-0176077P.

PR 14-MAR-2000; 2000US-0189167P.

PR 24-MAR-2000; 2000US-0192099P.

PR 29-MAR-2000; 2000US-0193480P.

PR 15-MAY-2000; 2000US-0205230P.

PR 09-JUN-2000; 2000US-0211315P.

PR 25-JUL-2000; 2000US-0220534P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;

XX WPI; 2001-451856/48.

XX New peptide useful as a marker for the diagnosis of breast cancer.

XX Claim 1; Page 2245; 3695pp; English.

XX The invention relates to human breast cancer expressed polynucleotides  
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
 CC afflicted with breast cancer by examining the correlation between the  
 CC expression of certain markers and the cancerous state of breast cells.  
 CC The polynucleotides and encoded polypeptides are potential markers for  
 CC detecting, diagnosing, monitoring, characterising treating and  
 CC potentially preventing breast cancer. The polynucleotides and encoded  
 CC polypeptides are also useful for isolating compounds with cytostatic  
 CC activity

XX Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 2; DB 4; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

QY 1 GT 2  
 ||  
 Db 2 GT 1

RESULT 4  
 AAA94655  
 ID AAA94655 standard; DNA; 3 BP.  
 XX



PR 06-NOV-2000; 2000WO-IB001607.  
 XX (SCSC-) ACAD APPLIED SCI.  
 PA Viig J;  
 XX WPI; 2002-471507/50.  
 DR Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting  
 PT amplification products to 2-dimensional gel electrophoresis to produce a  
 PT characteristic spot pattern for a specific mutation in either the BRCA1  
 PT or the hMLH1 gene.  
 XX  
 PS Claim 1; Page 27; 57pp; English.  
 XX The invention relates to detecting mutations in the BRCA1 and hMLH1 gene  
 CC comprising subjecting a set of amplification products to two-dimensional  
 CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a  
 CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included  
 CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short  
 CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM  
 CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for  
 CC detecting mutations in the BRCA1 (breast and ovarian cancer  
 CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA  
 CC mismatch repair gene). The present sequence is a PCR clamp sequence used  
 CC in the method of the invention  
 XX Sequence 2 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 33.3%; Score 1; DB 6; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 G 1  
 Db 1 G 1  
 RESULT 7  
 ART33326/c  
 ID AAT33326 standard; RNA; 3 BP.  
 XX  
 AC AAT33326;  
 XX  
 DT 12-NOV-1996 (first entry)  
 XX  
 DE CAPL trinucleotide.  
 XX  
 KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;  
 KW osteosarcoma; therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9625499-A1.  
 XX  
 PD 22-AUG-1996.  
 XX  
 PF 16-FEB-1996; 96WO-US002108.  
 XX  
 PR 17-FEB-1995; 95US-00391375.  
 XX  
 PA (HYBR-) HYBRIDON INC.  
 PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.  
 XX  
 PI Fodstad O, Hovig E, Engebraaten O, Maelandsmo GJ, Agrawal S;  
 PI Von Hofe E;  
 XX  
 DR WPI; 1996-393400/39.  
 XX  
 XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression - useful to  
 PT inhibit metastatic cancer, partic. osteo:sarcoma.  
 PS Claim 2; Page 56; 70pp; English.

XX Novel antisense oligonucleotides capable of inhibiting CAPL gene  
 CC expression may include the trinucleotide GUC (AAT33326, given in 5' to 3'  
 CC direction) found in codon 14 of CAPL mRNA. These and other antisense  
 CC oligonucleotides (AAT33327-36) complementary to specific regions of the  
 CC CAPL gene (see also AAT33345), as well as CAPL-specific ribozymes  
 CC (AAT33337-40) can be administered to a patient as a means of inhibiting  
 CC metastatic cancer  
 XX  
 SQ Sequence 3 BP; 0 A; 1 C; 1 G; 0 T; 1 U; 0 Other;  
 Query Match 33.3%; Score 1; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 G 1  
 Db 1 G 1  
 RESULT 8  
 AAL20244  
 ID AAL20244 standard; cDNA; 3 BP.  
 XX  
 AC AAL20244;  
 XX  
 DT 07-DEC-2001 (first entry)  
 XX  
 DE Human breast cancer expressed polynucleotide 12701.  
 XX  
 KW Human; breast cancer; cell marker; cytostatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200151628-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 10-JAN-2001; 2001WO-US000798.  
 XX  
 PR 14-JAN-2000; 2000US-0176077P.  
 PR 14-MAR-2000; 2000US-0189167P.  
 PR 24-MAR-2000; 2000US-0192099P.  
 PR 29-MAR-2000; 2000US-0193480P.  
 PR 15-MAY-2000; 2000US-0205230P.  
 PR 09-JUN-2000; 2000US-0211315P.  
 PR 25-JUL-2000; 2000US-0220534P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX  
 DR WPI; 2001-451856/48.  
 XX  
 PT New peptide useful as a marker for the diagnosis of breast cancer.  
 XX  
 PS Claim 1; Page 2245; 3695pp; English.  
 XX  
 CC The invention relates to human breast cancer expressed polynucleotides  
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
 CC afflicted with breast cancer by examining the correlation between the  
 CC expression of certain markers and the cancerous state of breast cells.  
 CC The polynucleotides and encoded polypeptides are potential markers for  
 CC detecting, diagnosing, monitoring, characterising, treating and  
 CC potentially preventing breast cancer. The polynucleotides and encoded  
 CC polypeptides are also useful for isolating compounds with cytostatic  
 CC activity  
 XX  
 SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 33.3%; Score 1; DB 4; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 2 T 2  
Db 3 T 3

RESULT 9  
ABN73392  
ID ABN73392 standard; cDNA; 3 BP.

XX AC ABN73392;

XX DT 03-JUL-2002 (first entry)

XX DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.

XX KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;  
XX KW development; gene; ss.

XX OS Bos taurus.

XX PN WO200194550-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018576.

XX PR 07-JUN-2000; 2000US-0209874P.

XX PS 06-JUN-2001; 2001US-00876143.

XX PA (INFI-) INFIGEN INC.

XX PI Eilertsen KJ, Pfister-Genskow M, Childs L;

XX DR WPI; 2002-351289/38.

XX PT An expressed sequence tag (EST), the expression of which, or its  
XX PT complementary sequence, in a cell identifies the cell as a  
XX PT developmentally competent or incompetent cell.

XX PS Example 16; Page 163; 584pp; English.

XX CC The present invention describes an expressed sequence tag (EST), where  
XX CC the EST is an isolated, enriched, or purified nucleic acid sequence  
XX CC representing all or part of a gene, the expression of which, or its  
XX CC complementary sequence, in a cell identifies the cell as a  
XX CC developmentally competent or incompetent cell. Molecules which induce  
XX CC developmental competence in a cell line are useful for inducing  
XX CC totipotence in one or more cells. Molecules which induce developmental  
XX CC incompetence in a cell line are useful for preventing a full term  
XX CC pregnancy in an animal and inhibiting totipotence. The molecules are also  
XX CC useful for treating a disease in an animal by inducing development of one  
XX CC or more cells of the animal into a specific cell type. The present  
XX CC sequence represents a bovine EST which is given in the exemplification of  
XX CC the present invention

XX SQ Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2e+09;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2  
Db 1 T 1

RESULT 10  
ABN73392/c  
ID ABN73392 standard; cDNA; 3 BP.

XX AC ABN73392;

XX

DT 03-JUL-2002 (first entry)

XX DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.

XX KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;  
XX KW development; gene; ss.

XX OS Bos taurus.

XX PN WO200194550-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018576.

XX PR 07-JUN-2000; 2000US-0209874P.

XX PS 06-JUN-2001; 2001US-00876143.

XX PA (INFI-) INFIGEN INC.

XX PI Eilertsen KJ, Pfister-Genskow M, Childs L;

XX DR WPI; 2002-351289/38.

XX PT An expressed sequence tag (EST), the expression of which, or its  
XX PT complementary sequence, in a cell identifies the cell as a  
XX PT developmentally competent or incompetent cell.

XX PS Example 16; Page 163; 584pp; English.

XX CC The present invention describes an expressed sequence tag (EST), where  
XX CC the EST is an isolated, enriched, or purified nucleic acid sequence  
XX CC representing all or part of a gene, the expression of which, or its  
XX CC complementary sequence, in a cell identifies the cell as a  
XX CC developmentally competent or incompetent cell. Molecules which induce  
XX CC developmental competence in a cell line are useful for inducing  
XX CC totipotence in one or more cells. Molecules which induce developmental  
XX CC incompetence in a cell line are useful for preventing a full term  
XX CC pregnancy in an animal and inhibiting totipotence. The molecules are also  
XX CC useful for treating a disease in an animal by inducing development of one  
XX CC or more cells of the animal into a specific cell type. The present  
XX CC sequence represents a bovine EST which is given in the exemplification of  
XX CC the present invention

XX SQ Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2e+09;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2  
Db 2 T 2

RESULT 11  
ABN73302  
ID ABN73302 standard; cDNA; 3 BP.

XX AC ABN73302;

XX DT 03-JUL-2002 (first entry)

XX DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.

XX KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;  
XX KW development; gene; ss.

XX OS Bos taurus.

XX PN WO200194550-A2.

XX PD 13-DEC-2001.

```
XX PF 07-JUN-2001; 2001WO-US018576.
XX XX
XX PR 07-JUN-2000; 2000US-0209874P.
XX PR 06-JUN-2001; 2001US-00876143.
XX (INFI-) INFIGEN INC.
XX PA
XX PI Bilertsen KJ, Pfister-Genskow M, Childs L;
XX XX
XX DR WPI; 2002-351289/38.
XX XX
XX PT An expressed sequence tag (EST), the expression of which, or its
XX PT complementary sequence, in a cell identifies the cell as a
XX PT developmentally competent or incompetent cell.
XX XX
XX PS Example 16; Page 146; 584pp; English.
XX CC
XX CC The present invention describes an expressed sequence tag (EST), where
XX CC the EST is an isolated, enriched, or purified nucleic acid sequence
XX CC representing all or part of a gene, the expression of which, or its
XX CC complementary sequence, in a cell identifies the cell as a
XX CC developmentally competent or incompetent cell. Molecules which induce
XX CC developmental competence in a cell line are useful for inducing
XX CC totipotency in one or more cells. Molecules which induce developmental
XX CC incompetence in a cell line are useful for preventing a full term
XX CC pregnancy in an animal and inhibiting totipotency. The molecules are also
XX CC useful for treating a disease in an animal by inducing development of one
XX CC or more cells of the animal into a specific cell type. The present
XX CC sequence represents a bovine EST which is given in the exemplification of
XX CC the present invention
XX SQ Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 33.3%; Score 1; DB 6; Length 3;
XX Best Local Similarity 100.0%; Pred. No. 2e+09;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 T 2
XX DB 1 T 1
XX
XX RESULT 12
XX ABN73302/C
XX ID ABN73302 standard; cDNA; 3 BP.
XX AC
XX XX
XX DT 03-JUL-2002 (first entry)
XX DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.
XX XX
XX KW Bovine; Bos taurus; EST; expressed sequence tag; totipotency;
XX KW development; gene; ss.
XX XX
XX OS Bos taurus.
XX XX
XX PN WO200194550-A2.
XX XX
XX PD 13-DEC-2001.
XX XX
XX PF 07-JUN-2001; 2001WO-US018576.
XX XX
XX PR 07-JUN-2000; 2000US-0209874P.
XX PR 06-JUN-2001; 2001US-00876143.
XX XX
XX PA (INFI-) INFIGEN INC.
XX XX
XX PI Bilertsen KJ, Pfister-Genskow M, Childs L;
XX XX
XX DR WPI; 2002-351289/38.
XX CC
XX CC The present invention describes an expressed sequence tag (EST), where
XX CC the EST is an isolated, enriched, or purified nucleic acid sequence
XX CC representing all or part of a gene, the expression of which, or its
XX CC complementary sequence, in a cell identifies the cell as a
XX CC developmentally competent or incompetent cell. Molecules which induce
XX CC developmental competence in a cell line are useful for inducing
XX CC totipotency in one or more cells. Molecules which induce developmental
XX CC incompetence in a cell line are useful for preventing a full term
XX CC pregnancy in an animal and inhibiting totipotency. The molecules are also
XX CC useful for treating a disease in an animal by inducing development of one
XX CC or more cells of the animal into a specific cell type. The present
XX CC sequence represents a bovine EST which is given in the exemplification of
XX CC the present invention
XX SQ Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 33.3%; Score 1; DB 6; Length 3;
XX Best Local Similarity 100.0%; Pred. No. 2e+09;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 T 2
XX DB 1 T 1
XX
XX RESULT 13
XX ADE58066
XX ID ADE58066 standard; DNA; 3 BP.
XX XX
XX AC ADE58066;
XX XX
XX DT 29-JAN-2004 (first entry)
XX DE Human gene L11696, SEQ ID NO 3935.
XX XX
XX KW Human; ds; gene; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO2003016475-A2.
XX XX
XX PD 27-FEB-2003.
XX XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-033347P.
XX XX
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX XX
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX XX
XX DR WPI; 2003-268312/26.
XX DR GENBANK; L11696.
XX XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX XX
XX PS Claim 1; Page; 1017pp; English.
XX CC
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
```

CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human DNA (shown in Table 2 of the  
 CC specification) which encodes one of the polypeptides of the invention  
 CC which is differentially expressed during pain. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 3 BP; 0 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2  
 DB 3 T 3

RESULT 14  
 ADE58066/c  
 ID ADE58066 standard; DNA; 3 BP.

AC ADE58066;

XX 29-JAN-2004 (first entry)

DE Human gene L11696, SEQ ID NO 3935.

XX Human; ds; gene; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; L11696.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human DNA (shown in Table 2 of the  
 CC specification) which encodes one of the polypeptides of the invention  
 CC which is differentially expressed during pain. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 3 BP; 0 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1  
 DB 2 G 2

RESULT 15  
 ADG28481/c

ID ADG28481 standard; DNA; 3 BP.

XX AC ADG28481;

XX 26-FEB-2004 (first entry)

XX Modified oligonucleotide seq id 2.

XX antibacterial; protozoacide; antialgal; fungicide;

XX internucleotide linkage; 2',5'-internucleotide linkage; 3'-substituent;

XX antisense; pharmaceutical; RNA-DNA transcription;

XX RNA-protein translation; infection; diagnostic; therapeutic;

XX nuclease resistance; ss.

XX Synthetic.

XX US6653458-B1.

XX 25-NOV-2003.

XX 08-NOV-1999; 99US-00435806.

XX 03-SEP-1993; 93US-00117363.

XX 02-SEP-1994; 94WO-US010131.

XX 28-FEB-1996; 96US-00602862.

XX 14-JUL-1998; 98US-00115043.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Cook PD, Guinosso CU;  
 PI WPI; 2004-079586/08.  
 XX New oligonucleotide comprising at least one 2',5'-internucleotide linkage  
 PT useful for treating organisms having disease caused by undesired  
 PT production of protein e.g. bacteria, yeast, protozoa and algae.  
 XX Example 49; SEQ ID NO 2; 30pp; English.  
 XX The invention describes an oligonucleotide comprising several nucleotides  
 CC covalently linked together by internucleotide linkages. At least one of  
 CC the nucleotides is linked to an adjacent nucleotide by 2',5'-  
 CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides  
 CC are useful: as antisense oligonucleotides; in pharmaceutical compositions  
 CC for treating organisms having disease caused by undesired production of  
 CC protein e.g. organism that utilises RNA-DNA transcription or RNA-protein  
 CC translation, bacteria, yeast, protozoa, algae and warm-blooded animals;  
 CC for developing diagnostic and therapeutic agents. The modified  
 CC oligonucleotide exhibits improved properties of nuclease resistance and  
 CC binding affinity. The oligonucleotides are easy to synthesise and exhibit  
 CC good properties of nuclease resistance and hybridisation to target  
 CC nucleic acids. The oligonucleotide is potent antisense agent with longer  
 CC duration of action. This sequence represents an oligonucleotide of the  
 CC invention.  
 XX Sequence 3 BP; 3 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 33.3%; Score 1; DB 12; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09; 0; Gaps 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 T 2  
 Db 3 T 3  
 RESULT 16  
 AD014091  
 ID AD014091 standard; DNA; 3 BP.  
 AC AD014091;  
 XX 29-JUL-2004 (first entry)  
 DT Part of rolling circle padlock probe used to detect p53 SNP3.  
 DE ss; probe; single nucleotide polymorphism; SNP; p53; p53 SNP3.  
 XX Synthetic.  
 OS US2004086892-A1.  
 XX 06-MAY-2004.  
 PD 24-APR-2003; 2003US-00424542.  
 XX 06-NOV-2002; 2002US-0424656P.  
 PR (CROT/) CROTHERS D M.  
 PA (HOLM/) HOLMLIN R E.  
 XX Crothers DM, Holmlin RE;  
 PI WPI; 2004-418412/39.  
 DR Detecting target nucleotide sequence in sample involves incubating tagged  
 XX molecules having identifier tags corresponding to targets, with detection  
 PT probes, and hybridization of tag to complementary probe indicates  
 PT presence of target.  
 XX Example 1; SEQ ID NO 6; 35pp; English.

XX The invention relates to methods of detecting a target nucleotide  
 CC sequence (T) in a sample. The methods involve generating at least one  
 CC tagged molecule (G) comprising at least one identifier tag (I) selected  
 CC as an identifier for (T), where (I) is generated only when (T)  
 CC corresponding to (I) is present in sample; incubating (G) with a  
 CC universal detector having at least one detection probe (P) complementary  
 CC to (I); and measuring hybridisation of (I) to (P) complementary to (I);  
 CC where hybridisation of (I) to (P) complementary to (I) indicates (T)  
 CC corresponding to (I) is present in sample. The methods are useful for  
 CC detecting several target nucleotide sequences in a sample, where each (T)  
 CC in several (T) has a distinct (I), such that hybridisation of each  
 CC distinct (I) to a complementary (P) indicates the presence of the  
 CC corresponding (T). The methods are useful for detecting at least one  
 CC variant sequence of (T), where the variant sequence is a single  
 CC nucleotide polymorphism (SNP), an allelic variant, or a splice variant,  
 CC preferably SNP. The methods are useful for identifying an organism or  
 CC individual by detecting one or more target nucleotide sequences chosen to  
 CC serve as distinguishing features for the organisms or individuals. The  
 CC universal tag assay utilises target-dependent procedures to generate  
 CC tagged molecules, advantageously increasing accuracy and minimising  
 CC spurious signals without the need to employ special conditions or special  
 CC reagents. The universal tag assay can easily be used to assay a wide  
 CC variety of samples. The universal tag assay can be performed in a single  
 CC vessel and easily be automated. The present sequence represents the a 3  
 CC nucleotide gap used to help transcription from T7 promoter of a rolling  
 CC circle padlock probe used to detect a SNP in the p53 gene known as p53  
 CC SNP3.  
 XX Sequence 3 BP; 1 A; 0 C; 1 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 33.3%; Score 1; DB 12; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2e+09; 0; Gaps 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 G 1  
 Db 1 G 1  
 RESULT 17  
 AD014091/c  
 ID AD014091 standard; DNA; 3 BP.  
 AC AD014091;  
 XX 29-JUL-2004 (first entry)  
 DT Part of rolling circle padlock probe used to detect p53 SNP3.  
 DE ss; probe; single nucleotide polymorphism; SNP; p53; p53 SNP3.  
 XX Synthetic.  
 OS US2004086892-A1.  
 XX 06-MAY-2004.  
 PD 24-APR-2003; 2003US-00424542.  
 XX 06-NOV-2002; 2002US-0424656P.  
 PR (CROT/) CROTHERS D M.  
 PA (HOLM/) HOLMLIN R E.  
 XX Crothers DM, Holmlin RE;  
 PI WPI; 2004-418412/39.  
 DR Detecting target nucleotide sequence in sample involves incubating tagged  
 XX molecules having identifier tags corresponding to targets, with detection  
 PT probes, and hybridization of tag to complementary probe indicates  
 PT presence of target.

```

XX PS Example 1; SEQ ID NO 6; 35pp; English.
XX CC
XX CC The invention relates to methods of detecting a target nucleotide
XX CC sequence (T) in a sample. The methods involve generating at least one
XX CC tagged molecule (G) comprising at least one identifier tag (I) selected
XX CC as an identifier for (T), where (I) is generated only when (T)
XX CC corresponding to (I) is present in sample; incubating (G) with a
XX CC universal detector having at least one detection probe (P) complementary
XX CC to (I); and measuring hybridisation of (I) to (P) complementary to (I);
XX CC where hybridisation of (I) to (P) complementary to (I) indicates (T)
XX CC corresponding to (I) is present in sample. The methods are useful for
XX CC detecting several target nucleotide sequences in a sample, where each (T)
XX CC distinct (T) has a distinct (I), such that hybridisation of each
XX CC distinct (I) to a complementary (P) indicates the presence of the
XX CC corresponding (T). The methods are useful for detecting at least one
XX CC variant sequence of (T), where the variant sequence is a single
XX CC nucleotide polymorphism (SNP), an allelic variant, or a splice variant,
XX CC preferably SNP. The methods are useful for identifying an organism or
XX CC individual by detecting one or more target nucleotide sequences chosen to
XX CC serve as distinguishing features for the organisms or individuals. The
XX CC universal tag assay utilises target-dependent procedures to generate
XX CC tagged molecules, advantageously increasing accuracy and minimising
XX CC spurious signals without the need to employ special conditions or special
XX CC reagents. The universal tag assay can easily be used to assay a wide
XX CC variety of samples. The universal tag assay can be performed in a single
XX CC vessel and easily be automated. The present sequence represents the a 3
XX CC nucleotide gap used to help transcription from T7 promoter of a rolling
XX CC circle padlock probe used to detect a SNP in the p53 gene known as p53
XX CC SNP3.
XX SQ Sequence 3 BP; 1 A; 0 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 33.3%; Score 1; DB 12; Length 3;
XX Best Local Similarity 100.0%; Pred. No. 2e+09;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 T 2
XX Db 2 T 2
XX
XX RESULT 18
XX AAN80743
XX ID AAN80743 standard; DNA; 3 BP.
XX AC AAN80743;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-SEP-1990 (first entry)
XX XX
XX DE Sequence encoding complete mature and precursor forms of human tissue
XX DE factor heavy chain proteins (hufTh & pre-hufTh, respectively).
XX XX
XX KW Human tissue factor heavy chain (hufTh); immunoassays;
XX KW precursor human tissue factor heavy chain (pre-hufTh);
XX KW human tissue factor detection.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX CDS 34..921
XX FT /*tag= a
XX FT /product= "pre-hufTh"
XX FT mat_peptide 130..921
XX FT /*tag= b
XX FT /product= "hufTh"
XX XX
XX PN WO8807543-A.
XX XX
XX PD 06-OCT-1988.
XX XX
XX PF 31-MAR-1987; 87US-00033047.
XX XX
XX PR 31-MAR-1987; 87US-00033047.
XX PR 25-JUN-1987; 87US-00067103.
XX PR 09-MAR-1988; 87US-00165939.
XX XX

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XX PR 31-MAR-1987; 87US-00033047.
XX PR 25-JUN-1987; 87US-00067103.
XX PR 09-MAR-1988; 88US-00165939.
XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.
XX XX
XX PI Edgington TS, Morrissey JH;
XX XX
XX DR WPI; 1988-292837/41.
XX DR P-PSDB; AAP80713.
XX XX
XX PT New DNA segment - has gene encoding human tissue factor heavy chain
XX PT protein and is useful for inhibiting coagulation.
XX PS Disclosure; Page ?; 148pp; English.
XX XX
XX CC A DNA segment with a nucleotide sequence from about 130 to about 918 of
XX CC the sequence given here is claimed. Also claimed are antibodies which
XX CC immunoreact with hufTh and the claimed peptides (given in AAP80713). The
XX CC antibodies may be used in immunoassays for detection of hufTh. The
XX CC claimed peptides may be used to inhibit the binding of hufTh to
XX CC coagulation factor VII/VIII in vivo. (Updated on 25-MAR-2003 to correct
XX CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
XX CC MAR-2003 to correct PI field.)
XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;
XX
XX Query Match 6.7%; Score 0.2; DB 1; Length 3;
XX Best Local Similarity 0.0%; Pred. No. 2e+09;
XX Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 G 1
XX Db 2 D 2
XX
XX RESULT 19
XX AAN80743/c
XX ID AAN80743 standard; DNA; 3 BP.
XX AC AAN80743;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-SEP-1990 (first entry)
XX XX
XX DE Sequence encoding complete mature and precursor forms of human tissue
XX DE factor heavy chain proteins (hufTh & pre-hufTh, respectively).
XX XX
XX KW Human tissue factor heavy chain (hufTh); immunoassays;
XX KW precursor human tissue factor heavy chain (pre-hufTh);
XX KW human tissue factor detection.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX CDS 34..921
XX FT /*tag= a
XX FT /product= "pre-hufTh"
XX FT mat_peptide 130..921
XX FT /*tag= b
XX FT /product= "hufTh"
XX XX
XX PN WO8807543-A.
XX XX
XX PD 06-OCT-1988.
XX XX
XX PF 31-MAR-1987; 87US-00033047.
XX XX
XX PR 31-MAR-1987; 87US-00033047.
XX PR 25-JUN-1987; 87US-00067103.
XX PR 09-MAR-1988; 88US-00165939.
XX XX

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(SCRI ) SCRIPPS CLINIC & RES FOUND.  
 PA Edgington TS, Morrissey JH;  
 PI WPI; 1988-292837/41.  
 XX P-PSDB; AAP80713.  
 DR New DNA segment - has gene encoding human tissue factor heavy chain  
 XX protein and is useful for inhibiting coagulation.  
 PT Disclosure; Page ?; 148pp; English.  
 XX A DNA segment with a nucleotide sequence from about 130 to about 918 of  
 CC the sequence given here is claimed. Also claimed are antibodies which  
 CC immunoreact with hTGF and the claimed peptides (given in AAP80713). The  
 CC antibodies may be used in immunoassays for detection of hTGF. The  
 CC claimed peptides may be used to inhibit the binding of hTGF to  
 CC coagulation factor VII/VIII in vivo. (Updated on 25-MAR-2003 to correct  
 CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-  
 CC MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;  
 Query Match 6.7%; Score 0.2; DB 1; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 2e+09;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 T 2  
 Db 2 H 2  
 RESULT 20  
 AAX57131  
 ID AAX57131 standard; DNA; 1 BP.  
 XX  
 AC AAX57131;  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human mutant KCNQ3 primer 26.  
 XX  
 KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;  
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;  
 KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;  
 KW gene therapy; drug screening; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9921875-A1.  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 23-OCT-1998; 98WO-US022375.  
 XX  
 PR 24-OCT-1997; 97US-0063147P.  
 XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI Singh NA, Leppert MF, Charlier C;  
 XX  
 DR WPI; 1999-312938/26.  
 XX  
 PT Nucleic acid encoding potassium channels KCNQ2 and 3.  
 XX  
 PS Claim 65; Page 151; 195pp; English.  
 XX  
 CC This invention describes novel human and mouse potassium channel proteins  
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or  
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and  
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic  
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)  
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves  
 CC in cell-free form) are used to screen for agents that can be used to  
 CC treat or prevent these forms of epilepsy. Fragments of the encoding  
 CC nucleic acids are used as probes or primers, either for detecting  
 CC mutations or for isolation of related sequences, while the complete  
 CC sequences may be used in gene therapy to provide wild-type protein.  
 CC Antibodies specific for mutant or wild-type proteins are used as

CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves  
 CC in cell-free form) are used to screen for agents that can be used to  
 CC treat or prevent these forms of epilepsy. Fragments of the encoding  
 CC nucleic acids are used as probes or primers, either for detecting  
 CC mutations or for isolation of related sequences, while the complete  
 CC sequences may be used in gene therapy to provide wild-type protein.  
 CC Antibodies specific for mutant or wild-type proteins are used as

CC Query Match 0.0%; Score 0; DB 2; Length 1;  
 Best Local Similarity 0.0%; Pred. No. 5.9e+09;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 G 1  
 Db 1 A 1  
 RESULT 21  
 AAX57131/c  
 ID AAX57131 standard; DNA; 1 BP.  
 XX  
 AC AAX57131;  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human mutant KCNQ3 primer 26.  
 XX  
 KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;  
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;  
 KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;  
 KW gene therapy; drug screening; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9921875-A1.  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 23-OCT-1998; 98WO-US022375.  
 XX  
 PR 24-OCT-1997; 97US-0063147P.  
 XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI Singh NA, Leppert MF, Charlier C;  
 XX  
 DR WPI; 1999-312938/26.  
 XX  
 PT Nucleic acid encoding potassium channels KCNQ2 and 3.  
 XX  
 PS Claim 65; Page 151; 195pp; English.  
 XX  
 CC This invention describes novel human and mouse potassium channel proteins  
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or  
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and  
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic  
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)  
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves  
 CC in cell-free form) are used to screen for agents that can be used to  
 CC treat or prevent these forms of epilepsy. Fragments of the encoding  
 CC nucleic acids are used as probes or primers, either for detecting  
 CC mutations or for isolation of related sequences, while the complete  
 CC sequences may be used in gene therapy to provide wild-type protein.  
 CC Antibodies specific for mutant or wild-type proteins are used as

CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are  
 CC useful in rational design of drugs and therapeutically (in replacement  
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and  
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),  
 CC and better treatment options will be available. AAX57074-X57139 are  
 CC primers used in the method of the invention

XX  
 SQ Sequence 1 BP; 1 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 2; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2  
 DB 1 T 1

## RESULT 22

ABK94535  
 ID ABK94535 standard; DNA; 1 BP.

XX  
 AC ABK94535;

XX  
 DT 27-AUG-2002 (first entry)

XX  
 DE Human BRCA1 gene, PCR clamping sequence #3.

XX hMLH1; DNA mismatch repair; BRCA1; ss; clamp sequence; BRCA1;  
 KW breast and ovarian cancer susceptibility gene; TGDS; PCR;  
 KW two-dimensional DNA electrophoresis; tumour suppressor gene;  
 KW breast cancer; ovarian cancer; tumour.

XX  
 OS Homo sapiens.

XX  
 PN WO200236819-A1.

XX  
 PD 10-MAY-2002.

XX  
 PF 06-NOV-2000; 2000WO-IB001607.

XX  
 PR 06-NOV-2000; 2000WO-IB001607.

XX  
 PA (SCSC-) ACAD APPLIED SCI.

XX  
 PI Vijg J;

XX  
 DR WPI; 2002-471507/50.

XX  
 PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting  
 PT amplification products to 2-dimensional gel electrophoresis to produce a  
 PT characteristic spot pattern for a specific mutation in either the BRCA1  
 PT or the hMLH1 gene.

XX  
 PS Claim 1; Page 54; 57pp; English.

XX  
 SQ The invention relates to detecting mutations in the BRCA1 and hMLH1 gene  
 CC comprising subjecting a set of amplification products to two-dimensional  
 CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a  
 CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included  
 CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short  
 CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM  
 CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for  
 CC detecting mutations in the BRCA1 (breast and ovarian cancer  
 CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA  
 CC mismatch repair gene). The present sequence is a PCR clamp sequence used  
 CC in the method of the invention

XX  
 SQ Sequence 1 BP; 0 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 6; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1  
 DB 1 G 1

## RESULT 23

ABK94535/c  
 ID ABK94535 standard; DNA; 1 BP.

XX  
 AC ABK94535;

XX  
 DT 27-AUG-2002 (first entry)

XX  
 DE Human BRCA1 gene, PCR clamping sequence #3.

XX hMLH1; DNA mismatch repair; BRCA1; ss; clamp sequence; BRCA1;  
 KW breast and ovarian cancer susceptibility gene; TGDS; PCR;  
 KW two-dimensional DNA electrophoresis; tumour suppressor gene;  
 KW breast cancer; ovarian cancer; tumour.

XX  
 OS Homo sapiens.

XX  
 PN WO200236819-A1.

XX  
 PD 10-MAY-2002.

XX  
 PF 06-NOV-2000; 2000WO-IB001607.

XX  
 PR 06-NOV-2000; 2000WO-IB001607.

XX  
 PA (SCSC-) ACAD APPLIED SCI.

XX  
 PI Vijg J;

XX  
 DR WPI; 2002-471507/50.

XX  
 PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting  
 PT amplification products to 2-dimensional gel electrophoresis to produce a  
 PT characteristic spot pattern for a specific mutation in either the BRCA1  
 PT or the hMLH1 gene.

XX  
 PS Claim 1; Page 54; 57pp; English.

XX  
 SQ The invention relates to detecting mutations in the BRCA1 and hMLH1 gene  
 CC comprising subjecting a set of amplification products to two-dimensional  
 CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a  
 CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included  
 CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short  
 CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM  
 CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for  
 CC detecting mutations in the BRCA1 (breast and ovarian cancer  
 CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA  
 CC mismatch repair gene). The present sequence is a PCR clamp sequence used  
 CC in the method of the invention

XX  
 SQ Sequence 1 BP; 0 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 6; Length 1;  
 Best Local Similarity 0.0%; Pred. No. 5.9e+09;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 G 1  
 DB 1 C 1

## RESULT 24

ACH82100  
 ID ACH82100 standard; DNA; 1 BP.

XX  
 AC ACH82100;

|    |                                                                           |  |
|----|---------------------------------------------------------------------------|--|
| DT | 29-JUL-2004 (first entry)                                                 |  |
| XX | Human genome derived single exon probe #15295.                            |  |
| DE | Human; probe; ss; gene expression; single exon probe; microarray;         |  |
| XX | alternative splicing event; genomic alteration.                           |  |
| KW | Homo sapiens.                                                             |  |
| OS | US2003194704-A1.                                                          |  |
| XX | 16-OCT-2003.                                                              |  |
| XX | 03-APR-2002; 2002US-00029386.                                             |  |
| XX | 03-APR-2002; 2002US-00029386.                                             |  |
| PR | (PENN/) PENN S G.                                                         |  |
| XX | (RANK/) RANK D R.                                                         |  |
| PA | (HANZ/) HANZEL D K.                                                       |  |
| XX | Penn SG, Rank DR, Hanzel DK;                                              |  |
| PI | WPI; 2004-119264/12.                                                      |  |
| DR | New human genome-derived single exon nucleic acid probes useful for human |  |
| XX | gene expression analysis, for identifying or characterizing alternative   |  |
| PT | splicing events, for assessing genomic alterations or as tools for        |  |
| PT | surveying tissues.                                                        |  |
| XX | Claim 1; SEQ ID NO 15295; 80pp; English.                                  |  |
| PS | The invention relates to a nucleic acid probe for measuring human gene    |  |
| XX | expression, comprising any of the 27,400 fully defined nucleotide         |  |
| CC | sequences in the specification, or their complements or fragments, and    |  |
| CC | encoding at least 8 amino acids of any of the 6888 amino acid sequences   |  |
| CC | fully defined in the specification. The probe is a single exon probe that |  |
| CC | hybridises under high stringency conditions to a nucleic acid molecule    |  |
| CC | expressed in human cells or tissues. Also included are a spatially-       |  |
| CC | addressable set of single exon nucleic acid probes for measuring human    |  |
| CC | gene expression (comprising a plurality of single exon nucleic acid       |  |
| CC | probes cited above, where each of the plurality of probes is separately   |  |
| CC | and addressably isolatable or amplifiable from the plurality), a single   |  |
| CC | exon microarray for measuring human gene expression, a method of          |  |
| CC | measuring human gene expression, a vector comprising the single exon      |  |
| CC | probe cited above, an ORF-encoded peptide comprising at least 8           |  |
| CC | contiguous amino acids of any of the above-mentioned amino acid           |  |
| CC | sequences (optionally with conservative amino acid substitutions), an     |  |
| CC | isolated antibody that binds specifically to a peptide cited above,       |  |
| CC | methods of selling and/or licensing single exon probes or microarrays to  |  |
| CC | a customer desiring to measure gene expression, a method of providing     |  |
| CC | human gene expression data by subscription, and a computer-readable       |  |
| CC | storage medium which contains a database having a plurality of records    |  |
| CC | (each record including data on the expression of a single exon probe      |  |
| CC | cited above. The probe, methods and apparatus are useful in gene          |  |
| CC | expression analysis. The probes may be used as tools for surveying        |  |
| CC | tissues to detect the presence of expressed messages that contain their   |  |
| CC | specific exon, or in constructing genome-derived single exon microarrays. |  |
| CC | In addition, the probes are used in identifying and characterising        |  |
| CC | alternative splicing events, in detecting and characterising gross        |  |
| CC | alterations in the genomic locus that includes their exon, in assessing   |  |
| CC | smaller genomic alterations, in priming the synthesis of nucleic acids,   |  |
| CC | or in expressing the ORF-encoded peptide. The present sequence is a human |  |
| CC | single exon probe of the invention. Note: The sequence data for this      |  |
| CC | patent did not form part of the printed specification, but was obtained   |  |
| CC | in electronic format directly from USPTO at                               |  |
| CC | seqdata.uspto.gov/sequence.html?DocID=20030194704                         |  |
| XX | Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 U; 0 Other;                          |  |
| SQ | Query Match 0.0%; Score 0; DB 12; Length 1;                               |  |
|    | Best Local Similarity 0.0%; Pred. No. 5.9e+09;                            |  |
|    | Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                |  |



CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 XX  
 SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 0.0%; Score 0; DB 12; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 G 1  
 Db 1 G 1  
 RESULT 26  
 ACH81204  
 ID ACH81204 standard; DNA; 1 BP.  
 XX  
 AC ACH81204;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human genome derived single exon probe #14399.  
 XX  
 KW Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003194704-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 03-APR-2002; 2002US-00029386.  
 XX  
 PR 03-APR-2002; 2002US-00029386.  
 XX  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 XX  
 DR WPI; 2004-119264/12.  
 XX  
 PT New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 PS Claim 1; SEQ ID NO 14399; 80pp; English.  
 XX  
 CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above). The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 XX  
 SQ Sequence 1 BP; 0 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 0.0%; Score 0; DB 12; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+09;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 G 1  
 Db 1 G 1  
 RESULT 27  
 ACH81204/c  
 ID ACH81204 standard; DNA; 1 BP.  
 XX  
 AC ACH81204;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human genome derived single exon probe #14399.  
 XX  
 KW Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003194704-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 03-APR-2002; 2002US-00029386.  
 XX  
 PR 03-APR-2002; 2002US-00029386.  
 XX  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 XX  
 DR WPI; 2004-119264/12.  
 XX  
 PT New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 PS Claim 1; SEQ ID NO 14399; 80pp; English.  
 XX  
 CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,

CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 CC  
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QY 1 G 1  
 DB 1 C 1

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 ID ABK24295 standard; DNA; 2 BP.  
 XX AC ABK24295;  
 XX DT 09-APR-2002 (first entry)  
 XX DE Human microsatellite D1S191 detection PCR primer #3.  
 XX KW Microsatellite; ligase-assisted spacer addition assay; LISA; cancer;  
 KW nucleotide length polymorphism detection; neurodegenerative disease;  
 KW fragile X syndrome; Huntington's disease; muscular dystrophy; forensic;  
 KW gene mapping; population study; human; primer; ss.  
 OS Homo sapiens.  
 XX WO200185987-A1.  
 XX PN 15-NOV-2001.  
 XX PP 09-MAY-2001; 2001WO-AU000526.  
 XX PR 09-MAY-2000; 2000US-0202771P.  
 XX PR 10-MAY-2000; 2000US-0202559P.  
 XX PA (DIAT-) DIATECH PTY LTD.  
 XX PI Brockhurst V, Timms P, Wolter L, Barnard R, Giffard PM;  
 XX WPI; 2002-121948/16.  
 XX

XX Detecting a nucleotide repeat region in a nucleic acid having a  
 PT particular length, useful for identifying nucleotide length polymorphism  
 PT associated with a neurodegenerative disease, comprises using a ligase-  
 PT assisted spacer addition assay.

XX Example 10; Page 55; 89pp; English.

XX The invention relates to a method of identifying or detecting a  
 CC nucleotide repeat region in a nucleic acid molecule characterised by a  
 CC particular length, comprising employing ligase-assisted spacer addition  
 CC (LISA) assay. The method is useful in the identifying or detecting a  
 CC nucleotide repeat region in a nucleic acid molecule characterised by a  
 CC particular length. In particular, the method is useful for identification  
 CC of a nucleotide length polymorphism in animals or humans, which is  
 CC associated with a neurodegenerative disease including fragile X syndrome,  
 CC Huntington's disease, or muscular dystrophy. Furthermore, the method may  
 CC be used for identifying and/or typing microorganisms including yeasts and  
 CC lower uni- and multi-cellular organisms, as well as prokaryotic  
 CC microorganisms; and for genotyping subjects including humans. The method  
 CC is also useful for detecting certain cancers and other malignancies.  
 CC Moreover, the method can be used to provide markers for use in  
 CC identification of human and non-human individuals, plants and  
 CC microorganisms, to ascertain parentage of human or non-human individual,  
 CC and to monitor responses to therapies including the possibility of  
 CC nucleic acid damage. The nucleotide polymorphisms may be used in forensic  
 CC science to identify a particular victim or an alleged perpetrator of a  
 CC crime, in gene mapping and population studies. LISA may also be used in  
 CC the manufacture of a kit for detecting and/or identifying nucleotide  
 CC repeat regions such as a nucleotide length polymorphism in a eukaryotic  
 CC genome. The LISA method avoids the time and cost required by prior art  
 CC methods using gel electrophoresis and Southern transfer analysis. In  
 CC particular, current diagnosis of Huntington's disease relies heavily upon  
 CC the use of gel electrophoresis, a process that has proved difficult to  
 CC automate or miniaturise. The LISA method allows total avoidance of this  
 CC limiting step, making it a strong candidate for future use in clinical  
 CC and laboratory procedures. ABK24276-ABK24313 represent primers used to  
 CC detect polymorphisms or microsatellites as described in the method of the  
 CC invention  
 XX  
 SQ Sequence 2 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

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 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 G 1  
 DB 1 C 1

RESULT 29  
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 ID AAQ85491 standard; cDNA; 3 BP.  
 XX AC AAQ85491;  
 XX DT 25-MAR-2003 (revised)  
 DT 18-AUG-1995 (first entry)  
 XX DE Plasmid pEZ2318.thy2.  
 XX KW OMTKY3; turkey ovomucoid third domain peptide inhibitor; furin inhibitor;  
 KW protease inhibitor; pEZ2318.thy2; probe; Escherichia coli; ss.  
 OS Synthetic.  
 XX WO9502055-A1.  
 XX PN 19-JAN-1995.  
 XX PD 08-JUL-1994; 94WO-US007779.  
 XX PF  
 XX

PR 09-JUL-1993; 93US-00089248.  
XX (LASK/) LASKOWSKI M.  
PA (ANDE/) ANDERSON S.  
XX Laskowski M, Anderson S;  
XX WPI; 1995-066900/09.  
DR  
XX Protein inhibitors of serine proteinase(s), e.g. furin, deriv. from  
XX turkey ovomucoid third domain - used as laboratory reagents to study the  
PT proteinase(s), or as chemotherapeutic agents to treat diseases associated  
PT with them.  
XX  
PS Disclosure; Page 42-45; 66pp; English.  
XX  
XX In synthetic analogs of turkey ovomucoid domain protein (6-56) (OMTKY3),  
CC given in AAR69818-24, the region immediately adjacent to the reactive  
CC site peptide bond is mutated to include the consensus sequence of furin  
CC or other serine protease. Polynucleotides encoding such analogs are  
CC incorporated into pEZ318.thy2 and expressed in Escherichia coli RV308  
CC (ATCC 31608). (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;  
Query Match 0.0%; Score 0; DB 2; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2e+09;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 G 1  
Db 1 N 1  
RESULT 30  
AAQ85491/C  
ID AAQ85491 standard; cDNA; 3 BP.  
XX AC AAQ85491;  
XX  
XX 25-MAR-2003 (revised)  
DT 18-AUG-1995 (first entry)  
XX  
XX Plasmid pEZ318.thy2.  
XX  
XX OMTKY3; turkey ovomucoid third domain peptide inhibitor; furin inhibitor;  
KW protease inhibitor; pEZ318.thy2; probe; Escherichia coli; ss.  
XX  
XX Synthetic.  
XX  
XX WO9502055-A1.  
XX  
XX 19-JAN-1995.  
XX  
XX 08-JUL-1994; 94WO-US007779.  
XX  
XX 09-JUL-1993; 93US-00089248.  
XX  
XX (LASK/) LASKOWSKI M.  
PA (ANDE/) ANDERSON S.  
XX  
XX Laskowski M, Anderson S;  
XX WPI; 1995-066900/09.  
XX  
XX Protein inhibitors of serine proteinase(s), e.g. furin, deriv. from  
PT turkey ovomucoid third domain - used as laboratory reagents to study the  
PT proteinase(s), or as chemotherapeutic agents to treat diseases associated  
PT with them.  
XX  
XX Disclosure; Page 42-45; 66pp; English.  
PS  
XX In synthetic analogs of turkey ovomucoid domain protein (6-56) (OMTKY3),  
CC given in AAR69818-24, the region immediately adjacent to the reactive  
CC site peptide bond is mutated to include the consensus sequence of furin  
CC or other serine protease. Polynucleotides encoding such analogs are  
CC incorporated into pEZ318.thy2 and expressed in Escherichia coli RV308  
CC (ATCC 31608). (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;  
Query Match 0.0%; Score 0; DB 2; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2e+09;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 G 1  
Db 3 N 3  
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Job time : 280 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:59:06 ; Search time 1696 Seconds  
(without alignments)  
85.711 Million cell updates/sec

Title: US-09-735-363A-8

Perfect score: 3

Sequence: 1 stg 3

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 550

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_on:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| C 2        | 3     | 100.0         | 3      | 6  | CQ787827 Sequence |
| C 3        | 3     | 100.0         | 3      | 6  | AX092473 Sequence |
| C 4        | 3     | 100.0         | 3      | 6  | AX092502 Sequence |
| C 5        | 3     | 100.0         | 3      | 6  | AX175244 Sequence |
| C 6        | 3     | 100.0         | 3      | 6  | AX743312 Sequence |
| C 7        | 3     | 100.0         | 3      | 6  | AX743316 Sequence |
| C 8        | 3     | 100.0         | 3      | 6  | AX816713 Sequence |
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| C 16       | 2     | 66.7          | 2      | 6  | CQ787923 Sequence |
| C 17       | 2     | 66.7          | 2      | 6  | CQ787936 Sequence |
| C 18       | 2     | 66.7          | 2      | 6  | CQ787937 Sequence |
| C 19       | 2     | 66.7          | 2      | 6  | CQ787938 Sequence |

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97 1.6 53.3 2 6 BD001933 BD001933 Sensitize  
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## ALIGNMENTS

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CQ787755/c  
LOCUS CQ787755 Sequence 61 from Patent WO2004020664. linear PAT 24-MAR-2004  
DEFINITION CQ787755  
ACCESSION CQ787755  
VERSION CQ787755.1 GI:45722713  
KEYWORDS Bos taurus (cow)  
SOURCE Bos taurus  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1  
AUTHORS Geldermann,H., Preuss,S. and Han,Y.  
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic purposes  
JOURNAL Patent: WO 2004020664-A 61 11-MAR-2004;  
Universitaet Hohenheim (DE)  
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Db 3 GTG 1

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ACCESSION CQ787827  
VERSION CQ787827.1 GI:45722785  
KEYWORDS Ovis aries (sheep)  
SOURCE Ovis aries  
ORGANISM Ovis aries  
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Caprinae; Ovis.

REFERENCE 1  
AUTHORS Geldermann,H., Preuss,S. and Han,Y.  
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic purposes  
JOURNAL Patent: WO 2004020664-A 133 11-MAR-2004;  
Universitaet Hohenheim (DE)  
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Db 3 GTG 1

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AX092473/c  
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DEFINITION AX092473  
ACCESSION AX092473  
VERSION AX092473.1 GI:13444568  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 34 08-MAR-2001;  
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3  
|||  
Db 3 GTG 1

RESULT 4  
AX092502  
LOCUS AX092502 Sequence 63 from Patent WO0116366. linear PAT 21-MAR-2001  
DEFINITION AX092502  
ACCESSION AX092502  
VERSION AX092502.1 GI:13444597  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 63 08-MAR-2001;  
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

## FEATURES

source Location/Qualifiers  
1..3  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

## ORIGIN

Query Match 100.0%; Score 3; DB 6; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3  
 ||||  
 Db 1 GTG 3

## RESULT 5

AX175244  
 LOCUS AX175244 3 bp DNA linear PAT 03-JUL-2001  
 DEFINITION Sequence 8 from Patent WO014465.  
 ACCESSION AX175244  
 VERSION AX175244.1 GI:14598612

KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

## REFERENCE

1 (bases 1 to 3)  
 AUTHORS Phillips,N.C. and Filion,M.C.  
 TITLE Therapeutically useful synthetic oligonucleotides  
 JOURNAL Patent: WO 014465-A 8 21-JUN-2001;

## FEATURES

source  
 1..3  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 100.0%; Score 3; DB 6; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3  
 ||||  
 Db 1 GTG 3

## RESULT 6

AX743312  
 LOCUS AX743312 3 bp DNA linear PAT 12-MAY-2003  
 DEFINITION Sequence 4 from Patent WO03028764.  
 ACCESSION AX743312  
 VERSION AX743312.1 GI:30577238

KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

## REFERENCE

1  
 AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.  
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides  
 JOURNAL Patent: WO 03028764-A 4 10-APR-2003;  
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)

## FEATURES

source  
 1..3  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic Oligonucleotide"

## ORIGIN

Query Match 100.0%; Score 3; DB 6; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3  
 ||||  
 Db 1 GTG 3

## RESULT 7

AX743316  
 LOCUS AX743316 3 bp DNA linear PAT 12-MAY-2003  
 DEFINITION Sequence 8 from Patent WO03028764.  
 ACCESSION AX743316  
 VERSION AX743316.1 GI:30577242

KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

## REFERENCE

1  
 AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.  
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides

## JOURNAL

Patent: WO 03028764-A 8 10-APR-2003;  
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)

## FEATURES

source  
 1..3  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic Oligonucleotide-3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide"

## ORIGIN

Query Match 100.0%; Score 3; DB 6; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3  
 ||||  
 Db 1 GTG 3

## RESULT 8

AX816713  
 LOCUS AX816713 3 bp DNA linear PAT 09-DEC-2003  
 DEFINITION Sequence 1 from Patent WO02085340.  
 ACCESSION AX816713  
 VERSION AX816713.1 GI:39647042

KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

## REFERENCE

1  
 AUTHORS Filion,M.C. and Phillips,N.C.  
 TITLE Oligonucleotide compositions and their use to induce differentiation of cells  
 JOURNAL Patent: WO 02085340-A 1 31-OCT-2002;  
 Bioniche Life Sciences Inc. (CA)

## FEATURES

source  
 1..3  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide"

## ORIGIN

Query Match 100.0%; Score 3; DB 6; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3  
 ||||  
 Db 1 GTG 3

## RESULT 9

CQ787746/c  
 LOCUS CQ787746 2 bp DNA linear PAT 24-MAR-2004  
 DEFINITION Sequence 52 from Patent WO2004020664.

```

ACCESSION CQ787746
VERSION CQ787746.1 GI:45722704
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 52 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES Location/Qualifiers
 source
 1..2
 /organism="Bos taurus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9913"
 misc_feature
 1..2
 /note="MS-Motiv in R11"
 repeat_unit
 1..2
 /note="Anzahl der Wiederholungen: 12"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 ||
Db 2 TG 1

RESULT 10
CQ787759/c
LOCUS CQ787759
DEFINITION Sequence 65 from Patent WO2004020664.
ACCESSION CQ787759
VERSION CQ787759.1 GI:45722717
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 65 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES Location/Qualifiers
 source
 1..2
 /organism="Bos taurus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9913"
 misc_feature
 1..2
 /note="MS-Motiv in R27"
 repeat_unit
 1..2
 /note="Anzahl der Wiederholungen: 3"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
 ||
Db 2 GT 1

RESULT 11
CQ787816/c
LOCUS CQ787816
DEFINITION Sequence 122 from Patent WO2004020664.
ACCESSION CQ787816
VERSION CQ787816.1 GI:45722774
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Ovis.

REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 122 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES Location/Qualifiers
 source
 1..2
 /organism="Ovis aries"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9940"
 misc_feature
 1..2
 /note="MS-Motiv in S11"
 repeat_unit
 1..2
 /note="Anzahl der Wiederholungen: 12"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 ||
Db 2 TG 1

RESULT 12
CQ787830/c
LOCUS CQ787830
DEFINITION Sequence 136 from Patent WO2004020664.
ACCESSION CQ787830
VERSION CQ787830.1 GI:45722788
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Ovis.

REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 136 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES Location/Qualifiers
 source
 1..2
 /organism="Ovis aries"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9940"
 misc_feature
 1..2
 /note="MS-Motiv in S27"
 repeat_unit
 1..2
 /note="Anzahl der Wiederholungen: 4"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
 ||
Db 2 GT 1

```



```

RESULT 13
CQ787891/c
LOCUS CQ787891 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 197 from Patent WO2004020664.
ACCESSION CQ787891
VERSION CQ787891.1 GI:45722849
KEYWORDS .
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 197 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES source
 1..2
 /organism="Bos taurus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9913"
 repeat_unit 1..2
 /notes="Anzahl der Wiederholungen: 12"
 satellite 1..2
 /notes="R11, Allel R"
ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 ||
Db 2 TG 1

RESULT 14
CQ787892/c
LOCUS CQ787892 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 198 from Patent WO2004020664.
ACCESSION CQ787892
VERSION CQ787892.1 GI:45722850
KEYWORDS .
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 198 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES source
 1..2
 /organism="Bos taurus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9913"
 repeat_unit 1..2
 /notes="Anzahl der Wiederholungen: 10"
 satellite 1..2
 /notes="R11, Allel A"
ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 TG 3
 ||
Db 2 TG 1

RESULT 15
CQ787893/c
LOCUS CQ787893 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 199 from Patent WO2004020664.
ACCESSION CQ787893
VERSION CQ787893.1 GI:45722851
KEYWORDS .
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 199 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES source
 1..2
 /organism="Bos taurus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9913"
 repeat_unit 1..2
 /notes="Anzahl der Wiederholungen: 13"
 satellite 1..2
 /notes="R11, Allel C"
ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 ||
Db 2 TG 1

RESULT 16
CQ787923/c
LOCUS CQ787923 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 229 from Patent WO2004020664.
ACCESSION CQ787923
VERSION CQ787923.1 GI:45722881
KEYWORDS .
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 229 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES source
 1..2
 /organism="Bos taurus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9913"
 repeat_unit 1..2
 /notes="Anzahl der Wiederholungen: 3"
 satellite 1..2
 /notes="R27, Allel R"
ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 2 GT 1

RESULT 17
CQ787936/c
LOCUS CQ787936 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 242 from Patent WO2004020664.
ACCESSION CQ787936
VERSION CQ787936.1 GI:45722894
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 242 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"
repeat_unit 1..2
satellite 1..2
/notes="Anzahl der Wiederholungen: 12"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

RESULT 18
CQ787937/c
LOCUS CQ787937 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 243 from Patent WO2004020664.
ACCESSION CQ787937
VERSION CQ787937.1 GI:45722895
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 243 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"
repeat_unit 1..2
satellite 1..2
/notes="Anzahl der Wiederholungen: 8"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

RESULT 19
CQ787938/c
LOCUS CQ787938 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 244 from Patent WO2004020664.
ACCESSION CQ787938
VERSION CQ787938.1 GI:45722896
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 244 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"
repeat_unit 1..2
satellite 1..2
/notes="Anzahl der Wiederholungen: 9"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

RESULT 20
CQ787939/c
LOCUS CQ787939 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 245 from Patent WO2004020664.
ACCESSION CQ787939
VERSION CQ787939.1 GI:45722897
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 245 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"
repeat_unit 1..2
satellite 1..2
/notes="Anzahl der Wiederholungen: 9"

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satellite /note="Anzahl der Wiederholungen: 10"
1. .2
/note="S11, Allel C"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
Db 2 TG 1

RESULT 21
CQ787940/c
LOCUS CQ787940 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 246 from Patent WO2004020664.
ACCESSION CQ787940
VERSION CQ787940.1 GI:45722898
KEYWORDS
SOURCE
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.

REFERENCE
1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 246 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES
source
1. .2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"

repeat_unit 1. .2
satellite /note="Anzahl der Wiederholungen: 11"
1. .2
/note="S11, Allel D"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
Db 2 TG 1

RESULT 22
CQ787941/c
LOCUS CQ787941 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 247 from Patent WO2004020664.
ACCESSION CQ787941
VERSION CQ787941.1 GI:45722899
KEYWORDS
SOURCE
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.

REFERENCE
1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 247 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES
source
1. .2
/organism="Ovis aries"

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repeat_unit 1. .2
satellite /note="Anzahl der Wiederholungen: 12"
1. .2
/note="S11, Allel E"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
Db 2 TG 1

RESULT 23
CQ787964/c
LOCUS CQ787964 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 270 from Patent WO2004020664.
ACCESSION CQ787964
VERSION CQ787964.1 GI:45722922
KEYWORDS
SOURCE
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.

REFERENCE
1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 270 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES
source
1. .2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"

repeat_unit 1. .2
satellite /note="Anzahl der Wiederholungen: 4"
1. .2
/note="S27, Allel R"

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
 ||
Db 2 GT 1

RESULT 24
CQ787967
LOCUS CQ787967 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 273 from Patent WO2004020664.
ACCESSION CQ787967
VERSION CQ787967.1 GI:45722925
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
JOURNAL Patent: WO 2004020664-A 273 11-MAR-2004;
 Universitaet Hohenheim (DE)
FEATURES
source
1. .2
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"

```

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| misc_feature          |        | 1. .2                                                                                                                        |  | /organism="Homo sapiens"              |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /mol_type="unassigned DNA"            |  |
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| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="MS-Motiv in M03 (PrP-Gen)"     |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="Anzahl der Wiederholungen: 21" |  |
| ORIGIN                |        |                                                                                                                              |  |                                       |  |
| Query Match           |        | 66.7%; Score 2; DB 6; Length 2;                                                                                              |  |                                       |  |
| Best Local Similarity |        | 100.0%; Pred. No. 0;                                                                                                         |  |                                       |  |
| Matches               |        | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                           |  |                                       |  |
| QY                    | 1 GT 2 | 2 TG 3                                                                                                                       |  |                                       |  |
| Db                    | 1 GT 2 | 2 TG 1                                                                                                                       |  |                                       |  |
| RESULT 25             |        |                                                                                                                              |  |                                       |  |
| CQ787969/c            |        |                                                                                                                              |  |                                       |  |
| LOCUS                 |        | 2 bp DNA                                                                                                                     |  | linear                                |  |
| DEFINITION            |        | Sequence 275 from Patent WO2004020664.                                                                                       |  |                                       |  |
| ACCESSION             |        | CQ787969                                                                                                                     |  |                                       |  |
| VERSION               |        | CQ787969.1                                                                                                                   |  | GI:45722927                           |  |
| KEYWORDS              |        | Homo sapiens (human)                                                                                                         |  |                                       |  |
| SOURCE                |        | Homo sapiens                                                                                                                 |  |                                       |  |
| ORGANISM              |        | Homo sapiens                                                                                                                 |  |                                       |  |
| REFERENCE             |        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |  |                                       |  |
| AUTHORS               |        | Geldermann,H., Preuss,S. and Han,Y.                                                                                          |  |                                       |  |
| TITLE                 |        | Polymorphous microsatellite loci in genes for pre-diagnostic purposes                                                        |  |                                       |  |
| JOURNAL               |        | Patent: WO 2004020664-A 275 11-MAR-2004; Universitaet Hohenheim (DE)                                                         |  |                                       |  |
| FEATURES              |        | Location/Qualifiers                                                                                                          |  |                                       |  |
| source                |        | 1. .2                                                                                                                        |  |                                       |  |
| misc_feature          |        | 1. .2                                                                                                                        |  | /organism="Homo sapiens"              |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /mol_type="unassigned DNA"            |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /db_xref="taxon:9606"                 |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="MS-Motiv in M05 (PrP-Gen)"     |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="Anzahl der Wiederholungen: 5"  |  |
| ORIGIN                |        |                                                                                                                              |  |                                       |  |
| Query Match           |        | 66.7%; Score 2; DB 6; Length 2;                                                                                              |  |                                       |  |
| Best Local Similarity |        | 100.0%; Pred. No. 0;                                                                                                         |  |                                       |  |
| Matches               |        | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                           |  |                                       |  |
| QY                    | 1 GT 2 | 2 TG 1                                                                                                                       |  |                                       |  |
| Db                    | 1 GT 2 | 2 GT 1                                                                                                                       |  |                                       |  |
| RESULT 26             |        |                                                                                                                              |  |                                       |  |
| CQ787976/c            |        |                                                                                                                              |  |                                       |  |
| LOCUS                 |        | 2 bp DNA                                                                                                                     |  | linear                                |  |
| DEFINITION            |        | Sequence 282 from Patent WO2004020664.                                                                                       |  |                                       |  |
| ACCESSION             |        | CQ787976                                                                                                                     |  |                                       |  |
| VERSION               |        | CQ787976.1                                                                                                                   |  | GI:45722934                           |  |
| KEYWORDS              |        | Homo sapiens (human)                                                                                                         |  |                                       |  |
| SOURCE                |        | Homo sapiens                                                                                                                 |  |                                       |  |
| ORGANISM              |        | Homo sapiens                                                                                                                 |  |                                       |  |
| REFERENCE             |        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |  |                                       |  |
| AUTHORS               |        | Geldermann,H., Preuss,S. and Han,Y.                                                                                          |  |                                       |  |
| TITLE                 |        | Polymorphous microsatellite loci in genes for pre-diagnostic purposes                                                        |  |                                       |  |
| JOURNAL               |        | Patent: WO 2004020664-A 282 11-MAR-2004; Universitaet Hohenheim (DE)                                                         |  |                                       |  |

|                       |        |                                                                                                                              |  |                                       |  |
|-----------------------|--------|------------------------------------------------------------------------------------------------------------------------------|--|---------------------------------------|--|
| source                |        | 1. .2                                                                                                                        |  | Location/Qualifiers                   |  |
| misc_feature          |        | 1. .2                                                                                                                        |  | /organism="Homo sapiens"              |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /mol_type="unassigned DNA"            |  |
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| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="MS-Motiv in M12 (PrP-Gen)"     |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="Anzahl der Wiederholungen: 18" |  |
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| Query Match           |        | 66.7%; Score 2; DB 6; Length 2;                                                                                              |  |                                       |  |
| Best Local Similarity |        | 100.0%; Pred. No. 0;                                                                                                         |  |                                       |  |
| Matches               |        | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                           |  |                                       |  |
| QY                    | 2 TG 3 | 2 TG 1                                                                                                                       |  |                                       |  |
| Db                    | 2 TG 1 | 2 TG 1                                                                                                                       |  |                                       |  |
| RESULT 27             |        |                                                                                                                              |  |                                       |  |
| CQ788021              |        |                                                                                                                              |  |                                       |  |
| LOCUS                 |        | 2 bp DNA                                                                                                                     |  | linear                                |  |
| DEFINITION            |        | Sequence 327 from Patent WO2004020664.                                                                                       |  |                                       |  |
| ACCESSION             |        | CQ788021                                                                                                                     |  |                                       |  |
| VERSION               |        | CQ788021.1                                                                                                                   |  | GI:45722978                           |  |
| KEYWORDS              |        | Homo sapiens (human)                                                                                                         |  |                                       |  |
| SOURCE                |        | Homo sapiens                                                                                                                 |  |                                       |  |
| ORGANISM              |        | Homo sapiens                                                                                                                 |  |                                       |  |
| REFERENCE             |        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |  |                                       |  |
| AUTHORS               |        | Geldermann,H., Preuss,S. and Han,Y.                                                                                          |  |                                       |  |
| TITLE                 |        | Polymorphous microsatellite loci in genes for pre-diagnostic purposes                                                        |  |                                       |  |
| JOURNAL               |        | Patent: WO 2004020664-A 327 11-MAR-2004; Universitaet Hohenheim (DE)                                                         |  |                                       |  |
| FEATURES              |        | Location/Qualifiers                                                                                                          |  |                                       |  |
| source                |        | 1. .2                                                                                                                        |  |                                       |  |
| misc_feature          |        | 1. .2                                                                                                                        |  | /organism="Homo sapiens"              |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /mol_type="unassigned DNA"            |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /db_xref="taxon:9606"                 |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="Anzahl der Wiederholungen: 21" |  |
| repeat_unit           |        | 1. .2                                                                                                                        |  | /note="M03, Allel R (PrP-Gen)"        |  |
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| Best Local Similarity |        | 100.0%; Pred. No. 0;                                                                                                         |  |                                       |  |
| Matches               |        | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                           |  |                                       |  |
| QY                    | 1 GT 2 | 2 TG 2                                                                                                                       |  |                                       |  |
| Db                    | 1 GT 2 | 1 GT 2                                                                                                                       |  |                                       |  |
| RESULT 28             |        |                                                                                                                              |  |                                       |  |
| CQ788022              |        |                                                                                                                              |  |                                       |  |
| LOCUS                 |        | 2 bp DNA                                                                                                                     |  | linear                                |  |
| DEFINITION            |        | Sequence 328 from Patent WO2004020664.                                                                                       |  |                                       |  |
| ACCESSION             |        | CQ788022                                                                                                                     |  |                                       |  |
| VERSION               |        | CQ788022.1                                                                                                                   |  | GI:45722979                           |  |
| KEYWORDS              |        | Homo sapiens (human)                                                                                                         |  |                                       |  |
| SOURCE                |        | Homo sapiens                                                                                                                 |  |                                       |  |
| ORGANISM              |        | Homo sapiens                                                                                                                 |  |                                       |  |
| REFERENCE             |        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |  |                                       |  |
| AUTHORS               |        | Geldermann,H., Preuss,S. and Han,Y.                                                                                          |  |                                       |  |
| TITLE                 |        | Polymorphous microsatellite loci in genes for pre-diagnostic purposes                                                        |  |                                       |  |
| JOURNAL               |        | Patent: WO 2004020664-A 328 11-MAR-2004; Universitaet Hohenheim (DE)                                                         |  |                                       |  |

JOURNAL Patent: WO 2004020664-A 331 11-MAR-2004;  
Universitaet Hohenheim (DE)

FEATURES  
source  
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Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

repeat\_unit  
1..2  
/note="Anzahl der Wiederholungen: 15"

satellite  
1..2  
/note="WM03, Allel B (PrP-Gen)"

ORIGIN

Query Match 66.7%; Score 2; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
||  
Db 1 GT 2

Search completed: July 20, 2005, 21:15:06  
Job time : 1699 secs

JOURNAL Patent: WO 2004020664-A 329 11-MAR-2004;  
Universitaet Hohenheim (DE)

FEATURES  
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/note="Anzahl der Wiederholungen: 19"

satellite  
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/note="WM03, Allel D (PrP-Gen)"

ORIGIN

Query Match 66.7%; Score 2; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
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Db 1 GT 2

RESULT 29  
LOCUS CQ788023 2 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 329 from Patent WO2004020664.  
ACCESSION CQ788023  
VERSION CQ788023.1 GI:45722980  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Geldermann,H., Preuss,S. and Han,Y.  
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic purposes  
JOURNAL Purposes  
Patent: WO 2004020664-A 329 11-MAR-2004;  
Universitaet Hohenheim (DE)

FEATURES  
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repeat\_unit  
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/note="Anzahl der Wiederholungen: 19"

satellite  
1..2  
/note="WM03, Allel D (PrP-Gen)"

ORIGIN

Query Match 66.7%; Score 2; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2  
||  
Db 1 GT 2

RESULT 30  
LOCUS CQ788025 2 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 331 from Patent WO2004020664.  
ACCESSION CQ788025  
VERSION CQ788025.1 GI:45722981  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Geldermann,H., Preuss,S. and Han,Y.  
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic purposes

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds  
(without alignments)  
393.838 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 ggtgtg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
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| 1          | 6     | 100.0       | 6      | 6  | AX175246         |
| 2          | 6     | 100.0       | 6      | 6  | AX175307         |
| 3          | 5     | 83.3        | 6      | 6  | E06868 Substrate |
| 4          | 5     | 83.3        | 6      | 6  | AX175245         |
| 5          | 5     | 83.3        | 6      | 6  | AX175306         |
| 6          | 5     | 83.3        | 6      | 6  | AX239662         |
| 7          | 4.4   | 73.3        | 6      | 6  | CQ755831         |
| 8          | 4.4   | 73.3        | 6      | 6  | CQ755836         |
| 9          | 4.4   | 73.3        | 6      | 6  | CQ758069         |
| 10         | 4.4   | 73.3        | 6      | 6  | CQ758074         |
| 11         | 4.4   | 73.3        | 6      | 6  | CQ788027         |
| 12         | 4.4   | 73.3        | 6      | 6  | AX764869         |
| 13         | 4.4   | 73.3        | 6      | 6  | AX764874         |
| 14         | 4.4   | 73.3        | 6      | 6  | AX805867         |
| 15         | 4.4   | 66.7        | 4      | 6  | AX175290         |
| 16         | 4     | 66.7        | 4      | 6  | AX175295         |
| 17         | 4     | 66.7        | 5      | 6  | CQ868954         |
| 18         | 4     | 66.7        | 5      | 6  | CQ868982         |
| 19         | 4     | 66.7        | 5      | 6  | CQ869103         |

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|------|-----|------|---|---|----------|-------------|
| C 20 | 4   | 66.7 | 5 | 6 | CQ869131 | Sequence    |
| C 21 | 4   | 66.7 | 5 | 6 | AX163835 | Sequence    |
| C 22 | 4   | 66.7 | 5 | 6 | AX449528 | Sequence    |
| C 23 | 4   | 66.7 | 5 | 6 | AX805861 | Sequence    |
| C 24 | 4   | 66.7 | 5 | 6 | CQ755803 | Sequence    |
| C 25 | 4   | 66.7 | 6 | 6 | CQ758041 | Sequence    |
| C 26 | 4   | 66.7 | 6 | 6 | AX104453 | Sequence    |
| C 27 | 4   | 66.7 | 6 | 6 | AX107946 | Sequence    |
| C 28 | 4   | 66.7 | 6 | 6 | AX107947 | Sequence    |
| C 29 | 4   | 66.7 | 6 | 6 | AX107950 | Sequence    |
| C 30 | 4   | 66.7 | 6 | 6 | AX175275 | Sequence    |
| C 31 | 4   | 66.7 | 6 | 6 | AX355021 | Sequence    |
| C 32 | 4   | 66.7 | 6 | 6 | AX359851 | Sequence    |
| C 33 | 4   | 66.7 | 6 | 6 | AX547506 | Sequence    |
| C 34 | 4   | 66.7 | 6 | 6 | AX764841 | Sequence    |
| C 35 | 3.4 | 56.7 | 5 | 6 | A97990   | Sequence 20 |
| C 36 | 3.4 | 56.7 | 5 | 6 | CQ787740 | Sequence    |
| C 37 | 3.4 | 56.7 | 5 | 6 | CQ787812 | Sequence    |
| C 38 | 3.4 | 56.7 | 5 | 6 | CQ787970 | Sequence    |
| C 39 | 3.4 | 56.7 | 5 | 6 | CQ868947 | Sequence    |
| C 40 | 3.4 | 56.7 | 5 | 6 | CQ868949 | Sequence    |
| C 41 | 3.4 | 56.7 | 5 | 6 | CQ869003 | Sequence    |
| C 42 | 3.4 | 56.7 | 5 | 6 | CQ869027 | Sequence    |
| C 43 | 3.4 | 56.7 | 5 | 6 | CQ869035 | Sequence    |
| C 44 | 3.4 | 56.7 | 5 | 6 | CQ869096 | Sequence    |
| C 45 | 3.4 | 56.7 | 5 | 6 | CQ869098 | Sequence    |
| C 46 | 3.4 | 56.7 | 5 | 6 | CQ869152 | Sequence    |
| C 47 | 3.4 | 56.7 | 5 | 6 | CQ869176 | Sequence    |
| C 48 | 3.4 | 56.7 | 5 | 6 | CQ869184 | Sequence    |
| C 49 | 3.4 | 56.7 | 5 | 6 | CQ869237 | Sequence    |
| C 50 | 3.4 | 56.7 | 5 | 6 | AX046167 | Sequence    |
| C 51 | 3.4 | 56.7 | 5 | 6 | AX175297 | Sequence    |
| C 52 | 3.4 | 56.7 | 5 | 6 | AX186622 | Sequence    |
| C 53 | 3.4 | 56.7 | 5 | 6 | AX268756 | Sequence    |
| C 54 | 3.4 | 56.7 | 5 | 6 | AX268758 | Sequence    |
| C 55 | 3.4 | 56.7 | 5 | 6 | AX805865 | Sequence    |
| C 56 | 3.4 | 56.7 | 6 | 6 | A79021   | Sequence 1  |
| C 57 | 3.4 | 56.7 | 6 | 6 | A79022   | Sequence 2  |
| C 58 | 3.4 | 56.7 | 6 | 6 | A91411   | Sequence 1  |
| C 59 | 3.4 | 56.7 | 6 | 6 | A91412   | Sequence 2  |
| C 60 | 3.4 | 56.7 | 6 | 6 | CQ755676 | Sequence    |
| C 61 | 3.4 | 56.7 | 6 | 6 | CQ755702 | Sequence    |
| C 62 | 3.4 | 56.7 | 6 | 6 | CQ755706 | Sequence    |
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| C 64 | 3.4 | 56.7 | 6 | 6 | CQ755734 | Sequence    |
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| C 66 | 3.4 | 56.7 | 6 | 6 | CQ755763 | Sequence    |
| C 67 | 3.4 | 56.7 | 6 | 6 | CQ755771 | Sequence    |
| C 68 | 3.4 | 56.7 | 6 | 6 | CQ755772 | Sequence    |
| C 69 | 3.4 | 56.7 | 6 | 6 | CQ755849 | Sequence    |
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| C 71 | 3.4 | 56.7 | 6 | 6 | CQ756230 | Sequence    |
| C 72 | 3.4 | 56.7 | 6 | 6 | CQ756501 | Sequence    |
| C 73 | 3.4 | 56.7 | 6 | 6 | CQ757914 | Sequence    |
| C 74 | 3.4 | 56.7 | 6 | 6 | CQ757940 | Sequence    |
| C 75 | 3.4 | 56.7 | 6 | 6 | CQ757944 | Sequence    |
| C 76 | 3.4 | 56.7 | 6 | 6 | CQ757964 | Sequence    |
| C 77 | 3.4 | 56.7 | 6 | 6 | CQ757972 | Sequence    |
| C 78 | 3.4 | 56.7 | 6 | 6 | CQ757982 | Sequence    |
| C 79 | 3.4 | 56.7 | 6 | 6 | CQ758001 | Sequence    |
| C 80 | 3.4 | 56.7 | 6 | 6 | CQ758009 | Sequence    |
| C 81 | 3.4 | 56.7 | 6 | 6 | CQ758010 | Sequence    |
| C 82 | 3.4 | 56.7 | 6 | 6 | CQ758087 | Sequence    |
| C 83 | 3.4 | 56.7 | 6 | 6 | CQ758286 | Sequence    |
| C 84 | 3.4 | 56.7 | 6 | 6 | CQ758468 | Sequence    |
| C 85 | 3.4 | 56.7 | 6 | 6 | CQ758739 | Sequence    |
| C 86 | 3.4 | 56.7 | 6 | 6 | CQ787756 | Sequence    |
| C 87 | 3.4 | 56.7 | 6 | 6 | CQ787918 | Sequence    |
| C 88 | 3.4 | 56.7 | 6 | 6 | CQ787945 | Sequence    |
| C 89 | 3.4 | 56.7 | 6 | 6 | CQ787946 | Sequence    |
| C 90 | 3.4 | 56.7 | 6 | 6 | CQ787947 | Sequence    |
| C 91 | 3.4 | 56.7 | 6 | 6 | CQ787948 | Sequence    |
| C 92 | 3.4 | 56.7 | 6 | 6 | CQ788051 | Sequence    |

93 3.4 56.7 6 6 E17123 Pythium sp.  
 94 3.4 56.7 6 6 AX069170 Sequence  
 c 95 3.4 56.7 6 6 AX166334 Sequence  
 96 3.4 56.7 6 6 AX175239 Sequence  
 97 3.4 56.7 6 6 AX175260 Sequence  
 98 3.4 56.7 6 6 AX175261 Sequence  
 99 3.4 56.7 6 6 AX175262 Sequence  
 100 3.4 56.7 6 6 AX175266 Sequence

## ALIGNMENTS

RESULT 1  
 AX175246  
 LOCUS AX175246 6 bp DNA linear PAT 03-JUL-2001  
 DEFINITION Sequence 10 from Patent WO0144465.  
 ACCESSION AX175246  
 VERSION AX175246.1 GI:14598614  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM  
 other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 6)  
 AUTHORS Phillips,N.C. and Fillion,M.C.  
 TITLE Therapeutically useful synthetic oligonucleotides  
 JOURNAL Patent: WO 0144465-A 10 21-JUN-2001;  
 Bioniche Life Sciences Inc. (CA)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+09;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTGT 6  
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 Db 1 GTGTGT 6

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 AX175307  
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 DEFINITION Sequence 71 from Patent WO0144465.  
 ACCESSION AX175307  
 VERSION AX175307.1 GI:14598675  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM  
 other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 6)  
 AUTHORS Phillips,N.C. and Fillion,M.C.  
 TITLE Therapeutically useful synthetic oligonucleotides  
 JOURNAL Patent: WO 0144465-A 71 21-JUN-2001;  
 Bioniche Life Sciences Inc. (CA)  
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E06868  
 LOCUS E06868 6 bp RNA linear PAT 29-SEP-1997  
 DEFINITION Substrate of ribozyme.  
 ACCESSION E06868  
 VERSION E06868.1 GI:5708533  
 KEYWORDS JP 1994070774-A/16.  
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 other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 6)  
 AUTHORS Otsuka,E. and Koizumi,M.  
 TITLE RIBOZYME HAVING THERMODYNAMICALLY STABLE LOOP STRUCTURE  
 JOURNAL Patent: JP 1994070774-A 16 15-MAR-1994;  
 SANKYO CO LTD

## COMMENT

OS Artificial gene  
 OC Artificial sequence; Genes.  
 PN JP 1994070774-A/16  
 PD 15-MAR-1994  
 PF 01-JUL-1993 JP 1993163530  
 PR 02-JUL-1992 JP 92P 175706  
 PI OTSUKA EIKO, KOIZUMI MAKOTO  
 PC C12N15/11,C12N1/21,C12N9/00,C12N15/10,(C12N1/21,C12R1:19); CC  
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AX175245  
 LOCUS AX175245 6 bp DNA linear PAT 03-JUL-2001  
 DEFINITION Sequence 9 from Patent WO0144465.  
 ACCESSION AX175245  
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JOURNAL A method for the simultaneous production of multiple proteins;
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 /note="oligonucleotide patterns over-represented in STAR
 elements"
ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
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Db 6 GTGGGT 1

RESULT 11
LOCUS CQ788027/c
DEFINITION Sequence 333 from Patent WO2004020664.
ACCESSION CQ788027
VERSION CQ788027.1 GI:45722983
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes

REFERENCE
AUTHORS 1
TITLE Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
JOURNAL A method for the simultaneous production of multiple proteins;
FEATURES vectors and cells for use therein
 Patent: WO 2003106684-A 373 24-DEC-2003;
 Chromagenics B.V. (NL)
 Location/Qualifiers
 1..6
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="M05, Allel R (PrP-Gen)"
 1..6
 /note="Anzahl der Wiederholungen: 2"
 5..6
 /note="Anzahl der Wiederholungen: 2"
ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
 |||||
Db 6 GTTTGT 1

RESULT 12
LOCUS AX764869/c
DEFINITION Sequence 339 from Patent WO03004704.
ACCESSION AX764869
VERSION AX764869.1 GI:32259077
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P. and Kruckeberg,A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 Patent: WO 03004704-A 339 16-JAN-2003;
 Chromagenics B.V. (NL)
 Location/Qualifiers
 1..6
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide patterns over-represented in STAR
 elements"
ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
 |||||
Db 6 GTGGGT 1

RESULT 13
LOCUS AX764874/c
DEFINITION Sequence 344 from Patent WO03004704.
ACCESSION AX764874
VERSION AX764874.1 GI:32259082
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P. and Kruckeberg,A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 Patent: WO 03004704-A 344 16-JAN-2003;
 Chromagenics B.V. (NL)
 Location/Qualifiers
 1..6
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide patterns over-represented in STAR
 elements"
ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
 |||||
Db 6 GTGGGT 1

RESULT 14
LOCUS AX764874/c
DEFINITION Sequence 344 from Patent WO03004704.
ACCESSION AX764874
VERSION AX764874.1 GI:32259082
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P. and Kruckeberg,A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 Patent: WO 03004704-A 344 16-JAN-2003;
 Chromagenics B.V. (NL)
 Location/Qualifiers
 1..6
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide patterns over-represented in STAR
 elements"
ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
 |||||
Db 6 GTGGGT 1

RESULT 15
LOCUS CQ788027/c
DEFINITION Sequence 333 from Patent WO2004020664.
ACCESSION CQ788027
VERSION CQ788027.1 GI:45722983
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes

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Chromagenics B.V. (NL)
Location/Qualifiers
1. .6
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
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Db 6 GGGTGT 1

RESULT 14
AX805867/c
LOCUS AX805867 6 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 13 from Patent WO03060163.
ACCESSION AX805867
VERSION AX805867.1 GI:38522778
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS van Eijk, M.J. and van Schaik, C.
TITLE Discrimination and detection of target nucleotide sequences using
JOURNAL mass spectrometry
Patent: WO 03060163-A 13 24-JUL-2003;
Keygene N.V. (NL)
FEATURES
source
1. .6
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="stuffer sequence"

ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
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Db 6 GTGGGT 1

RESULT 15
AX175290
LOCUS AX175290 4 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 54 from Patent WO0144465.
ACCESSION AX175290
VERSION AX175290.1 GI:14598658
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 4)
AUTHORS Phillips, N.C. and Fillion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 54 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .4
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match
Best Local Similarity 66.7%; Score 4; DB 6; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
 | | |
Db 1 GTGT 4

RESULT 16
AX175295
LOCUS AX175295 4 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 59 from Patent WO0144465.
ACCESSION AX175295
VERSION AX175295.1 GI:14598663
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 4)
AUTHORS Phillips, N.C. and Fillion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 59 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .4
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match
Best Local Similarity 66.7%; Score 4; DB 6; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
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Db 1 TGTG 4

RESULT 17
CQ868954
LOCUS CQ868954 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 108 from Patent WO2004074429.
ACCESSION CQ868954
VERSION CQ868954.1 GI:51998881
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd, P.O., Goulliaev, A.H., Thisted, T. and Olsen, E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 108 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES
source
1. .5
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic construct"

ORIGIN

Query Match
Best Local Similarity 66.7%; Score 4; DB 6; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
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Db 1 GTGT 4
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RESULT 18
CQ868982/c
LOCUS CQ868982 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 136 from Patent WO2004074429.
ACCESSION CQ868982
VERSION CQ868982.1 GI:51998909
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 136 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES Location/Qualifiers
 1..5
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic construct"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
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Db 4 GTGT 1

RESULT 19
CQ869103
LOCUS CQ869103 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 257 from Patent WO2004074429.
ACCESSION CQ869103
VERSION CQ869103.1 GI:51999030
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 257 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES Location/Qualifiers
 1..5
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic construct"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
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Db 4 GTGT 1

RESULT 20
CQ869131/c
LOCUS CQ869131 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 285 from Patent WO2004074429.
ACCESSION CQ869131
VERSION CQ869131.1 GI:51999058
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
TITLE Nucleic acid molecules encoding plant cell cycle proteins and uses
JOURNAL Patent: WO 0185946-A 247 15-NOV-2001;

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other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 285 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES Location/Qualifiers
 1..5
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic construct"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
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Db 4 GTGT 1

RESULT 21
AX163835/c
LOCUS AX163835 5 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4 from Patent WO0140804.
ACCESSION AX163835
VERSION AX163835.1 GI:14544907
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5)
AUTHORS Hol,E.M. and van Leeuwen,F.W.
TITLE Clearance of aberrant protein in correlation with disease
JOURNAL Patent: WO 0140804-A 4 07-JUN-2001;
Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES Location/Qualifiers
 1..5
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 misc_feature 1..5 Repeat sequence, wherein N represents any
 nucleotide"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
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Db 4 TGTG 1

RESULT 22
AX449528/c
LOCUS AX449528 5 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 247 from Patent WO0185946.
ACCESSION AX449528
VERSION AX449528.1 GI:21698177
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
 other sequences; artificial sequences.
REFERENCE 1
AUTHORS Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
TITLE Nucleic acid molecules encoding plant cell cycle proteins and uses
JOURNAL Patent: WO 0185946-A 247 15-NOV-2001;

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CropDesign N.V. (BE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="motif"

ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
Db 5 TGTG 2

RESULT 23
AX805861/c
LOCUS
DEFINITION
Sequence 7 from Patent WO03060163.
ACCESSION
AX805861
VERSION
AX805861.1 GI:38522772
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
van Eijk,M.J. and van Schaik,C.
TITLE
Discrimination and detection of target nucleotide sequences using
mass spectrometry
JOURNAL
Patent: WO 03060163-A 7 24-JUL-2003;
Keygene N.V. (NL)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="stuffer sequence"

ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
Db 5 TGTG 2

RESULT 24
CQ755803/c
LOCUS
DEFINITION
Sequence 304 from Patent WO2003106674.
ACCESSION
CQ755803
VERSION
CQ755803.1 GI:44846608
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE
Means and methods for regulating gene expression
JOURNAL
Patent: WO 2003106674-A 304 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
1..6
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide patterns over-represented in STAR
elements"

CropDesign N.V. (BE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="motif"

ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
Db 5 GTGT 2

RESULT 25
CQ758041/c
LOCUS
DEFINITION
Sequence 345 from Patent WO2003106684.
ACCESSION
CQ758041
VERSION
CQ758041.1 GI:44848062
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE
A method for the simultaneous production of multiple proteins;
vectors and cells for use therein
JOURNAL
Patent: WO 2003106684-A 345 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
1..6
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
Db 5 GTGT 2

RESULT 26
AX104453
LOCUS
DEFINITION
Sequence 645 from Patent WO0122972.
ACCESSION
AX104453
VERSION
AX104453.1 GI:13920650
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Krieg,A.M., Schetter,C. and Vollmar,J.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 645 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
1..6
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
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QY 1 GTGT 4

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Db 3 GTGT 6
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RESULT 27
LOCUS AX107946/c
DEFINITION Sequence 3 from Patent WO0123559.
ACCESSION AX107946
VERSION AX107946.1 GI:13923327
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6)
AUTHORS Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE Osteoclast differentiation factor regulatory region
JOURNAL Patent: WO 0123559-A 3 05-APR-2001;
 ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
 Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
FEATURES source
 1..6
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
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Db 6 TGTG 3

RESULT 30
LOCUS AX175275
DEFINITION Sequence 39 from Patent WO014465.
ACCESSION AX175275
VERSION AX175275.1 GI:14598643
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
 other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 39 21-JUN-2001;
 Bioniche Life Sciences Inc. (CA)
FEATURES source
 1..6
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
 |||||
Db 2 TGTG 5

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Job time : 745.2 secs

Db 3 GTGT 6
|||||
RESULT 27
LOCUS AX107946/c
DEFINITION Sequence 3 from Patent WO0123559.
ACCESSION AX107946
VERSION AX107946.1 GI:13923327
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6)
AUTHORS Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE Osteoclast differentiation factor regulatory region
JOURNAL Patent: WO 0123559-A 3 05-APR-2001;
 ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
 Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
FEATURES source
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
 |||||
Db 6 TGTG 3

RESULT 28
LOCUS AX107947
DEFINITION Sequence 4 from Patent WO0123559.
ACCESSION AX107947
VERSION AX107947.1 GI:13923328
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6)
AUTHORS Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE Osteoclast differentiation factor regulatory region
JOURNAL Patent: WO 0123559-A 4 05-APR-2001;
 ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
 Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
FEATURES source
 1..6
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
 |||||
Db 1 TGTG 4

RESULT 29
LOCUS AX107950/c
DEFINITION Sequence 7 from Patent WO0123559.
ACCESSION AX107950
VERSION AX107950.1 GI:13923331
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6)
AUTHORS Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE Osteoclast differentiation factor regulatory region
JOURNAL Patent: WO 0123559-A 7 05-APR-2001;
 ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
 Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
FEATURES source
 1..6
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
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Db 2 TGTG 5

Search completed: July 21, 2005, 00:00:35
Job time : 745.2 secs
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 seconds  
(without alignments)  
189.533 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 ggtgt 6

Scoring table: IDENTITY NUC

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID       | Description        |
|------------|-------|---------------|--------|----------|--------------------|
| C 1        | 6     | 100.0         | 6      | AD081155 | Ad081155 Prion pro |
| C 2        | 5     | 83.3          | 6      | ADR7580  | Adr7580 AC repeat  |
| C 3        | 5     | 83.3          | 6      | ADR33261 | Adr33261 Human nlc |
| C 4        | 5     | 83.3          | 6      | ADR33262 | Adr33262 Human nlc |
| C 5        | 4.4   | 73.3          | 6      | AAQ78699 | Aaq78699 Pstail ge |
| C 6        | 4.4   | 73.3          | 6      | ABN73213 | Abn73213 Bovine em |
| C 7        | 4     | 66.7          | 5      | AAQ96420 | Aaq96420 Kozak seq |
| C 8        | 4     | 66.7          | 6      | AAQ58436 | Aaq58436 Sequencin |
| C 9        | 4     | 66.7          | 6      | ABK72534 | Abk72534 Human OPA |
| C 10       | 4     | 66.7          | 6      | ABK78161 | Abk78161 Angiogene |
| C 11       | 4     | 66.7          | 6      | ACD99933 | AcD99933 Immunosti |
| C 12       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 13       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 14       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 15       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 16       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 17       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 18       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 19       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |
| C 20       | 4     | 66.7          | 6      | AD081155 | Ad081155 Prion pro |

|      |     |      |   |          |                    |
|------|-----|------|---|----------|--------------------|
| C 21 | 4   | 66.7 | 6 | AD005792 | Ad005792 Telomere- |
| C 22 | 4   | 66.7 | 6 | ADR35664 | Adr35664 Human nlc |
| C 23 | 4   | 66.7 | 6 | ADR35687 | Adr35687 Human nlc |
| C 24 | 4   | 66.7 | 6 | ADR35663 | Adr35663 Human nlc |
| C 25 | 4   | 66.7 | 6 | ADR35667 | Adr35667 Human nlc |
| C 26 | 4   | 66.7 | 6 | ADR35668 | Adr35668 Human nlc |
| C 27 | 4   | 66.7 | 6 | ADR35665 | Adr35665 Human nlc |
| C 28 | 4   | 66.7 | 6 | ADR35666 | Adr35666 Human nlc |
| C 29 | 4   | 66.7 | 6 | ADR35669 | Adr35669 Human nlc |
| C 30 | 3.4 | 56.7 | 5 | AAZ10696 | Aaz10696 Oligonucl |
| C 31 | 3.4 | 56.7 | 5 | AAZ10695 | Aaz10695 Oligonucl |
| C 32 | 3.4 | 56.7 | 5 | AAZ14910 | Aaz14910 Melanogen |
| C 33 | 3.4 | 56.7 | 5 | AAZ14908 | Aaz14908 Melanogen |
| C 34 | 3.4 | 56.7 | 5 | AAH71043 | Aah71043 Human cer |
| C 35 | 3.4 | 56.7 | 5 | ABZ75664 | Abz75664 Helicase- |
| C 36 | 3.4 | 56.7 | 5 | ACD25823 | AcD25823 Telomere- |
| C 37 | 3.4 | 56.7 | 5 | ACD25825 | AcD25825 Telomere- |
| C 38 | 3.4 | 56.7 | 6 | AAZ93282 | Aaz93282 Promoter  |
| C 39 | 3.4 | 56.7 | 6 | AAZ93285 | Aaz93285 Promoter  |
| C 40 | 3.4 | 56.7 | 6 | AAZ93305 | Aaz93305 Fungal te |
| C 41 | 3.4 | 56.7 | 6 | AAZ93576 | Aaz93576 Cis-actin |
| C 42 | 3.4 | 56.7 | 6 | AAZ06241 | Aaz06241 PCR prime |
| C 43 | 3.4 | 56.7 | 6 | ABX50029 | Abx50029 Telomere  |
| C 44 | 3.4 | 56.7 | 6 | ACH50850 | Ach50850 Hypotheti |
| C 45 | 3.4 | 56.7 | 6 | ACA88955 | AcA88955 Selection |
| C 46 | 3.4 | 56.7 | 6 | ADJ35342 | Adj35342 Stabilisi |
| C 47 | 3.4 | 56.7 | 6 | ADJ35723 | Adj35723 Stabilisi |
| C 48 | 3.4 | 56.7 | 6 | ADJ35541 | Adj35541 Stabilisi |
| C 49 | 3.4 | 56.7 | 6 | ADK14278 | Adk14278 Candida p |
| C 50 | 3.4 | 56.7 | 6 | ADK14307 | Adk14307 Candida p |
| C 51 | 3.4 | 56.7 | 6 | ADK14309 | Adk14309 Candida p |
| C 52 | 3.4 | 56.7 | 6 | ADR34497 | Adr34497 Human nlc |
| C 53 | 3.4 | 56.7 | 6 | ADR33244 | Adr33244 Human nlc |
| C 54 | 3.4 | 56.7 | 6 | ADR37222 | Adr37222 Human nlc |
| C 55 | 3.4 | 56.7 | 6 | ADR32691 | Adr32691 Human nlc |
| C 56 | 3.4 | 56.7 | 6 | ADR32738 | Adr32738 Human nlc |
| C 57 | 3.4 | 56.7 | 6 | ADR33009 | Adr33009 Human nlc |
| C 58 | 3.4 | 56.7 | 6 | ADR34495 | Adr34495 Human nlc |
| C 59 | 3.4 | 56.7 | 6 | ADR37224 | Adr37224 Human nlc |
| C 60 | 3.4 | 56.7 | 6 | ADR37225 | Adr37225 Human nlc |
| C 61 | 3.4 | 56.7 | 6 | ADR33005 | Adr33005 Human nlc |
| C 62 | 3.4 | 56.7 | 6 | ADR33070 | Adr33070 Human nlc |
| C 63 | 3.4 | 56.7 | 6 | ADR37203 | Adr37203 Human nlc |
| C 64 | 3.4 | 56.7 | 6 | ADR34498 | Adr34498 Human nlc |
| C 65 | 3.4 | 56.7 | 6 | ADR37223 | Adr37223 Human nlc |
| C 66 | 3.4 | 56.7 | 6 | ADR33068 | Adr33068 Human nlc |
| C 67 | 3.4 | 56.7 | 6 | ADR33066 | Adr33066 Human nlc |
| C 68 | 3.4 | 56.7 | 6 | ADR37221 | Adr37221 Human nlc |
| C 69 | 3.4 | 56.7 | 6 | ADR32877 | Adr32877 Human nlc |
| C 70 | 3.4 | 56.7 | 6 | ADR33069 | Adr33069 Human nlc |
| C 71 | 3.4 | 56.7 | 6 | ADR34496 | Adr34496 Human nlc |
| C 72 | 3.4 | 56.7 | 6 | ADR37226 | Adr37226 Human nlc |
| C 73 | 3.4 | 56.7 | 6 | ADR37202 | Adr37202 Human nlc |
| C 74 | 3.4 | 56.7 | 6 | ADR33067 | Adr33067 Human nlc |
| C 75 | 3   | 50.0 | 4 | AAQ81664 | Aaq81664 bFGF bind |
| C 76 | 3   | 50.0 | 4 | ABV75157 | Abv75157 Nucleotid |
| C 77 | 3   | 50.0 | 5 | AAZ96299 | Aaz96299 Fungal te |
| C 78 | 3   | 50.0 | 5 | AAZ93601 | Aaz93601 Transcrip |
| C 79 | 3   | 50.0 | 5 | AAZ44181 | Aaz44181 Probe #4  |
| C 80 | 3   | 50.0 | 5 | ABK99557 | Abk99557 Nucleic a |
| C 81 | 3   | 50.0 | 5 | ABZ75666 | Abz75666 Helicase- |
| C 82 | 3   | 50.0 | 5 | ABX49997 | Abx49997 Telomere  |
| C 83 | 3   | 50.0 | 5 | ADN33270 | Adn33270 E. coli 2 |
| C 84 | 3   | 50.0 | 5 | ADN33278 | Adn33278 E. coli 2 |
| C 85 | 3   | 50.0 | 5 | AAZ71342 | Aaz71342 Restricti |
| C 86 | 3   | 50.0 | 6 | AAZ71342 | Aaz71342 Restricti |
| C 87 | 3   | 50.0 | 6 | AAZ93284 | Aaz93284 Promoter  |
| C 88 | 3   | 50.0 | 6 | AAQ47786 | Aaq47786 Mammalian |
| C 89 | 3   | 50.0 | 6 | AAQ38713 | Aaq38713 Mac:Max c |
| C 90 | 3   | 50.0 | 6 | AAQ38713 | Aaq38713 Mac:Max c |
| C 91 | 3   | 50.0 | 6 | AAQ37364 | Aaq37364 HRR25 rea |
| C 92 | 3   | 50.0 | 6 | AAQ58433 | Aaq58433 Sequencin |
| C 93 | 3   | 50.0 | 6 | AAQ58434 | Aaq58434 Sequencin |

94 3 50.0 6 2 AAQ58435 Sequencin  
 C 95 3 50.0 6 2 AAV11643  
 C 96 3 50.0 6 3 AA289322 Human UCP  
 C 97 3 50.0 6 3 AA289327 Human UCP  
 Aa289327 Human UCP  
 Aa28793 Tethered  
 Aaf91831 Breast-ca  
 Aaf91845 Breast-ca

# ALIGNMENTS

RESULT 1  
 AD081155/c  
 ID AD081155 standard; DNA; 6 BP.  
 XX  
 AC AD081155;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Prion protein polymorphic microsatellite marker consensus sequence #33.  
 XX

gene typing; polymorphic microsatellite loci; PML;  
 disease predisposition; microsatellite marker; prion disease;  
 KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
 KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;  
 KW microsatellite; ds.  
 XX

OS Synthetic.  
 XX  
 PN DE10236711-A1.  
 XX  
 PD 26-FEB-2004.  
 XX

PF 09-AUG-2002; 2002DE-01036711.  
 XX  
 PR 09-AUG-2002; 2002DE-01036711.  
 XX  
 XX (UYHO-) UNIV HOHENHEIM.  
 PA  
 XX Geldermann H, Preuss S, Han Y;  
 PI  
 XX WPI; 2004-215730/21.  
 DR

XX Typing genes that contain polymorphic microsatellite loci, useful for  
 PT identifying predisposition to disease, by amplification and determining  
 PT length of amplicons.  
 XX  
 PS Claim 9; Page 50; 64pp; German.  
 XX

CC The invention describes a method of typing (M1) a gene (I) that has one  
 CC or more polymorphic microsatellite loci (PML). The method comprises: PCR  
 CC amplification of at least one DNA region of (I) that includes PML, using  
 CC as template a DNA sample containing at least one segment of (I); and  
 CC determining the length of the resulting amplicon(s). Also described are:  
 CC a method of determining (M2) microsatellite markers (MM) for  
 CC predisposition to a disease, associated with a gene that includes one or  
 CC more PML; and prediagnosis (M3) of diseases associated with gene that  
 CC include PML. The method is used to identify microsatellite markers, in a  
 CC disease-related gene, that are associated with a predisposition to  
 CC diseases and for prediagnosis of such diseases, especially prion diseases  
 CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
 CC metabolic diseases; also to type genes that encode milk proteins  
 CC hormones or transcription factors. The method is simpler, quicker and  
 CC particularly less expensive than known methods based on sequencing. This  
 CC sequence represents a prion protein polymorphic microsatellite marker  
 CC consensus sequence.  
 XX

XX Sequence 6 BP; 3 A; 3 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
 Db 6 GTGTGT 1  
 RESULT 2  
 AAD17580/c  
 ID AAD17580 standard; DNA; 6 BP.  
 XX  
 AC AAD17580;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE AC repeat sequence #2 of 5' variation generator.  
 XX  
 KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;  
 KW endangered animal identification; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN EP130114-A1.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 03-MAR-2000; 2000EP-00200757.  
 XX  
 PR 03-MAR-2000; 2000EP-00200757.  
 XX  
 PA (VHAE-) VAN HAERINGEN LAB BV.  
 XX  
 PI Van Haringen H, Van Haringen WA;  
 XX  
 DR WPI; 2001-572636/65.  
 XX

PT Analyzing genomic DNA in a sample, useful for analyzing genes of  
 PT organisms (e.g. a species or individual) or identifying endangered  
 PT animals or plants, by using oligonucleotide primers comprising universal  
 PT variable fragments.  
 XX  
 PS Disclosure; Page 3; 23pp; English.  
 XX  
 CC The patent discloses a method and associated kit for analysing genomic  
 CC DNA in a sample. The method comprises conducting a nucleic acid  
 CC amplification on the genomic DNA in the sample using both first and  
 CC second oligonucleotide primer to produce DNA fragments based on repeat  
 CC sequences on at least one end of the genomic DNA. The first primer is a  
 CC 5' variation generator including a repeat sequence and at least one non-  
 CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment  
 CC generator starting within such a genetic distance that amplification of  
 CC the genomic DNA can be performed and preferably includes inosine. The  
 CC method is useful for the genetic analysis of an individual organism,  
 CC particularly of a species or individual. It is also useful for the rapid  
 CC and straight forward identification of endangered animals or plants. The  
 CC present DNA sequence is an AC repeat of 5' variation generator  
 XX  
 SQ Sequence 6 BP; 3 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
 Db 5 GTGTG 1

RESULT 3  
 ADR33261/c  
 ID ADR33261 standard; DNA; 6 BP.  
 XX  
 AC ADR33261;  
 XX



```

DT 04-NOV-2004 (first entry)
DE Human nicking agent target DNA #802.
XX
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX WO2004067765-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX
XX Example 1; Page 84; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX subspecies, and especially strains or individuals of the subspecies. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/quality control of
XX bacterial contamination, monitoring microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. This sequence
XX corresponds to nucleic acid used in the method of the invention.
XX
XX Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 83.3%; Score 5; DB 13; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TGTGT 6
XX |||||
XX Db 5 TGTGT 1
XX
XX RESULT 4
XX ADR33262/c
XX ID ADR33262 standard; DNA; 6 BP.
XX

```

```

AC ADR33262;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX DE Human nicking agent target DNA #803.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DNA fingerprinting; nosocomial infection; microbiological assay;
XX bacterial contamination; genome mapping; bioremediation.
XX
XX OS Homo sapiens.
XX WO2004067765-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX
XX Example 1; Page 84; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX subspecies, and especially strains or individuals of the subspecies. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/quality control of
XX bacterial contamination, monitoring microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. This sequence
XX corresponds to nucleic acid used in the method of the invention.
XX
XX Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 83.3%; Score 5; DB 13; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TGTGT 6
XX |||||
XX Db 5 TGTGT 1
XX
XX RESULT 5
XX AAQ78699
XX

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```

ID AAQ78699 standard; DNA; 6 BP.
XX
AC AAQ78699;
XX
DT 25-MAR-2003 (revised)
DT 06-JUN-1995 (first entry)
XX
DE Pistil gene promoter consensus sequence.
XX
KW Pistil; anther; gene expression; female sterile; male sterile;
KW S-locus glycoprotein; SLG; S-locus related gene; SLR1; promoter;
KW transgenic plant; crop improvement; da.
XX
OS Brassica sp.
XX
PN WO9425613-A1.
XX
PD 10-NOV-1994.
XX
PF 03-MAY-1994; 94WO-US004557.
XX
PR 03-MAY-1993; 93US-00054362.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Nasrallah ME, Nasrallah JB, Thorsness MK;
XX
DR WPI; 1994-358288/44.
XX
PT Isolated DNA elements directing pistil- or anther-specific gene
PT expression - used to cause female and male sterility in plants.
XX
PS Disclosure; Page 32; 54pp; English.
XX
CC Comparison of the promoter regions of Brassica sp. S-locus glycoprotein
CC SLG13, SLG2, SLG8 and S-locus related SLR1 genes (given in AAQ78703-06)
CC identified consensus sequences, which can be used as minimal promoter
CC elements for pistil- or anther-specific gene expression in plants. The
CC pistil-specific element has at least 70% homology to the consensus
CC elements given in AAQ78698-700. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 6 BP; 0 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
DB 1 GTTTGT 6

RESULT 6
ABN73213/c
ID ABN73213 standard; cDNA; 6 BP.
XX
AC ABN73213;
XX
DT 03-JUL-2002 (first entry)
XX
DE Bovine embryonic germ (EG) cell cDNA EST 000128a CONTIG 73.
XX
KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW development; gene; ss.
XX
OS Bos taurus.
XX
PN WO200194550-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018576.

Query Match 73.3%; Score 4.4; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
DB 1 GTTTGT 6

RESULT 7
AAS96420/c
ID AAS96420 standard; DNA; 5 BP.
XX
AC AAS96420;
XX
DT 26-FEB-2002 (first entry)
XX
DE Kozak sequence containing PCR primer.
XX
KW Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;
KW plant growth regulator; plant development; abiotic stress; biotic stress;
KW nutrient deprivation; pathogen attack; crop yield; PCR primer.
XX
OS Unidentified.
XX
PN WO200185946-A2.
XX
PD 15-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-IB001307.
XX
PR 12-MAY-2000; 2000US-0204045P.
XX
PA (CROP-) CROPDISEIGN NV.
XX
PI Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;
XX
DR WPI; 2002-062249/08.
XX
PT New cell cycle protein and nucleic acid molecule encoding it useful for
PT regulating cell cycle progression in plants and for identifying

```

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XX
PR 07-JUN-2000; 2000US-0209874P.
PR 06-JUN-2001; 2001US-00876143.
XX
PA (INFI-) INFIGEN INC.
XX
PI Eilertsen KJ, Pfister-Genskow M, Childs L;
XX
DR WPI; 2002-351289/38.
XX
PT An expressed sequence tag (EST), the expression of which, or its
PT complementary sequence, in a cell identifies the cell as a
PT developmentally competent or incompetent cell.
XX
PS Example 16; Page 129; 584pp; English.
XX
CC The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC totipotence in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotence. The molecules are also
CC useful for treating a disease in an animal by inducing development of one
CC or more cells of the animal into a specific cell type. The present
CC sequence represents a bovine EST which is given in the exemplification of
CC the present invention
XX
SQ Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
DB 6 GTTTTT 1

RESULT 7
AAS96420/c
ID AAS96420 standard; DNA; 5 BP.
XX
AC AAS96420;
XX
DT 26-FEB-2002 (first entry)
XX
DE Kozak sequence containing PCR primer.
XX
KW Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;
KW plant growth regulator; plant development; abiotic stress; biotic stress;
KW nutrient deprivation; pathogen attack; crop yield; PCR primer.
XX
OS Unidentified.
XX
PN WO200185946-A2.
XX
PD 15-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-IB001307.
XX
PR 12-MAY-2000; 2000US-0204045P.
XX
PA (CROP-) CROPDISEIGN NV.
XX
PI Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;
XX
DR WPI; 2002-062249/08.
XX
PT New cell cycle protein and nucleic acid molecule encoding it useful for
PT regulating cell cycle progression in plants and for identifying

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CC immunological assays to screen for, and to detect the presence of, either  
 CC a normal or a defective OP1 gene or gene product. ABK72533-ABK72593  
 CC represent the human OP1 gene and intron/exon splice junctions  
 XX

SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGTG 5  
 Db 2 TGTG 5

RESULT 10  
 ID ABS78161 standard; DNA; 6 BP.  
 XX ABS78161;  
 AC  
 XX  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #645.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.

OS Synthetic.  
 XX  
 XX WO200253141-A2.  
 PN  
 XX  
 XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.  
 PF  
 XX  
 XX 14-DEC-2000; 2000US-0255534P.  
 PR  
 XX  
 XX (COLE-) COLEY PHARM GROUP INC.

PA Bratzler RL;  
 PI  
 XX  
 XX WPI; 2002-566690/60.  
 DR  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 PT  
 XX  
 XX Claim 2; Page 31; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention

SQ Sequence 6 BP; 1 A; 1 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 6; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGT 4  
 Db 3 GTGT 6

RESULT 11  
 ACD99933  
 ID ACD99933 standard; DNA; 6 BP.  
 XX  
 XX ACD99933;  
 AC  
 XX  
 XX 25-SEP-2003 (first entry)  
 DT  
 XX  
 DE Immunostimulatory nucleic acid #619.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

OS Synthetic.  
 XX  
 XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.

XX Krieg AM, Berg DJ;  
 XX  
 XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 XX Disclosure; Page 25; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid

SQ Sequence 6 BP; 1 A; 1 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGT 4  
 Db 3 GTGT 6

RESULT 12  
 ADE14140  
 ID ADE14140 standard; DNA; 6 BP.  
 XX  
 XX ADE14140;  
 AC  
 XX  
 XX 29-JAN-2004 (first entry)

XX DE Optineurin promoter motif, repeat element or regulatory region #249.  
 XX DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
 KW SNP; glaucoma; progressive ocular hypertensive disorder;  
 KW glaucoma related disorder; motif; repeat element; regulatory region.  
 XX OS Homo sapiens.  
 XX US2003190617-A1.  
 XX 09-OCT-2003.  
 XX 06-MAR-2002; 2002US-00091281.  
 XX 06-MAR-2002; 2002US-00091281.  
 XX (SIEE/) SI E.  
 PA (RAYM/) RAYMOND V.  
 PA (MORI/) MORISSETTE J.  
 PI Raymond V, Morissette J, Si E;  
 DR WPI; 2003-864168/80.  
 XX New nucleic acid sequences of the optineurin gene are useful to detect  
 PT polymorphisms particularly single nucleotide polymorphisms in the  
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
 PT disorders.  
 XX Claim 11; SEQ ID NO 251; 159pp; English.  
 XX The invention relates to an isolated nucleic acid (N1) comprising at  
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
 CC promoter appearing as ADE13890. Also included are the optineurin promoter  
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
 CC promoter, a host cell comprising the promoter operably linked to a  
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
 CC in a promoter region of the optineurin gene, associated with a glaucoma  
 CC phenotype), detecting a SNP sequence variation in a sample containing  
 CC DNA, detecting the presence of an optineurin promoter sequence variation  
 CC in a sample containing DNA, determining the presence or increased  
 CC susceptibility to glaucoma or to a progressive ocular hypertensive  
 CC disorder resulting in loss of visual field in a patient (or the severity  
 CC or progression of glaucoma in a patient, comprising providing  
 CC amplification reaction primers that direct amplification of a selected  
 CC nucleic acid region containing the variation within the optineurin  
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
 CC capable of detecting a SNP located within an optineurin promoter, and  
 CC detecting the polymorphism). The invention is used to diagnose and  
 CC prognose glaucoma and also to treat glaucoma related disorders. The  
 CC present sequence is an optineurin promoter motif, repeat element or  
 CC putative regulatory region.  
 XX Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 66.7%; Score 4; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TGTG 5  
 ||||  
 Db 1 TGTG 4  
 RESULT 13  
 ADE14096  
 ID ADE14096 standard; DNA; 6 BP.  
 XX ADE14096;

XX 29-JAN-2004 (first entry)  
 DT Optineurin promoter motif, repeat element or regulatory region #205.  
 DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
 KW SNP; glaucoma; progressive ocular hypertensive disorder;  
 KW glaucoma related disorder; motif; repeat element; regulatory region.  
 XX OS Homo sapiens.  
 XX US2003190617-A1.  
 XX 09-OCT-2003.  
 XX 06-MAR-2002; 2002US-00091281.  
 XX 06-MAR-2002; 2002US-00091281.  
 XX (SIEE/) SI E.  
 PA (RAYM/) RAYMOND V.  
 PA (MORI/) MORISSETTE J.  
 PI Raymond V, Morissette J, Si E;  
 DR WPI; 2003-864168/80.  
 XX New nucleic acid sequences of the optineurin gene are useful to detect  
 PT polymorphisms particularly single nucleotide polymorphisms in the  
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
 PT disorders.  
 XX Claim 11; SEQ ID NO 207; 159pp; English.  
 XX The invention relates to an isolated nucleic acid (N1) comprising at  
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
 CC promoter appearing as ADE13890. Also included are the optineurin promoter  
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
 CC promoter, a host cell comprising the promoter operably linked to a  
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
 CC in a promoter region of the optineurin gene, associated with a glaucoma  
 CC phenotype), detecting a SNP sequence variation in a sample containing  
 CC DNA, detecting the presence of an optineurin promoter sequence variation  
 CC in a sample containing DNA, determining the presence or increased  
 CC susceptibility to glaucoma or to a progressive ocular hypertensive  
 CC disorder resulting in loss of visual field in a patient (or the severity  
 CC or progression of glaucoma in a patient, comprising providing  
 CC amplification reaction primers that direct amplification of a selected  
 CC nucleic acid region containing the variation within the optineurin  
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
 CC capable of detecting a SNP located within an optineurin promoter, and  
 CC detecting the polymorphism). The invention is used to diagnose and  
 CC prognose glaucoma and also to treat glaucoma related disorders. The  
 CC present sequence is an optineurin promoter motif, repeat element or  
 CC putative regulatory region.  
 XX Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 66.7%; Score 4; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TGTG 5  
 ||||  
 Db 1 TGTG 4  
 RESULT 14  
 ADE13916  
 ID ADE13916 standard; DNA; 6 BP.



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RESULT 16
ADEI4265
ID ADEI4265 standard; DNA; 6 BP.
XX AC ADEI4265;
XX DT 29-JAN-2004 (first entry)
XX DE Optineurin promoter motif, repeat element or regulatory region #374.
XX KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX KW SNP; glaucoma; progressive ocular hypertensive disorder;
XX KW glaucoma related disorder; motif; repeat element; regulatory region.
XX OS Homo sapiens.
XX PN US2003190617-A1.
XX PD 09-OCT-2003.
XX PF 06-MAR-2002; 2002US-00091281.
XX PR 06-MAR-2002; 2002US-00091281.
XX PA (SIEE/) SI E.
XX PA (RAYM/) RAYMOND V.
XX PA (MORI/) MORISSETTE J.
XX PI Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
XX PT New nucleic acid sequences of the optineurin gene are useful to detect
XX PT polymorphisms particularly single nucleotide polymorphisms in the
XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
XX PT disorders.
XX PS Claim 11; SEQ ID NO 376; 159pp; English.
XX CC The invention relates to an isolated nucleic acid (N1) comprising at
XX CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX CC promoter appearing as ADEI3890. Also included are the optineurin promoter
XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin
XX CC promoter, a host cell comprising the promoter operably linked to a
XX CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX CC in a promoter region of the optineurin gene, associated with a glaucoma
XX CC phenotype), detecting a SNP sequence variation in a sample containing
XX CC DNA, detecting the presence of an optineurin promoter sequence variation
XX CC in a sample containing DNA, determining the presence or increased
XX CC susceptibility to glaucoma or to a progressive ocular hypertensive
XX CC disorder resulting in loss of visual field in a patient (or the severity
XX CC or progression of glaucoma in a patient, comprising providing
XX CC amplification reaction primers that direct amplification of a selected
XX CC nucleic acid region containing the variation within the optineurin
XX CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX CC obtaining a sample containing human genomic DNA, providing a nucleic acid
XX CC capable of detecting a SNP located within an optineurin promoter, and
XX CC detecting the polymorphism). The invention is used to diagnose and
XX CC prognose glaucoma and also to treat glaucoma related disorders. The
XX CC present sequence is an optineurin promoter motif, repeat element or
XX CC putative regulatory region.
XX SQ Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTG 5
|||||

RESULT 17
ADES2744
ID ADES2744 standard; DNA; 6 BP.
XX AC ADES2744;
XX DT 29-JAN-2004 (first entry)
XX DE Oligonucleotide SEQ ID 110.
XX KW DNA-binding protein; interferon-activatable protein; ss.
XX OS Synthetic.
XX PN WO2003089466-A1.
XX PD 30-OCT-2003.
XX PF 18-APR-2003; 2003WO-JP004981.
XX PR 19-APR-2002; 2002JP-00117840.
XX PR 30-APR-2002; 2002JP-00128418.
XX PR 30-APR-2002; 2002JP-00128779.
XX PR 04-DEC-2002; 2002JP-00352469.
XX PA (RIKE) RIKEN KK.
XX PA (DNAP-) DNAFORM KK.
XX PA (MITU) MITSUBISHI CHEM CORP.
XX PI Hayaahizaki Y, Kamiya M, Kubodera H;
XX WPI; 2004-011681/01.
XX PT Proteins with DNA binding activity and substances that affect their
XX PT activity or expression, useful for treating associated disorders.
XX PS Example 9; SEQ ID NO 110; 237pp; Japanese.
XX CC The present invention relates to novel proteins (ADES2648-ADES2660,
XX CC ADES2670 and ADES2672) and their coding sequences (ADES2635-ADES2647,
XX CC ADES2669 and ADES2671). The proteins have a DNA-binding activity or an
XX CC interferon-activatable protein (IAP)-like activity. The present
XX CC oligonucleotide is related to AML1a.
XX SQ Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTG 5
|||||
1 TTGTG 4

RESULT 18
ADK14289/c
ID ADK14289 standard; DNA; 6 BP.
XX AC ADK14289;
XX DT 20-MAY-2004 (first entry)
XX DE Candida promoter motif URS1-like sequence SEQ ID NO:18.
XX KW Candida tropicalis; CYP gene promoter; modified CYP gene promoter;
XX KW yeast host cell; URS1; URS2; URS1-like; URS2-like;
XX KW beta oxidation pathway; omega oxidation pathway; gene; ds.
XX OS Candida sp.
```

XX WO2004016756-A2.  
 PN  
 XX  
 XX 26-FEB-2004.  
 PD  
 XX  
 XX 15-AUG-2003; 2003WO-US025545.  
 PF  
 XX 16-AUG-2002; 2002US-0403979P.  
 PR  
 XX 14-AUG-2003; 2003US-00640962.  
 PR  
 XX (COGN-) COGNIS CORP.  
 PA  
 XX Wilson RC, Craft DL, Zhang Y, Stavenhagen JB;  
 PI  
 XX WPI; 2004-203787/19.  
 DR  
 XX New modified Candida tropicalis CYP gene promoters comprising nucleotide  
 PT sequence for a CYP gene promoter, useful for modulating expression of a  
 PT protein of the beta or omega oxidation pathway in a yeast cell.  
 PT  
 XX Claim 4; SEQ ID NO 18; 99pp; English.  
 PS  
 XX The present invention describes modified Candida tropicalis CYP gene  
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also  
 CC described: (1) a yeast host cell comprising the modified Candida  
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression  
 CC of a protein of the beta or omega oxidation pathway in a yeast cell.  
 CC comprising: (a) isolating a CYP gene promoter from C. tropicalis; (b)  
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like  
 CC or URS2-like sequences; (c) operably linking the modified promoter with a  
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)  
 CC transforming a yeast cell with the modified promoter operably linked to  
 CC the coding sequence; and (e) growing the yeast under conditions  
 CC favourable for expression of the coding sequence under the control of the  
 CC modified promoter. The promoters are useful for modulating expression of  
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 XX Sequence 6 BP; 3 A; 2 C; 1 G; 0 T; 0 U; 0 Other;  
 SQ

Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
 DB 4 GTGT 1

RESULT 19  
 ADK14312/c  
 ID ADK14312 standard; DNA; 6 BP.  
 AC  
 XX ADK14312;  
 AC  
 XX 20-MAY-2004 (first entry)  
 DT  
 XX Candida promoter motif URS2-like sequence SEQ ID NO:41.  
 DE  
 XX Candida tropicalis; CYP gene promoter; modified CYP gene promoter;  
 KW yeast host cell; URS1; URS2; URS1-like; URS2-like;  
 KW beta oxidation pathway; omega oxidation pathway; gene; ds.  
 KW  
 XX Candida sp.  
 OS  
 XX WO2004016756-A2.  
 PN  
 XX 26-FEB-2004.  
 PD  
 XX 15-AUG-2003; 2003WO-US025545.  
 PF  
 XX 16-AUG-2002; 2002US-0403979P.  
 PR  
 XX 14-AUG-2003; 2003US-00640962.  
 PR

XX (COGN-) COGNIS CORP.  
 PA  
 XX Wilson RC, Craft DL, Zhang Y, Stavenhagen JB;  
 PI  
 XX WPI; 2004-203787/19.  
 DR  
 XX New modified Candida tropicalis CYP gene promoters comprising nucleotide  
 PT sequence for a CYP gene promoter, useful for modulating expression of a  
 PT protein of the beta or omega oxidation pathway in a yeast cell.  
 PT  
 XX Claim 9; SEQ ID NO 41; 99pp; English.  
 PS  
 XX The present invention describes modified Candida tropicalis CYP gene  
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also  
 CC described: (1) a yeast host cell comprising the modified Candida  
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression  
 CC of a protein of the beta or omega oxidation pathway in a yeast cell  
 CC comprising: (a) isolating a CYP gene promoter from C. tropicalis; (b)  
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like  
 CC or URS2-like sequences; (c) operably linking the modified promoter with a  
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)  
 CC transforming a yeast cell with the modified promoter operably linked to  
 CC the coding sequence; and (e) growing the yeast under conditions  
 CC favourable for expression of the coding sequence under the control of the  
 CC modified promoter. The promoters are useful for modulating expression of  
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 XX Sequence 6 BP; 2 A; 3 C; 1 G; 0 T; 0 U; 0 Other;  
 SQ

Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
 DB 4 GTGT 1

RESULT 20  
 ADL09233/c  
 ID ADL09233 standard; DNA; 6 BP.  
 AC  
 XX ADL09233;  
 AC  
 XX 20-MAY-2004 (first entry)  
 DT  
 XX SP6 promoter DNA fragment #12.  
 DE  
 XX amplification; primer; promoter; RNA polymerase; ds.  
 KW  
 XX Enterobacteria phage SP6.  
 OS  
 XX WO2004016757-A2.  
 PN  
 XX 26-FEB-2004.  
 PD  
 XX 15-AUG-2003; 2003WO-US025564.  
 PF  
 XX 16-AUG-2002; 2002US-0404075P.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Karin M, Park JM;  
 PI  
 XX WPI; 2004-203788/19.  
 DR  
 XX Producing a nucleic acid sequence comprises amplifying double stranded  
 PT DNA sequence in the presence of first and second primers to produce a  
 PT first nucleic acid molecule having the double stranded DNA sequence in a  
 PT head to head orientation.  
 PT  
 XX



PS Disclosure; SEQ ID NO 49; 55pp; English.

XX This invention describes a novel method for producing a nucleic acid  
CC sequence comprising amplifying the double stranded DNA sequence of  
CC interest in the presence of the first primer and the second primer to  
CC produce a first nucleic acid molecule comprising the double stranded DNA  
CC sequence of interest flanked by at least a portion of the first promoter  
CC in a head to head orientation. The method involves providing RNA  
CC polymerase that specifically binds to the first promoter and contacting  
CC the first nucleic acid molecule with the RNA polymerase to produce double  
CC stranded RNA that is complementary to the double stranded DNA sequence of  
CC interest. This method further comprises providing a third primer  
CC complementary to at least a portion of the first promoter and amplifying  
CC the first nucleic acid molecule produced in the presence of the third  
CC primer to produce a second nucleic acid molecule comprising the double  
CC stranded DNA sequence of interest flanked by the first promoter in a head  
CC to head orientation. The method further comprises providing RNA  
CC polymerase that specifically binds to the first promoter and contacting  
CC the second nucleic acid molecule with the RNA polymerase to produce  
CC double stranded RNA that is complementary to the double stranded DNA  
CC sequence of interest. The second strand of the double-stranded DNA  
CC sequence of interest comprises at least a portion of a second promoter.  
CC The second promoter is different from the first promoter. The first  
CC strand of the double stranded DNA comprises a nucleotide sequence linked to the 3' end of the  
CC first promoter, and the first primer further comprises a second sequence  
CC complementary to the nucleotide sequence, where the second sequence is  
CC linked to the 3' end of the first sequence of the first primer. The first  
CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The  
CC first sequence comprises a second primer complementary to at least a  
CC portion of a promoter. The methods and kits are useful for producing  
CC nucleic acid sequences as powerful alternative tools for functional  
CC genomics.

XX SQ Sequence 6 BP; 2 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
Db 5 GTGT 2

RESULT 21  
ADO05792/c  
ID ADO05792 standard; DNA; 6 BP.  
XX ADO05792;  
XX 15-JUL-2004 (first entry)  
XX Telomere-specific PNA-labelled probe repeat fragment, SEQ ID 6.  
DE PNA; peptide nucleic acid; telomere length assay; in vitro fertilization;  
XX telomere; quantitative fluorescent in situ hybridization; Q-FISH;  
KW aneuploidy; probe; ss.  
XX Synthetic.  
OS WO2004035597-A2.  
XX 29-APR-2004.  
XX 13-OCT-2003; 2003WO-US032672.  
PF 16-OCT-2002; 2002US-0419071P.  
XX 07-MAR-2003; 2003US-0452741P.  
XX (WOME-) WOMEN & INFANTS HOSPITAL RHODE ISLAND.  
PA Keefe DL;

XX WPI; 2004-348432/32.  
XX Determining the risk of reproductive failure or aneuploidy in an oocyte,  
PT useful for in vitro fertilization purposes, comprises measuring the  
PT telomere length of a chromosome obtained from the oocyte.  
XX Claim 49; Page 23; 47pp; English.  
XX The invention relates to determining the risk of reproductive failure or  
CC aneuploidy in a cell from a subject. The method involves obtaining at  
CC least one chromosome from the cell, measuring telomere length of the  
CC chromosome, and comparing the measured length of the telomere to the  
CC standardized average length of a control telomere to determine the risk  
CC of reproductive failure or aneuploidy in the cell. In determining the  
CC risk of reproductive failure and/or aneuploidy in a cell, the cell is an  
CC oocyte, an oocyte representative of a population of oocytes, a polar body  
CC from a fertilized oocyte, or a polar body from an unfertilized oocyte.  
CC Preferably, the cell is an oocyte. Selecting a fertilized oocyte with a  
CC low risk of reproductive failure or aneuploidy for in vitro fertilization  
CC comprises obtaining at least one chromosome from the polar body of the  
CC fertilized oocyte, measuring telomere length of the chromosome, and  
CC comparing the measured length of the telomere to the standardized average  
CC length of a control telomere to select a fertilized oocyte with a low  
CC risk of reproductive failure for in vitro fertilization. In the above  
CC methods, a labelled telomere-specific probe is hybridized to the  
CC chromosome prior to measuring telomere length of the chromosome. The  
CC probe is hybridized to telomere repeats. The probe is peptide nucleic  
CC acid (PNA)-labelled. The telomere is measured using quantitative  
CC fluorescent in situ hybridization (Q-FISH) analysis. In vitro  
CC fertilization comprises selecting a fertilized oocyte cited above and  
CC implanting the selected oocyte in the subject. The methods are useful for  
CC in vitro fertilization. The kit and methods may also be used for  
CC assessing the risk of reproductive failure and/or aneuploidy. Sequences  
CC ADO05788-ADO05795 represent specific examples of repeat fragments  
CC contained in the telomere-specific PNA-labelled probes.

XX SQ Sequence 6 BP; 2 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5  
Db 6 TGTG 3

RESULT 22  
ADR35664/c  
ID ADR35664 standard; DNA; 6 BP.  
XX ADR35664;  
XX 04-NOV-2004 (first entry)  
XX Human nicking agent DNA containing BstNBI restriction site #2084.  
DE ss; nicking agent; assay panel; diagnosis; expression pattern;  
XX DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bio remediation.  
XX Homo sapiens.  
OS WO2004067765-A2.  
XX 12-AUG-2004.  
PD 29-JAN-2004; 2004WO-US002720.  
XX 29-JAN-2003; 2003US-0443811P.  
XX (KECK-) KECK GRADUATE INST.

XX Van Ness J, Galas DJ, Van Ness LK;  
 PI WPI; 2004-581010/56.  
 DR  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX  
 PS Example 3; Page 105-219; 238pp; English.  
 XX  
 CC The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR3581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.  
 XX  
 SQ Sequence 6 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 1 Other;  
 Query Match 66.7%; Score 4; DB 13; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GTGTGT 6  
 Db | : |||  
 6 GASTGT 1  
 RESULT 23  
 ID ADR35687  
 XX ADR35687 standard; DNA; 6 BP.  
 AC ADR35687;  
 XX  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX Human nicking agent DNA containing BstNBI restriction site #2107.  
 DE  
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 OS  
 XX Homo sapiens.  
 XX WO2004067765-A2.  
 XX  
 XX 12-AUG-2004.  
 PD  
 XX 29-JAN-2004; 2004WO-US002720.  
 PF  
 XX

PR 29-JAN-2003; 2003US-0443811P.  
 XX (KECK-) KECK GRADUATE INST.  
 XX  
 PI Van Ness J, Galas DJ, Van Ness LK;  
 XX WPI; 2004-581010/56.  
 DR  
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 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX  
 PS Example 3; Page 105-219; 238pp; English.  
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 CC The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
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 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
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 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
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 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR3581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.  
 XX  
 SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;  
 Query Match 66.7%; Score 4; DB 13; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GTGTGT 6  
 Db | : |||  
 1 GASTGT 6  
 RESULT 24  
 ID ADR35663/c  
 XX ADR35663 standard; DNA; 6 BP.  
 AC ADR35663;  
 XX  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX Human nicking agent DNA containing BstNBI restriction site #2083.  
 DE  
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 OS  
 XX Homo sapiens.  
 XX WO2004067765-A2.  
 XX  
 XX 12-AUG-2004.  
 PD



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XX Homo sapiens.
OS WO2004067765-A2.
XX 12-AUG-2004.
XX 29-JAN-2004; 2004WO-US002720.
XX 29-JAN-2003; 2003US-0443811P.
XX (KECK-) KECK GRADUATE INST.
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX Example 3; Page 105-219; 238pp; English.
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
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CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
SQ Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db | :|||
1 GASTGT 6

RESULT 27
ADR35665/c
ID ADR35665 standard; DNA; 6 BP.
XX ADR35665;
XX ADR35665;
XX 04-NOV-2004 (first entry)
XX Human nicking agent DNA containing BstNBI restriction site #2085.
XX

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KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX Homo sapiens.
OS WO2004067765-A2.
XX 12-AUG-2004.
XX 29-JAN-2004; 2004WO-US002720.
XX 29-JAN-2003; 2003US-0443811P.
XX (KECK-) KECK GRADUATE INST.
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX Example 3; Page 105-219; 238pp; English.
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
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CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
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CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX Sequence 6 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
SQ Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db | :|||
6 GASTGT 1

RESULT 28
ADR35666/c
ID ADR35666 standard; DNA; 6 BP.
XX ADR35666;
XX ADR35666;
XX 04-NOV-2004 (first entry)
XX

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```
XX DE Human nicking agent DNA containing BstNBI restriction site #2086.
XX KW ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX PN WO2004067765-A2.
XX PD 12-AUG-2004.
XX PF 29-JAN-2004; 2004WO-US002720.
XX PR 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX DR WPI; 2004-581010/56.
XX PT Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PS conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
XX CC family of initiating oligonucleotide fragments to a characterization
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XX CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
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XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX CC subpopulations, and especially strains or individuals of the subspecies. It
XX CC is especially useful for identifying different bacterial strains involved
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XX CC diagnosing bacterial disease in plants and humans, monitoring for
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XX CC food for bacterial contamination, monitoring quality assurance/quality control of
XX CC bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTGTGT 6
XX | :|||
XX 6 GASTGT 1
XX
XX Db
XX
XX RESULT 29
XX ADR35669
XX ID ADR35669 standard; DNA; 6 BP.
XX
```

```
AC ADR35669;
XX 04-NOV-2004 (first entry)
XX Human nicking agent DNA containing BstNBI restriction site #2089.
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX PN WO2004067765-A2.
XX PD 12-AUG-2004.
XX PF 29-JAN-2004; 2004WO-US002720.
XX PR 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX DR WPI; 2004-581010/56.
XX PT Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PS conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
XX CC family of initiating oligonucleotide fragments to a characterization
XX CC process to thus provide results. The method is useful for creating an
XX CC assay panel of diagnostic oligonucleotides that can identify any organism
XX CC or individual. The method is useful for characterizing other DNA
XX CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX CC The method, kit or composition is useful for identifying the source
XX CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX CC non-human animal or human. The method is particularly useful for rapidly
XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX CC subpopulations, and especially strains or individuals of the subspecies. It
XX CC is especially useful for identifying different bacterial strains involved
XX CC in e.g., nosocomial infections. Furthermore, the method is useful for
XX CC diagnosing bacterial disease in plants and humans, monitoring for
XX CC bacterial content and/or contamination in the environment, monitoring
XX CC food for bacterial contamination, monitoring quality assurance/quality control of
XX CC bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTGTGT 6
XX | :|||
XX 1 GASTGT 6
XX
XX Db
XX
XX RESULT 30
```

AAZ10696/c  
ID AAZ10696 standard; DNA; 5 BP.  
XX  
AC AAZ10696;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
XX Oligonucleotide sequence that increases p53 activity in a cell.  
DE  
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KW skin cancer; ss.  
XX  
OS Synthetic.  
XX  
PN GB2336157-A.  
XX  
PD 13-OCT-1999.  
XX  
PF 24-MAR-1999; 99GB-00006758.  
XX  
PR 26-MAR-1998; 98US-00048927.  
XX  
PA (UYBO-) UNIV BOSTON.  
XX  
PI Gilchrist BA, Yaar M, Eller M;  
XX  
DR WPI; 1999-543520/46.  
XX  
PT DNA fragments useful for increasing p53 activity in a cell and reducing  
PT susceptibility to UV-induced hyperproliferative diseases.  
XX  
PS Claim 11; Page 30; 44pp; English.  
XX  
CC AAZ10692-97 represent DNA fragments that are used for increasing p53  
CC activity in a cell. The oligonucleotides are UV mimetics and protect  
CC cells against subsequent exposure to UV-irradiation or chemicals. The  
CC oligonucleotides are useful for increasing p53 activity in a cell,  
CC reducing the susceptibility to UV-induced hyperproliferative diseases,  
CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,  
CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and  
CC reducing susceptibility to skin cancer  
XX  
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 56.7%; Score 3.4; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. NO. 1.2e+09;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GTGTG 5  
Db 5 GRATG 1  
  
Search completed: July 20, 2005, 22:58:57  
Job time : 197.4 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds

(without alignments)  
169.325 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 ggtgtg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hlc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gssi:\*  
9: gb\_gss2:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| C 1        | 6     | 100.0       | 6      | CA851767 | CA851767 D17C12_E2 |
| C 2        | 4.4   | 73.3        | 6      | CF309881 | CF309881 ABF--04-E |
| C 3        | 4     | 66.7        | 6      | CF302557 | CF302557 7LEAF--08 |
| C 4        | 3.4   | 56.7        | 5      | CL423849 | CL423849 01S0750-0 |
| C 5        | 3.4   | 56.7        | 5      | CL685110 | CL685110 PRI0140b  |
| C 6        | 3.4   | 56.7        | 6      | CF312755 | CF312755 ABF--08-K |
| C 7        | 3.4   | 56.7        | 6      | CF332957 | CF332957 JMT--01-K |
| C 8        | 3.4   | 56.7        | 6      | CL680271 | CL680271 PRI0128C  |
| C 9        | 3     | 50.0        | 3      | CL423861 | CL423861 01S0750-0 |
| C 10       | 3     | 50.0        | 4      | CF318871 | CF318871 HD--09-C1 |
| C 11       | 3     | 50.0        | 4      | CF324308 | CF324308 HDN--06-D |
| C 12       | 3     | 50.0        | 4      | CO785960 | CO785960 B285A_B0  |
| C 13       | 3     | 50.0        | 5      | CF297897 | CF297897 7LEAF--01 |
| C 14       | 3     | 50.0        | 5      | CF300956 | CF300956 7LEAF--05 |
| C 15       | 3     | 50.0        | 5      | CF302927 | CF302927 7LEAF--08 |
| C 16       | 3     | 50.0        | 5      | CF307842 | CF307842 ABF--01-G |
| C 17       | 3     | 50.0        | 5      | CF318944 | CF318944 HD--09-E0 |
| C 18       | 3     | 50.0        | 5      | CF323326 | CF323326 HDN--03-I |
| C 19       | 3     | 50.0        | 5      | CF333993 | CF333993 JMT--03-B |
| C 20       | 3     | 50.0        | 5      | CF930992 | CF930992 CF--05-R  |
| C 21       | 3     | 50.0        | 6      | CA850905 | CA850905 D07H12_O2 |
| C 22       | 3     | 50.0        | 6      | CA851633 | CA851633 D15H03_O1 |
| C 23       | 3     | 50.0        | 6      | CF323984 | CF323984 HDN--05-E |
| C 24       | 3     | 50.0        | 6      | CF339252 | CF339252 RCL1--04- |

|      |     |      |   |   |          |                    |
|------|-----|------|---|---|----------|--------------------|
| 25   | 3   | 50.0 | 6 | 9 | CL687157 | CL687157 PRI0146a  |
| 26   | 2.4 | 40.0 | 4 | 7 | CF318085 | CF318085 HD--07-P2 |
| 27   | 2.4 | 40.0 | 4 | 8 | BZ382195 | BZ382195 SALK_1179 |
| 28   | 2.4 | 40.0 | 5 | 6 | CA850981 | CA850981 D08H03_F1 |
| 29   | 2.4 | 40.0 | 5 | 7 | CF314074 | CF314074 HD--02-H0 |
| C 30 | 2.4 | 40.0 | 5 | 7 | CF327578 | CF327578 NACL--02- |
| C 31 | 2.4 | 40.0 | 5 | 9 | CL667999 | CL667999 PRI0156C  |
| 32   | 2.4 | 40.0 | 5 | 9 | CL680087 | CL680087 PRI0127d  |
| C 33 | 2.4 | 40.0 | 5 | 6 | CA851592 | CA851592 D15D09_G2 |
| C 34 | 2.4 | 40.0 | 6 | 6 | CA853780 | CA853780 B12B09_se |
| C 35 | 2.4 | 40.0 | 6 | 7 | CF310635 | CF310635 ABF--05-G |
| C 36 | 2.4 | 40.0 | 6 | 7 | CF338772 | CF338772 RCL1--02- |
| C 37 | 2.4 | 40.0 | 6 | 9 | CL679615 | CL679615 PRI0126C  |
| C 38 | 2.4 | 40.0 | 6 | 9 | CL682618 | CL682618 PRI0134C  |
| C 39 | 2.4 | 40.0 | 6 | 9 | CL694328 | CL694328 PRI0163d  |
| C 40 | 2   | 33.3 | 2 | 7 | CF301411 | CF301411 7LEAF--06 |
| C 41 | 2   | 33.3 | 2 | 7 | CF306288 | CF306288 HDAL--03- |
| C 42 | 2   | 33.3 | 2 | 7 | CF331310 | CF331310 NACL--07- |
| C 43 | 2   | 33.3 | 2 | 7 | CF333014 | CF333014 JMT--01-L |
| C 44 | 2   | 33.3 | 2 | 7 | CO792627 | CO792627 NT015C_D1 |
| C 45 | 2   | 33.3 | 2 | 9 | CL661289 | CL661289 PRI0139b  |
| C 46 | 2   | 33.3 | 2 | 9 | CL670560 | CL670560 PRI0162b  |
| C 47 | 2   | 33.3 | 2 | 9 | CL682684 | CL682684 PRI0134C  |
| C 48 | 2   | 33.3 | 2 | 9 | CL688205 | CL688205 PRI0148d  |
| C 49 | 2   | 33.3 | 2 | 9 | CL872635 | CL872635 abe83q10  |
| C 50 | 2   | 33.3 | 2 | 9 | CL874640 | CL874640 abe96h02  |
| C 51 | 2   | 33.3 | 2 | 9 | CL876415 | CL876415 abf13c11  |
| C 52 | 2   | 33.3 | 2 | 9 | CL883717 | CL883717 abf63c08  |
| C 53 | 2   | 33.3 | 3 | 1 | AL043149 | AL043149 DKF2P434E |
| C 54 | 2   | 33.3 | 3 | 6 | CA850938 | CA850938 D08D06_H1 |
| C 55 | 2   | 33.3 | 3 | 6 | CA851961 | CA851961 D19E05_I1 |
| C 56 | 2   | 33.3 | 3 | 7 | CF305942 | CF305942 HDAL--02- |
| C 57 | 2   | 33.3 | 3 | 7 | CF308858 | CF308858 ABF--02-N |
| C 58 | 2   | 33.3 | 3 | 7 | CF310006 | CF310006 ABF--04-H |
| C 59 | 2   | 33.3 | 3 | 7 | CF311628 | CF311628 ABF--06-O |
| C 60 | 2   | 33.3 | 3 | 7 | CF313258 | CF313258 HD--01-F0 |
| C 61 | 2   | 33.3 | 3 | 7 | CF315632 | CF315632 HD--04-K0 |
| C 62 | 2   | 33.3 | 3 | 7 | CF317717 | CF317717 HD--07-I0 |
| C 63 | 2   | 33.3 | 3 | 7 | CF338538 | CF338538 RCL1--01- |
| C 64 | 2   | 33.3 | 3 | 7 | CF339357 | CF339357 RCL1--04- |
| C 65 | 2   | 33.3 | 3 | 7 | CF339421 | CF339421 RCL1--04- |
| C 66 | 2   | 33.3 | 3 | 7 | CF339646 | CF339646 RCL1--05- |
| C 67 | 2   | 33.3 | 3 | 7 | CF340077 | CF340077 RCL1--06- |
| C 68 | 2   | 33.3 | 3 | 7 | CF372478 | CF372478 CSECS052H |
| C 69 | 2   | 33.3 | 3 | 7 | CK575874 | CK575874 IST_WIS_9 |
| C 70 | 2   | 33.3 | 3 | 7 | CK632435 | CK632435 AM1-AP000 |
| C 71 | 2   | 33.3 | 3 | 7 | CO793948 | CO793948 NT019B_A0 |
| C 72 | 2   | 33.3 | 3 | 7 | CO819398 | CO819398 CSECS153H |
| C 73 | 2   | 33.3 | 3 | 7 | CV179297 | CV179297 CSECS016C |
| C 74 | 2   | 33.3 | 3 | 9 | CL656746 | CL656746 PRI0127b  |
| C 75 | 2   | 33.3 | 3 | 9 | CL664603 | CL664603 PRI0147C  |
| C 76 | 2   | 33.3 | 3 | 9 | CL668376 | CL668376 PRI0157C  |
| C 77 | 2   | 33.3 | 3 | 9 | CL669749 | CL669749 PRI0160b  |
| C 78 | 2   | 33.3 | 3 | 9 | CL679295 | CL679295 PRI0125C  |
| C 79 | 2   | 33.3 | 3 | 9 | CL884066 | CL884066 abf65h10  |
| C 80 | 2   | 33.3 | 3 | 9 | AL039425 | AL039425 DKF2P434L |
| C 81 | 2   | 33.3 | 4 | 1 | AL045617 | AL045617 KFE2P434O |
| C 82 | 2   | 33.3 | 4 | 1 | AL045617 | AL045617 KFE2P434O |
| C 83 | 2   | 33.3 | 4 | 6 | CA850965 | CA850965 D08F10_L2 |
| C 84 | 2   | 33.3 | 4 | 6 | CA850974 | CA850974 D08G08_N2 |
| C 85 | 2   | 33.3 | 4 | 7 | CF300707 | CF300707 7LEAF--05 |
| C 86 | 2   | 33.3 | 4 | 7 | CF306914 | CF306914 HDAL--05- |
| C 87 | 2   | 33.3 | 4 | 7 | CF317847 | CF317847 HD--07-L0 |
| C 88 | 2   | 33.3 | 4 | 7 | CF324158 | CF324158 HDN--05-M |
| C 89 | 2   | 33.3 | 4 | 7 | CF333086 | CF333086 JMT--01-N |
| C 90 | 2   | 33.3 | 4 | 7 | CF335346 | CF335346 JMT--04-P |
| C 91 | 2   | 33.3 | 4 | 7 | CF336880 | CF336880 JMT--07-B |
| C 92 | 2   | 33.3 | 4 | 7 | CF338536 | CF338536 RCL1--01- |
| C 93 | 2   | 33.3 | 4 | 7 | CF340391 | CF340391 RCL1--07- |
| C 94 | 2   | 33.3 | 4 | 7 | CF340642 | CF340642 RCL1--08- |
| C 95 | 2   | 33.3 | 4 | 7 | CF340653 | CF340653 RCL1--08- |
| C 96 | 2   | 33.3 | 4 | 8 | BZ424869 | BZ424869 100020550 |
| C 97 | 2   | 33.3 | 4 | 9 | CL655267 | CL655267 PRI0122d  |

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98 2 33.3 4 9 CL670570 CL670570 PRI0162C
99 2 33.3 4 9 CL889653 CL889653 abf96d10-
c 100 2 33.3 5 1 AL042985 AL042985 DXFZP434N

ALIGNMENTS

RESULT 1
LOCUS CA851767
DEFINITION D17C12_E24_06.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D17C12 5', mRNA sequence.
ACCESSION CA851767
VERSION CA851767.1 GI:33388560
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
REFERENCE Alkharouf,N.W., Khan,R. and Matthews,B.F.
AUTHORS Analysis of expressed sequence tags from roots of resistant soybean
infectd by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
source
1. .6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D17C12"
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/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred.No. 6.3e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTGT 6
Db |||||
6 GTGTGT 1

RESULT 2
LOCUS CF309881/c
DEFINITION ABF--04-E05_b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-E05, mRNA sequence.
ACCESSION CF309881
VERSION CF309881.1 GI:33681642
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
REFERENCE 1 (bases 1 to 6)

```

```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--04-E05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 73.3%; Score 4.4; DB 7; Length 6;
Best Local Similarity 83.3%; Pred.No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGTGT 6
Db |||||
6 GTTGT 1

RESULT 3
LOCUS CF302557/c
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-D07, mRNA
sequence.
ACCESSION CF302557
VERSION CF302557.1 GI:33674318
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--08-D07"
/tissue_type="leaf"

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/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGT 4
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Db 6 GTGT 3

RESULT 4
CL423849/c
LOCUS
DEFINITION
CL423849
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 5)
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
AUTHORS
TITLE
Sequence tagged transposon insertions from the UniformMu maize
population
JOURNAL
COMMENT
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu
line: 01S0750-04, Primer set: C
Class: transposon insertion site.
Class: transposon insertion site.
FEATURES
source
1..5
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0750-04C1-A12"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 56.7%; Score 3.4; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGT 5
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Db 5 GAGTG 1

RESULT 5
CL685110
LOCUS
DEFINITION
CL685110
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
AUTHORS
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

LOCUS
DEFINITION
CL685110
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 5)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AUTHORS
TITLE
AppaB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL
COMMENT
Contact: Sommer RJ
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Class: fosmid ends.
FEATURES
source
1..5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 56.7%; Score 3.4; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGT 5
 ||||
Db 1 GCGTG 5

RESULT 6
CF312755
LOCUS
DEFINITION
CF312755
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
AUTHORS
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
source
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF-08-K07"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /cna_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

ORIGIN
 Query Match
 Best Local Similarity 56.7%; Score 3.4; DB 7; Length 6;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
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Db 2 GGTG 6

RESULT 7
CF332957/c
LOCUS
DEFINITION
 CF332957 6 bp mRNA linear EST 18-AUG-2003
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT-01-K14, mRNA sequence.
ACCESSION
 CF332957
VERSION
 CF332957.1 GI:33814152
KEYWORDS
 EST.
SOURCE
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
 1 (bases 1 to 6)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="JMT-01-K14"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /cna_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

ORIGIN
 Query Match
 Best Local Similarity 56.7%; Score 3.4; DB 7; Length 6;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
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Db 2 GGTG 6

RESULT 8
CL680271
LOCUS
DEFINITION
 CL680271 6 bp DNA linear GSS 09-JUL-2004
 PRI0128C B04.2 - PRI0128C.BR (6) Mixed stage fosmid library of P.
 pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
ACCESSION
 CL680271
VERSION
 CL680271.1 GI:50187114
KEYWORDS
 GSS.
SOURCE
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
REFERENCE
 1 (bases 1 to 6)
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
 AppaDB: an AcedB database for the nematode satellite organism
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: raif.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.
FEATURES
source
 Location/Qualifiers
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 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strains="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
 Query Match
 Best Local Similarity 56.7%; Score 3.4; DB 9; Length 6;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6
 |||
Db 2 TCGT 6

RESULT 9
CL423861/c
LOCUS
DEFINITION
 CL423861 3 bp DNA linear GSS 16-MAR-2004
 01S0750-04C1-C02 UniformMu MutAIL Library Zea mays genomic clone
 01S0750-04C1-C02, genomic survey sequence.
ACCESSION
 CL423861
VERSION
 CL423861.1 GI:45501905
KEYWORDS
 GSS.
SOURCE
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
 1 (bases 1 to 3)
 Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
 Sequence tagged transposon insertions from the UniformMu maize

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```

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGT 4
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Db 3 TGT 1

RESULT 15
LOCUS CF302927
DEFINITION 7LEAF--08-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-N23, mRNA
sequence.
ACCESSION CF302927
VERSION 1 GI:33674688
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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cDNA library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGT 4
 |||
Db 3 TGT 1

RESULT 17
LOCUS CF318944
DEFINITION HD--09-E08.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-E08, mRNA sequence.
ACCESSION CF318944
VERSION 1 GI:33690705
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--08-N23"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGT 4
 |||
Db 3 TGT 5

RESULT 16
LOCUS CF307842/c
DEFINITION ABF--01-G18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-G18, mRNA sequence.
ACCESSION CF307842
VERSION 1 GI:33679603
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
 source
 1..5
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--01-G18"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-E08"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

## ORIGIN

```

Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 TGT 4
 |||
Db 3 TGT 5

```

## RESULT 18

CF323326/c

LOCUS

```

DEFINITION HDN--03-120.g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA

```

ACCESSION

CF323326

VERSION

CF323326.1

GI:33794892

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 5)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..5

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="HDN--03-120"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli SOLR"

/clone\_lib="OshDAC1-overexpressing transgenic rice lambda

phage cDNA library II (HDN)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

## ORIGIN

```

Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GTG 3
 |||
Db 5 GTG 3

```

## RESULT 19

CF333993

LOCUS

```

DEFINITION JMT--03-B22.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

```

ACCESSION

CF333993

VERSION

CF333993.1

GI:33816290

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 5)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..5

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="JMT--03-B22"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

## ORIGIN

```

Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 TGT 4
 |||
Db 2 TGT 4

```

## RESULT 20

CF930992/c

LOCUS

```

DEFINITION CF--05-R-N09 Bos taurus CF-24-HW cDNA library Bos taurus cDNA clone
 CF--05-R-N09(5'), mRNA sequence.

```

ACCESSION

CF930992

VERSION

CF930992.1

GI:38280813

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

Bos taurus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

1 (bases 1 to 5)

Yoon,D.H., Lee,S.H., Sang,J.H., Lee,J.H., Sang,B.C. and Oh,S.J.

## Gene Expression Profiling of the Bovine adipose tissues

TITLE  
JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Dr. Du-Hak Yoon  
National Livestock Research Institute, RDA  
564 Omoekchun-dong, Suwon, 441-350, Korea  
Tel: 82 31 290 1593  
Fax: 82 31 290 1792  
Email: dhyoon@rda.go.kr  
Insert Length: 5 Std Error: 0.00  
Seq primer: ATTAACCTCACTAAAG  
POLYA=No.

## FEATURES

Location/Qualifiers

1. .5  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="CF-05-R-N09(5')"  
/sex="four males mixed"  
/tissue\_type="adipose tissue"  
/cell\_type="adipocyte"  
/dev\_stage="24 months old"  
/lab\_host="X11-BlueWRF strain"  
/clone\_lib="Bos taurus CF-24-HW cDNA library"  
/note="Vector: Uni-ZAPXR; Site\_1: EcoRI; Site\_2: Xho I"

## ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3

Db 4 GTG 2

## RESULT 21

## CA850905

LOCUS D07H12.024.16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
DEFINITION cDNA clone D07H12 5', mRNA sequence.

ACCESSION CA850905

VERSION CA850905.1 GI:33387698

KEYWORDS EST.

SOURCE Glycine max (soybean)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

1 (bases 1 to 6)

Contact: Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharon@ba.ars.usda.gov.

## FEATURES

source

1. .6  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="D07H12"  
/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="cDNA Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA"

## ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.3e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3

Db 1 GTG 3

## RESULT 22

## CA851633/c

LOCUS D15H03.015.16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
DEFINITION cDNA clone D15H03 5', mRNA sequence.

ACCESSION CA851633

VERSION CA851633.1 GI:33388426

KEYWORDS EST.

SOURCE Glycine max (soybean)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

1 (bases 1 to 6)

Contact: Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharon@ba.ars.usda.gov.

## FEATURES

source

1. .6  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="D15H03"  
/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="cDNA Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA"  
extracted from Peking roots 2 and 4 days past invasion."

## ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.3e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4

Db 6 TGT 4

## RESULT 23

## CF323984/c

LOCUS HDN--05-E22.g1 OshDACL1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA  
clone HDN--05-E22, mRNA sequence.

ACCESSION CF323984

VERSION CF323984.1 GI:33796236

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)

extracted from Peking roots 2 and 4 days past invasion."

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 6)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.  
Location/Qualifiers

#### FEATURES

source

1. .6  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN--05-E22"  
/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"  
/notes="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."  
Query Match 50.0%; Score 3; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.3e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

#### ORIGIN

QY 1 GTG 3  
|||  
DB 4 GTG 2

#### RESULT 24

CF339252

LOCUS  
DEFINITION  
RCL1--04-E20.g1 Regenerated callus lambda phage cDNA library (RCL1)  
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-E20,  
mRNA sequence.

ACCESSION

CF339252

VERSION

CF339252.1

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 6)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .6

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="RCL1--04-E20"

/issue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli SOLR"

/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"

/note="Vector: pBluescript SK(+); Site\_1: SstI; Site\_2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on

regenerated media"

Query Match 50.0%; Score 3; DB 7; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.3e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4

|||

DB 4 TGT 6

|||

RESULT 25

CL687157

LOCUS

DEFINITION

PR10146a\_E04\_2 - PR10146a.BR (6) Mixed stage fosmid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic

survey sequence.

ACCESSION

CL687157

VERSION

CL687157.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 6)

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: raif.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1. .6

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 50.0%; Score 3; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.3e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4

|||

DB 2 TGT 4

|||

FEATURES

source

Location/Qualifiers

1. .6

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 50.0%; Score 3; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.3e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4

|||

DB 2 TGT 4

|||



```

RESULT 26
CF318065
LOCUS
DEFINITION
HD--07-P21-g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-P21, mRNA sequence.
CF318065
ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriartoideae; Oryzaceae; Oryza.
1 (bases 1 to 4)
Song, S.I., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Sung, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..4
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site:1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
ORIGIN
Query Match 40.0%; Score 2.4; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCT 4
Db 1 GTTT 4
RESULT 27
CF318065
LOCUS
DEFINITION
SALK_117983.27.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_117983.27.80.x, genomic
survey sequence.
CF318065
ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 4)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
FEATURES
source
1..5
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_117983.27.80.x"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 40.0%; Score 2.4; DB 8; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCT 4
Db 1 GTAT 4
RESULT 28
CA850981
LOCUS
DEFINITION
CDNA clone D08H03 5', mRNA sequence.
CA850981
ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 5)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
source
1..5
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D08H03"
/dev_stage="Roots"

```

Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..4

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_117983.27.80.x"

/notes="Arabidopsis thaliana TDNA insertion lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 40.0%; Score 2.4; DB 8; Length 4;

Best Local Similarity 75.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCT 4

Db 1 GTAT 4

RESULT 28

CA850981

LOCUS

DEFINITION

CDNA clone D08H03 5', mRNA sequence.

CA850981

ACCESSION

VERSION

SOURCE

KEYWORDS

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 5)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean

infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ars.usda.gov.

FEATURES

source

1..5

Location/Qualifiers

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Peking"

/db\_xref="taxon:3847"

/clone="D08H03"

/dev\_stage="Roots"

/clone lib="cdna Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA  
extracted from Peking roots 2 and 4 days past invasion."

## ORIGIN

Query Match 40.0%; Score 2.4; DB 6; Length 5;  
Best Local Similarity 75.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGT 4  
|||  
Db 1 GTAT 4

## RESULT 29

CF314074

LOCUS

DEFINITION HD--02-H09.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

CF314074

VERSION CF314074.1 GI:33685835

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 5)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1..5  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HD--02-H09"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDACL1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

Query Match 40.0%; Score 2.4; DB 7; Length 5;  
Best Local Similarity 75.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTG 5  
|||  
Db 1 TCTG 4

## RESULT 30

CF327578/c

LOCUS

DEFINITION NACL--02-B23.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--02-B23, mRNA

## sequence.

CF327578

VERSION CF327578.1 GI:33803408

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 5)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1..5  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="NACL--02-B23"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

## ORIGIN

Query Match 40.0%; Score 2.4; DB 7; Length 5;  
Best Local Similarity 75.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGT 4  
|||  
Db 4 GAGT 1

Search completed: July 21, 2005, 01:54:29  
Job time : 1361.8 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds  
(without alignments)  
172.240 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 g9tgt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| C 1        | 5     | 83.3        | 5      | 1  | US-08-717-526-56  |
| 2          | 5     | 83.3        | 5      | 3  | US-09-180-903-4   |
| 3          | 5     | 83.3        | 5      | 3  | US-09-180-903-5   |
| 4          | 5     | 83.3        | 6      | 1  | US-08-367-175A-24 |
| 5          | 5     | 83.3        | 6      | 2  | US-08-471-994-8   |
| 6          | 5     | 83.3        | 6      | 3  | US-08-154-364-8   |
| 7          | 5     | 83.3        | 6      | 3  | US-08-154-364-14  |
| 8          | 5     | 83.3        | 6      | 3  | US-09-180-903-9   |
| 9          | 5     | 83.3        | 6      | 3  | US-09-281-481A-22 |
| 10         | 5     | 83.3        | 6      | 4  | US-09-958-221A-2  |
| 11         | 5     | 83.3        | 6      | 5  | PCT-US94-06456-7  |
| 12         | 5     | 83.3        | 6      | 5  | PCT-US94-06456-36 |
| 13         | 4.4   | 73.3        | 6      | 2  | US-08-485-158A-2  |
| 14         | 4.2   | 70.0        | 6      | 2  | US-08-420-629-3   |
| 15         | 4     | 66.7        | 4      | 3  | US-09-180-903-3   |
| 16         | 4     | 66.7        | 4      | 3  | US-08-381-097A-12 |
| 17         | 4     | 66.7        | 6      | 1  | US-08-459-064B-22 |
| 18         | 4     | 66.7        | 6      | 2  | US-08-460-421A-22 |
| 19         | 4     | 66.7        | 6      | 2  | US-08-372-652-10  |
| 20         | 4     | 66.7        | 6      | 4  | US-09-086-663A-77 |
| 21         | 4     | 66.7        | 6      | 4  | US-09-830-401-2   |
| 22         | 4     | 66.7        | 6      | 5  | PCT-US95-16311-10 |
| 23         | 3.4   | 56.7        | 5      | 3  | US-08-855-372B-20 |
| 24         | 3.4   | 56.7        | 5      | 3  | US-08-855-372B-21 |
| 25         | 3.4   | 56.7        | 5      | 3  | US-08-855-372B-23 |
| 26         | 3.4   | 56.7        | 5      | 3  | US-09-048-927-4   |
| 27         | 3.4   | 56.7        | 5      | 3  | US-09-498-851-20  |
| C 1        | 5     | 83.3        | 5      | 1  | Sequence 56, Appl |
| 2          | 5     | 83.3        | 5      | 3  | Sequence 4, Appl  |
| 3          | 5     | 83.3        | 5      | 3  | Sequence 5, Appl  |
| 4          | 5     | 83.3        | 6      | 1  | Sequence 24, Appl |
| 5          | 5     | 83.3        | 6      | 2  | Sequence 8, Appl  |
| 6          | 5     | 83.3        | 6      | 3  | Sequence 8, Appl  |
| 7          | 5     | 83.3        | 6      | 3  | Sequence 14, Appl |
| 8          | 5     | 83.3        | 6      | 3  | Sequence 9, Appl  |
| 9          | 5     | 83.3        | 6      | 3  | Sequence 22, Appl |
| 10         | 5     | 83.3        | 6      | 4  | Sequence 2, Appl  |
| 11         | 5     | 83.3        | 6      | 5  | Sequence 7, Appl  |
| 12         | 5     | 83.3        | 6      | 5  | Sequence 36, Appl |
| 13         | 4.4   | 73.3        | 6      | 2  | Sequence 2, Appl  |
| 14         | 4.2   | 70.0        | 6      | 2  | Sequence 3, Appl  |
| 15         | 4     | 66.7        | 4      | 3  | Sequence 3, Appl  |
| 16         | 4     | 66.7        | 6      | 1  | Sequence 12, Appl |
| 17         | 4     | 66.7        | 6      | 1  | Sequence 22, Appl |
| 18         | 4     | 66.7        | 6      | 2  | Sequence 22, Appl |
| 19         | 4     | 66.7        | 6      | 2  | Sequence 10, Appl |
| 20         | 4     | 66.7        | 6      | 4  | Sequence 77, Appl |
| 21         | 4     | 66.7        | 6      | 4  | Sequence 2, Appl  |
| 22         | 4     | 66.7        | 6      | 5  | Sequence 10, Appl |
| 23         | 3.4   | 56.7        | 5      | 3  | Sequence 20, Appl |
| 24         | 3.4   | 56.7        | 5      | 3  | Sequence 21, Appl |
| 25         | 3.4   | 56.7        | 5      | 3  | Sequence 23, Appl |
| 26         | 3.4   | 56.7        | 5      | 3  | Sequence 4, Appl  |
| 27         | 3.4   | 56.7        | 5      | 3  | Sequence 20, Appl |
| 28         | 3.4   | 56.7        | 5      | 3  | US-09-498-851-21  |
| 29         | 3.4   | 56.7        | 5      | 3  | US-09-498-851-23  |
| C 30       | 3.4   | 56.7        | 5      | 4  | US-09-305-839-46  |
| C 31       | 3.4   | 56.7        | 5      | 5  | PCT-US91-03680-35 |
| 32         | 3.4   | 56.7        | 6      | 1  | US-07-630-288A-35 |
| 33         | 3.4   | 56.7        | 6      | 1  | US-08-153-051B-53 |
| 34         | 3.4   | 56.7        | 6      | 1  | US-08-060-952C-52 |
| 35         | 3.4   | 56.7        | 6      | 1  | US-08-468-049-35  |
| 36         | 3.4   | 56.7        | 6      | 2  | US-08-151-477A-53 |
| 37         | 3.4   | 56.7        | 6      | 3  | US-08-819-867-70  |
| C 38       | 3.4   | 56.7        | 6      | 3  | US-09-107-708-4   |
| 39         | 3.4   | 56.7        | 6      | 3  | US-08-793-634B-34 |
| C 40       | 3.4   | 56.7        | 6      | 3  | US-09-449-581-4   |
| 41         | 3.4   | 56.7        | 6      | 3  | US-08-464-011B-52 |
| C 42       | 3.4   | 56.7        | 6      | 3  | US-09-268-544B-43 |
| 43         | 3.4   | 56.7        | 6      | 4  | US-09-378-535-70  |
| 44         | 3.4   | 56.7        | 6      | 4  | US-09-830-401-3   |
| C 45       | 3.4   | 56.7        | 6      | 4  | US-09-244-438-12  |
| 46         | 3.4   | 56.7        | 6      | 5  | PCT-US95-04092-14 |
| C 47       | 3.2   | 53.3        | 6      | 4  | US-09-336-552A-4  |
| C 48       | 3     | 50.0        | 4      | 3  | US-08-630-019A-44 |
| C 49       | 3     | 50.0        | 4      | 3  | US-09-248-093-3   |
| C 50       | 3     | 50.0        | 5      | 1  | US-08-242-402-2   |
| C 51       | 3     | 50.0        | 5      | 1  | US-08-270-180-3   |
| C 52       | 3     | 50.0        | 5      | 1  | US-08-068-945A-47 |
| 53         | 3     | 50.0        | 5      | 1  | US-08-144-602B-12 |
| 54         | 3     | 50.0        | 5      | 1  | US-08-153-051B-47 |
| 55         | 3     | 50.0        | 5      | 1  | US-08-060-952C-20 |
| C 56       | 3     | 50.0        | 5      | 1  | US-08-442-806-47  |
| 57         | 3     | 50.0        | 5      | 2  | US-08-151-477A-47 |
| C 58       | 3     | 50.0        | 5      | 2  | US-08-319-052-10  |
| 59         | 3     | 50.0        | 5      | 2  | US-08-319-052-12  |
| 60         | 3     | 50.0        | 5      | 3  | US-08-819-867-44  |
| C 61       | 3     | 50.0        | 5      | 3  | US-08-682-423-3   |
| 62         | 3     | 50.0        | 5      | 3  | US-08-855-372B-22 |
| C 63       | 3     | 50.0        | 5      | 3  | US-08-973-068-59  |
| C 64       | 3     | 50.0        | 5      | 3  | US-08-973-068-60  |
| C 65       | 3     | 50.0        | 5      | 3  | US-08-846-301A-21 |
| 66         | 3     | 50.0        | 5      | 3  | US-08-793-634B-32 |
| C 67       | 3     | 50.0        | 5      | 3  | US-08-442-108B-10 |
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| C 70       | 3     | 50.0        | 5      | 3  | US-09-638-509C-20 |
| C 71       | 3     | 50.0        | 5      | 3  | US-09-638-509C-22 |
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| C 74       | 3     | 50.0        | 5      | 4  | US-09-723-685-4   |
| 75         | 3     | 50.0        | 5      | 4  | US-09-763-565-7   |
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| C 77       | 3     | 50.0        | 5      | 5  | PCT-US95-05141-3  |
| C 78       | 3     | 50.0        | 6      | 1  | US-07-847-743B-1  |
| 79         | 3     | 50.0        | 6      | 1  | US-08-011-398B-10 |
| C 80       | 3     | 50.0        | 6      | 1  | US-08-011-398B-10 |
| C 81       | 3     | 50.0        | 6      | 1  | US-08-365-189-13  |
| C 82       | 3     | 50.0        | 6      | 1  | US-08-171-389-625 |
| C 83       | 3     | 50.0        | 6      | 1  | US-08-456-201-1   |
| C 84       | 3     | 50.0        | 6      | 1  | US-08-211-682-1   |
| 85         | 3     | 50.0        | 6      | 1  | US-08-211-682-6   |
| 86         | 3     | 50.0        | 6      | 1  | US-08-211-682-9   |
| C 87       | 3     | 50.0        | 6      | 1  | US-08-211-682-13  |
| C 88       | 3     | 50.0        | 6      | 1  | US-07-996-783-25  |
| C 89       | 3     | 50.0        | 6      | 1  | US-08-484-499-25  |
| C 90       | 3     | 50.0        | 6      | 1  | US-08-123-936-625 |
| C 91       | 3     | 50.0        | 6      | 1  | US-08-475-221B-25 |
| C 92       | 3     | 50.0        | 6      | 1  | US-08-476-876-25  |
| 93         | 3     | 50.0        | 6      | 1  | US-08-309-644A-1  |
| C 94       | 3     | 50.0        | 6      | 1  | US-08-445-909A-2  |
| C 95       | 3     | 50.0        | 6      | 1  | US-08-445-909A-5  |
| 96         | 3     | 50.0        | 6      | 1  | US-08-464-051-10  |
| C 97       | 3     | 50.0        | 6      | 1  | US-08-464-051-10  |
| C 98       | 3     | 50.0        | 6      | 2  | US-08-330-161-1   |
| C 99       | 3     | 50.0        | 6      | 2  | US-08-456-241-1   |
| 100        | 3     | 50.0        | 6      | 2  | US-08-462-498-10  |

## ALIGNMENTS

## RESULT 1

US-08-717-526-56/c  
; Sequence 56, Application US/08717526  
; Patent No. 5786147  
; GENERAL INFORMATION:  
; APPLICANT: MABILAT, CLAUDE  
; APPLICANT: RAOULT, DIDIER  
; TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE  
; STREET: 700 SOUTH WASHINGTON STREET  
; CITY: ALEXANDRIA  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,526  
; FILING DATE: 17-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERRIDGE, WILLIAM P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38732  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6400  
; TELEFAX: 703-836-2787  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-717-526-56

Query Match 83.3%; Score 5; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 6  
Db 5 TGTGT 1

## RESULT 2

US-09-180-903-4  
; Sequence 4, Application US/09180903  
; Patent No. 6316190  
; GENERAL INFORMATION:  
; APPLICANT: Rein, Alan  
; Casas-Finet, Jose  
; Fisher, Robert  
; Fivash, Matthew  
; Henderson, Louis E.  
; TITLE OF INVENTION: Oligonucleotides Which Specifically Bind  
; Retroviral Nucleocapsid Proteins  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California

COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/180,903  
; FILING DATE: 12-Jul-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/017,128  
; FILING DATE: 20-MAY-1996  
; APPLICATION NUMBER: WO PCT/US97/08936  
; FILING DATE: 13-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Choi, Kathleen L.  
; REGISTRATION NUMBER: 43,433  
; REFERENCE/DOCKET NUMBER: 015280-279100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-180-903-4

Query Match 83.3%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 6  
Db 1 TGTGT 5

## RESULT 3

US-09-180-903-5  
; Sequence 5, Application US/09180903  
; Patent No. 6316190  
; GENERAL INFORMATION:  
; APPLICANT: Rein, Alan  
; Casas-Finet, Jose  
; Fisher, Robert  
; Fivash, Matthew  
; Henderson, Louis E.  
; TITLE OF INVENTION: Oligonucleotides Which Specifically Bind  
; Retroviral Nucleocapsid Proteins  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/180,903  
; FILING DATE: 12-Jul-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/017,128

;/ FILING DATE: 20-MAY-1996  
;/ APPLICATION NUMBER: WO PCT/US97/08936  
;/ FILING DATE: 19-MAY-1997  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Choi, Kathleen L.  
;/ REGISTRATION NUMBER: 43,433  
;/ REFERENCE/DOCKET NUMBER: 015280-279100US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 576-0200  
;/ TELEFAX: (415) 576-0300  
;/ INFORMATION FOR SEQ ID NO: 5:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-180-903-5

Query Match 83.3%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
DB 1 GTGTG 5

RESULT 4  
US-08-367-175A-24  
;/ Sequence 24, Application US/08367175A  
;/ Patent No. 5631115  
;/ GENERAL INFORMATION:  
;/ APPLICANT: OHTSUKA, Eiko  
;/ APPLICANT: KOIZUMI, Makoto  
;/ TITLE OF INVENTION: Looped, hairpin ribozyme  
;/ NUMBER OF SEQUENCES: 27  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: FRISHAUF, HOLTZ, GOODMAN,  
;/ ADDRESSEE: LANGER & CHICK, P.C.  
;/ STREET: 767 Third Avenue  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10017-2023  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.24  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/367,175A  
;/ FILING DATE: 29 Dec. 1994  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: GOODMAN, Herbert  
;/ REGISTRATION NUMBER: 17081  
;/ REFERENCE/DOCKET NUMBER: 920081  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212)319-4900  
;/ TELEFAX: (212)319-5101  
;/ TELEX: 236268  
;/ INFORMATION FOR SEQ ID NO: 24:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 6 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: mRNA  
;/ HYPOTHETICAL: N  
;/ ANTI-SENSE: N  
US-08-367-175A-24

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.5e+08;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGTG 5  
DB 1 GUGUG 5  
RESULT 5  
US-08-471-994-8  
;/ Sequence 8, Application US/08471994  
;/ Patent No. 5861245  
;/ GENERAL INFORMATION:  
;/ APPLICANT: McClelland, Michael  
;/ APPLICANT: Welsh, John T.  
;/ APPLICANT: Sorge, Joseph A.  
;/ TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN  
;/ REACTION METHOD FOR FINGERPRINTING GENOMES  
;/ NUMBER OF SEQUENCES: 13  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: United States of America  
;/ ZIP: 10036  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/471,994  
;/ FILING DATE: 06-JUN-1995  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Halluin, Albert P.  
;/ REGISTRATION NUMBER: 25,227  
;/ REFERENCE/DOCKET NUMBER: 8142-103  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415-854-3660  
;/ TELEFAX: 415-854-3694  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 8:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 6 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: DNA (genomic)  
US-08-471-994-8

Query Match 83.3%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
DB 2 GTGTG 6

RESULT 6  
US-08-154-364-8  
;/ Sequence 8, Application US/08154364  
;/ Patent No. 6207810  
;/ GENERAL INFORMATION:  
;/ APPLICANT: McClelland, Michael  
;/ APPLICANT: Welsh, John T.  
;/ APPLICANT: Sorge, Joseph A.  
;/ TITLE OF INVENTION: ARBITRARILY PRIMED  
;/ POLYMERASE CHAIN

;/ TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING  
;/ TITLE OF INVENTION: GENOMES  
;/ NUMBER OF SEQUENCES: 41  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Limbach and Limbach  
;/ STREET: 2001 Ferry Building  
;/ CITY: San Francisco  
;/ STATE: CA  
;/ COUNTRY: USA  
;/ ZIP: 94111  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0,  
;/ SOFTWARE: Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/154,364  
;/ FILING DATE:  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Borthner, Scott R.  
;/ REGISTRATION NUMBER: 34,298  
;/ REFERENCE/DOCKET NUMBER: STRG-20142 USA  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415-433-4150  
;/ TELEFAX: 414-433-8716  
;/ INFORMATION FOR SEQ ID NO: 8:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 6 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (genomic)  
;/ HYPOTHETICAL: NO  
;/ ANTI-SENSE: NO  
;/ US-08-154-364-8

Query Match 83.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
|||  
Db 2 GTGTG 6

RESULT 7  
US-08-154-364-14  
;/ Sequence 14, Application US/08154364  
;/ Patent No. 6207810  
;/ GENERAL INFORMATION:  
;/ APPLICANT: McCelland, Michael  
;/ APPLICANT: Welsh, John T.  
;/ APPLICANT: Sorge, Joseph A.  
;/ TITLE OF INVENTION: ARBITRARILY PRIMED  
;/ TITLE OF INVENTION: POLYMERASE CHAIN  
;/ TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING  
;/ TITLE OF INVENTION: GENOMES  
;/ NUMBER OF SEQUENCES: 41  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Limbach and Limbach  
;/ STREET: 2001 Ferry Building  
;/ CITY: San Francisco  
;/ STATE: CA  
;/ COUNTRY: USA  
;/ ZIP: 94111  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0,  
;/ SOFTWARE: Version #1.25

;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/154,364  
;/ FILING DATE:  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Borthner, Scott R.  
;/ REGISTRATION NUMBER: 34,298  
;/ REFERENCE/DOCKET NUMBER: STRG-20142 USA  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415-433-4150  
;/ TELEFAX: 414-433-8716  
;/ INFORMATION FOR SEQ ID NO: 14:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 6 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (genomic)  
;/ HYPOTHETICAL: NO  
;/ ANTI-SENSE: NO  
;/ US-08-154-364-14  
;/ Query Match 83.3%; Score 5; DB 3; Length 6;  
;/ Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
;/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;/ QY 1 GTGTG 5  
;/ |||  
;/ Db 2 GTGTG 6  
;/ RESULT 8  
;/ US-09-180-903-9  
;/ Sequence 9, Application US/09180903  
;/ Patent No. 6316190  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Rein, Alan  
;/ Casas-Finet, Jose  
;/ Fisher, Robert  
;/ Fivash, Matthew  
;/ Henderson, Louis E.  
;/ TITLE OF INVENTION: Oligonucleotides Which Specifically Bind  
;/ Retroviral Nucleocapsid Proteins  
;/ NUMBER OF SEQUENCES: 15  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, Eighth Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94111-3834  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/180,903  
;/ FILING DATE: 12-Jul-1999  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 60/017,128  
;/ FILING DATE: 20-MAY-1996  
;/ APPLICATION NUMBER: WO PCT/US97/08936  
;/ FILING DATE: 19-MAY-1997  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Choi, Kathleen L.  
;/ REGISTRATION NUMBER: 43,433  
;/ REFERENCE/DOCKET NUMBER: 015280-279100US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 576-0200  
;/ TELEFAX: (415) 576-0300  
;/ INFORMATION FOR SEQ ID NO: 9:

## SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-180-903-9

Query Match 83.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
Db 2 GTGTG 6

## RESULT 9

US-09-281-481A-22  
; Sequence 22, Application US/09281481A  
; Patent No. 6383747  
; GENERAL INFORMATION:  
; APPLICANT: DANKINS, Roger L. and ABRAHAM, Lawrence J.  
; TITLE OF INVENTION: GENETIC ANALYSIS

NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER  
STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK

COUNTRY: UNITED STATES OF AMERICA

ZIP: 11530-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/281,481A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/893,971

FILING DATE: 16-JUL-1997

APPLICATION NUMBER: US 232,229

FILING DATE: 29-APR-1994

APPLICATION NUMBER: PX9279 (AU)

FILING DATE: 01-NOV-1991

APPLICATION NUMBER: PCT/AU92/00583

FILING DATE: 30-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: DIGIGLIO, FRANK S

REFERENCE/DOCKET NUMBER: 9279

TELECOMMUNICATION INFORMATION:

TELEPHONE: +516 742 4343

TELEFAX: +516 742 4366

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-09-281-481A-22

Query Match 83.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
Db 2 GTGTG 6

## RESULT 10

US-09-958-221A-2/c  
; Sequence 2, Application US/09958221A  
; Patent No. 6886160  
; GENERAL INFORMATION:  
; APPLICANT: Haeringen van, Willem A.  
; APPLICANT: Haeringen van, Hendrik  
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
; FILE REFERENCE: 92750/64

CURRENT APPLICATION NUMBER: US/09/958,221A

CURRENT FILING DATE: 2001-10-03

PRIOR APPLICATION NUMBER: EP 00200757.3

PRIOR FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: PCT/NL01/00177

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 6

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-958-221A-2

Query Match 83.3%; Score 5; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.5e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5  
Db 5 GTGTG 1

## RESULT 11

PCT-US94-06456-7

; Sequence 7, Application PC/TUS9406456

GENERAL INFORMATION:

APPLICANT: Beutel, Bruce A.

APPLICANT: Coppola, George R.

APPLICANT: Sherman, Michael I.

TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC - DOS

SOFTWARE: DW4.V2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06456

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/073,873

FILING DATE: 09-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliott M.

REGISTRATION NUMBER: 24,025

REFERENCE/DOCKET NUMBER: 23550-89

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 6 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-06456-7

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+08;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GUGUG 6

RESULT 12
PCT-US94-06456-36
; Sequence 36, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
PCT-US94-06456-36

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GTGTG 6

RESULT 13
US-08-485-158A-2
; Sequence 2, Application US/08485158A
; Patent No. 5859328
; GENERAL INFORMATION:
; APPLICANT: Nasrallah, June B.
; APPLICANT: Nasrallah, Mikhail E.
; APPLICANT: Thoresness, Mary K.
; TITLE OF INVENTION: ISOLATED DNA ELEMENTS THAT DIRECT
; TITLE OF INVENTION: PISTIL-SPECIFIC AND ANTHER-SPECIFIC GENE EXPRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,158A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A-6217-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-485-158A-2

Query Match 73.3%; Score 4.4; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db 1 GTTGT 6

RESULT 14
US-08-420-629-3
; Sequence 3, Application US/08420629
; Patent No. 5891627
; GENERAL INFORMATION:
; APPLICANT: EVANS, GLEN A.
; APPLICANT: SELLERI, LUCIA
; APPLICANT: EUBANKS, JAMES H.
; TITLE OF INVENTION: POLYMORPHIC LOCUS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```



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/ APPLICATION NUMBER: US/08/420,629
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/773,099
/ FILING DATE: 09-OCT-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WETHERELL, JR., PH.D., JOHN R.
/ REGISTRATION NUMBER: 31,678
/ REFERENCE/DOCKET NUMBER: PD1512
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-455-5100
/ TELEFAX: 619-455-5110
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..6
/ US-08-420-629-3

Query Match
Best Local Similarity 70.0%; Score 4.2; DB 2; Length 6;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 6
DB 1 TRTGT 5

RESULT 15
US-09-180-903-3
/ Sequence 3, Application US/09180903
/ Patent No. 6316190
/ GENERAL INFORMATION:
/ APPLICANT: Rein, Alan
/ CASES-FINET, Jose
/ FISHER, Robert
/ FIVASH, Matthew
/ HENDERSON, Louis E.
/ TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
/ Retroviral Nucleocapsid Proteins
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 12-Jul-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/017,128
/ FILING DATE: 20-MAY-1996
/ APPLICATION NUMBER: WO PCT/US97/08936
/ FILING DATE: 19-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Choi, Kathleen L.
/ REGISTRATION NUMBER: 43,433
/ REFERENCE/DOCKET NUMBER: 015280-279100US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-180-903-3

Query Match
Best Local Similarity 66.7%; Score 4; DB 3; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
DB 1 TGTG 4

RESULT 16
US-08-381-097A-12
/ Sequence 12, Application US/08381097A
/ Patent No. 5643890
/ GENERAL INFORMATION:
/ APPLICANT: Iverson, Patrick L.
/ APPLICANT: Mata, John E.
/ TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
/ TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
/ TITLE OF INVENTION: of Cancer and Other Diseases
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
/ STREET: 801 Grand Suite 3200
/ CITY: Des Moines
/ STATE: Iowa
/ COUNTRY: United States
/ ZIP: 50309
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/381,097A
/ FILING DATE: 31-JAN-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nebel, Heidi S
/ REGISTRATION NUMBER: 37,719
/ REFERENCE/DOCKET NUMBER: unmc 63092
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 515-288-3667
/ TELEFAX: 515-288-1338
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-381-097A-12

Query Match
Best Local Similarity 66.7%; Score 4; DB 1; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
DB 1 TGTG 4
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RESULT 17  
US-08-459-064B-22/c  
; Sequence 22, Application US/08459064B  
; Patent No. 5747452  
; GENERAL INFORMATION:  
; APPLICANT: RUOSLAHTI, ERKKI I.  
; APPLICANT: MORLA, ALEX  
; TITLE OF INVENTION: A METHOD OF MODULATING TUMOR CELL MIGRATION  
; TITLE OF INVENTION: USING FIBRONECTIN TYPE III PEPTIDES  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES LLP  
; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,064B  
; FILING DATE: 01-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/829,462  
; FILING DATE: 31-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/021,626  
; FILING DATE: 16-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/340,812  
; FILING DATE: 17-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, CATHRYN A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 1543  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-535-9001  
; TELEFAX: 619-535-8949  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..6  
US-08-459-064B-22

Query Match 66.7%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
|||  
Db 4 GTGT 1

RESULT 18  
US-08-460-421A-22/c  
; Sequence 22, Application US/08460421A  
; Patent No. 5837813  
; GENERAL INFORMATION:  
; APPLICANT: RUOSLAHTI, ERKKI I.  
; APPLICANT: MORLA, ALEX  
; TITLE OF INVENTION: FIBRONECTIN BINDING SITES AND METHODS OF  
; TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY

NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES LLP  
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,421A  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/829,462  
FILING DATE: 31-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,626  
FILING DATE: 16-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/340,812  
FILING DATE: 17-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1542  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..6  
US-08-460-421A-22

Query Match 66.7%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
|||  
Db 4 GTGT 1

RESULT 19  
US-08-372-652-10  
; Sequence 10, Application US/08372652  
; Patent No. 5932699  
; GENERAL INFORMATION:  
; APPLICANT: Moore, David  
; APPLICANT: Seol, Wongi  
; APPLICANT: Choi, Hueng-Sik  
; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING  
; TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street, Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/372,652  
; FILING DATE: 13-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/246001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-372-652-10

Query Match 66.7%; Score 4; DB 2; Length 6;  
Best Local Similarity 33.3%; Pred. No. 2.5e+08;  
Matches 2; Conservative 3; Mismatches 1; Indels 0;

QY 1 GTGTGT 6  
|::|  
Db 1 GURAGU 6

## RESULT 20

US-09-086-663A-77/c  
; Sequence 77, Application US/09086663A  
; Patent No. 6518063  
; GENERAL INFORMATION:  
; APPLICANT: DUCY, PATRICIA  
; APPLICANT: KARSNTY, GERARD  
; TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF USE  
; FILE REFERENCE: UTSC:525  
; CURRENT APPLICATION NUMBER: US/09/086,663A  
; CURRENT FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 60/080,189  
; PRIOR FILING DATE: 1998-03-24  
; PRIOR APPLICATION NUMBER: 60/048,430  
; PRIOR FILING DATE: 1997-05-29  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 77  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-09-086-663A-77

Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 TGTG 5  
|::|  
Db 6 TGTG 3

## RESULT 21

US-09-830-401-2  
; Sequence 2, Application US/09830401  
; Patent No. 6593088  
; GENERAL INFORMATION:  
; APPLICANT: SAITO, Isao

; APPLICANT: FUJIMOTO, Kenzo  
; APPLICANT: MATSUDA, Shigeo  
; TITLE OF INVENTION: REVERSIBLE PHOTOLIGATING NUCLEIC ACID AND PHOSPHORAMIDITE  
; FILE REFERENCE: 2001-0514A/LC/00653  
; CURRENT APPLICATION NUMBER: US/09/830,401  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: PCT/JP00/05715  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 1999-240685  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHESIZED DNA OLIGOMER  
US-09-830-401-2

Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5  
|::|  
Db 1 TGTG 4

## RESULT 22

PCT-US95-16311-10  
; Sequence 10, Application PC/TUS9516311  
; GENERAL INFORMATION:  
; APPLICANT: Moore, David  
; APPLICANT: Seol, Wongi  
; APPLICANT: Choi, Hwang-Sik  
; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING  
; TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street, Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/16311  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/372,652  
; FILING DATE: 13-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/246001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
PCT-US95-16311-10

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Query Match 66.7%; Score 4; DB 5; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.5e+08; Indels 0; Gaps 0;
Matches 2; Conservative 3; Mismatches 1;

QY 1 GTGTGT 6
Db 1 GURAGU 6

RESULT 23
US-08-855-372B-20
; Sequence 20, Application US/08855372B
; Patent No. 6090549
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESS: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: Yes
US-08-855-372B-20

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08; Indels 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 1;

QY 1 GTGTG 5
Db 1 GTATG 5

RESULT 24
US-08-855-372B-21
; Sequence 21, Application US/08855372B
; Patent No. 6090549
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
```

```
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESS: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: Yes
US-08-855-372B-21

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08; Indels 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 1;

QY 2 TGTGT 6
Db 1 TGTAT 5

RESULT 25
US-08-855-372B-23
; Sequence 23, Application US/08855372B
; Patent No. 6090549
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESS: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
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;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/855,372B  
;/ FILING DATE: 13-MAY-97  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: U.S. 08/587,332  
;/ FILING DATE: 16-JAN-96  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Cherskov, Michael J.  
;/ REGISTRATION NUMBER: 33,664  
;/ REFERENCE/DOCKET NUMBER: ANL-IN-95-027  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (312) 621-1330  
;/ TELEFAX: (312) 621-0088  
;/ INFORMATION FOR SEQ ID NO: 23:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5 bases  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: No. 6090549 Applicable  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: Genomic DNA  
;/ HYPOTHETICAL: Yes  
;/ US-08-855-372B-23

Query Match 56.7%; Score 3.4; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 3e+08;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6  
|||  
Db 1 TATGT 5

RESULT 26  
US-09-048-927-4  
;/ Sequence 4, Application US/09048927  
;/ Patent No. 6147056  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Gilchrist, Barbara A.  
;/ APPLICANT: Yaar, Mina  
;/ APPLICANT: Eller, Mark  
;/ TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
;/ FILE REFERENCE: BU94-68A2  
;/ CURRENT APPLICATION NUMBER: US/09/048,927  
;/ CURRENT FILING DATE: 1998-03-26  
;/ EARLIER APPLICATION NUMBER: 08/952,697  
;/ EARLIER FILING DATE: 1996-06-03  
;/ EARLIER APPLICATION NUMBER: 08/467,012  
;/ EARLIER FILING DATE: 1995-06-06  
;/ NUMBER OF SEQ ID NOS: 4  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 4  
;/ LENGTH: 5  
;/ TYPE: DNA  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: DNA Fragment  
;/ US-09-048-927-4

Query Match 56.7%; Score 3.4; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 3e+08;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5  
|||  
Db 1 GTATG 5

RESULT 27  
US-09-498-851-20  
;/ Sequence 20, Application US/09498851  
;/ Patent No. 6440671  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Mirzabekov, Andrei D

;/ APPLICANT: Parinov, Sergei V  
;/ APPLICANT: Barsky, Victor E  
;/ APPLICANT: Kirillov, Eugene V  
;/ APPLICANT: Dubiley, Svetlana A  
;/ TITLE OF INVENTION: Use of Continuous/Contiguous  
;/ TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.  
;/ NUMBER OF SEQUENCES: 88  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: CHERSKOV & FLAYNIK  
;/ STREET: 20 N. Wacker Drive  
;/ CITY: Chicago  
;/ STATE: Illinois  
;/ COUNTRY: United States  
;/ ZIP: 60606  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.50 inch, 1.4 MB storage  
;/ COMPUTER: PC  
;/ OPERATING SYSTEM: Microsoft Windows 98  
;/ SOFTWARE: Wordperfect  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/498,851  
;/ FILING DATE:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/855,372  
;/ FILING DATE: 13-MAY-97  
;/ APPLICATION NUMBER: U.S. 08/587,332  
;/ FILING DATE: 16-JAN-96  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Cherskov, Michael J.  
;/ REGISTRATION NUMBER: 33,664  
;/ REFERENCE/DOCKET NUMBER: ANL-IN-95-027  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (312) 621-1330  
;/ TELEFAX: (312) 621-0088  
;/ INFORMATION FOR SEQ ID NO: 20:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5 bases  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: No. 6440671 Applicable  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: Genomic DNA  
;/ HYPOTHETICAL: yes  
;/ US-09-498-851-20

Query Match 56.7%; Score 3.4; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 3e+08;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5  
|||  
Db 1 GTATG 5

RESULT 28  
US-09-498-851-21  
;/ Sequence 21, Application US/09498851  
;/ Patent No. 6440671  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Mirzabekov, Andrei D  
;/ APPLICANT: Parinov, Sergei V  
;/ APPLICANT: Barsky, Victor E  
;/ APPLICANT: Kirillov, Eugene V  
;/ APPLICANT: Dubiley, Svetlana A  
;/ TITLE OF INVENTION: Use of Continuous/Contiguous  
;/ TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.  
;/ NUMBER OF SEQUENCES: 88  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: CHERSKOV & FLAYNIK  
;/ STREET: 20 N. Wacker Drive  
;/ CITY: Chicago  
;/ STATE: Illinois  
;/ COUNTRY: United States  
;/ ZIP: 60606

```
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.50 inch, 1.4 MB storage
/ COMPUTER: PC
/ OPERATING SYSTEM: Microsoft Windows 98
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/498,851
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/855,372
/ FILING DATE: 13-MAY-97
/ APPLICATION NUMBER: U.S. 08/587,332
/ FILING DATE: 16-JAN-96
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cherskov, Michael J.
/ REGISTRATION NUMBER: 33,664
/ REFERENCE/DOCKET NUMBER: ANL-IN-95-027
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 621-1330
/ TELEFAX: (312) 621-0088
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: No. 6440671 Applicable
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ HYPOTHETICAL: yes
/ US-09-498-851-21

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6
DB 1 TGTAT 5

RESULT 29
US-09-498-851-23
/ Sequence 23, Application US/09498851
/ Patent No. 6440671
/ GENERAL INFORMATION:
/ APPLICANT: Mirzabekov, Andrei D
/ APPLICANT: Parinov, Sergei V
/ APPLICANT: Barsky, Victor E
/ APPLICANT: Kirillov, Eugene V
/ APPLICANT: Dubiley, Svetlana A
/ TITLE OF INVENTION: Use of Continuous/Contiguous
/ NUMBER OF SEQUENCES: 88
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CHERSKOV & FLAYNIK
/ STREET: 20 N. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.50 inch, 1.4 MB storage
/ COMPUTER: PC
/ OPERATING SYSTEM: Microsoft Windows 98
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/498,851
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/855,372
/ FILING DATE: 13-MAY-97
/ APPLICATION NUMBER: U.S. 08/587,332
/ FILING DATE: 16-JAN-96
/ ATTORNEY/AGENT INFORMATION:
```

```
/
/ NAME: Cherskov, Michael J.
/ REGISTRATION NUMBER: 33,664
/ REFERENCE/DOCKET NUMBER: ANL-IN-95-027
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 621-1330
/ TELEFAX: (312) 621-0088
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: No. 6440671 Applicable
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ HYPOTHETICAL: yes
/ US-09-498-851-23

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6
DB 1 TATGT 5

RESULT 30
US-09-305-839-46/c
/ Sequence 46, Application US/09305839
/ Patent No. 6514935
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Mu-En
/ APPLICANT: Yet, Shaw-Fang
/ TITLE OF INVENTION: Methods of Treating Hypertension
/ FILE REFERENCE: 21508-064
/ CURRENT APPLICATION NUMBER: US/09/305,839
/ CURRENT FILING DATE: 1999-05-05
/ PRIOR APPLICATION NUMBER: 08/818,655
/ PRIOR FILING DATE: 1997-03-14
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 46
/ LENGTH: 5
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: artif: peptide
/ US-09-305-839-46

Query Match 56.7%; Score 3.4; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 5 GGGTG 1

Search completed: July 21, 2005, 04:29:16
Job time : 63 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 00:00:54 ; Search time 710.6 Seconds  
(without alignments)  
53.568 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6  
Sequence: 1 gtgtgt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 6704

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA.\*

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| 2:  | /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*   |
| 3:  | /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*  |
| 4:  | /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*  |
| 5:  | /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*  |
| 6:  | /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.* |
| 7:  | /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*  |
| 8:  | /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*  |
| 9:  | /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.* |
| 10: | /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.* |
| 11: | /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.* |
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| 16: | /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.* |
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| 21: | /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.* |
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| 23: | /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.* |
| 24: | /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*  |
| 25: | /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*  |
| 26: | /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 2          | 6     | 100.0       | 6      | 9  | US-09-735-363A-10 |
| 3          | 6     | 100.0       | 6      | 9  | US-09-879-668-2   |
| 4          | 6     | 100.0       | 6      | 15 | US-10-280-274-2   |
| 5          | 6     | 100.0       | 6      | 17 | US-10-297-008-11  |
| 6          | 6     | 100.0       | 6      | 18 | US-10-420-513A-1  |
| 7          | 6     | 100.0       | 6      | 21 | US-10-963-286-15  |
| 8          | 6     | 100.0       | 6      | 9  | US-09-735-363A-23 |
| 9          | 6     | 100.0       | 6      | 9  | US-09-735-363A-24 |
| 10         | 6     | 100.0       | 6      | 9  | US-09-735-363A-25 |
| 11         | 6     | 100.0       | 6      | 9  | US-09-735-363A-30 |
| 12         | 6     | 100.0       | 6      | 9  | US-09-735-363A-36 |
| 13         | 6     | 100.0       | 6      | 9  | US-09-735-363A-48 |
| 14         | 6     | 100.0       | 6      | 9  | US-09-735-363A-72 |
| 15         | 6     | 100.0       | 6      | 9  | US-09-735-363A-73 |
| 16         | 6     | 100.0       | 6      | 9  | US-09-735-363A-74 |
| 17         | 6     | 100.0       | 6      | 9  | US-09-735-363A-75 |
| 18         | 6     | 100.0       | 6      | 9  | US-09-735-363A-79 |
| 19         | 6     | 100.0       | 6      | 9  | US-09-879-668-3   |
| 20         | 6     | 100.0       | 6      | 9  | US-09-879-668-4   |
| 21         | 6     | 100.0       | 6      | 9  | US-09-879-668-5   |
| 22         | 6     | 100.0       | 6      | 9  | US-09-879-668-6   |
| 23         | 6     | 100.0       | 6      | 9  | US-09-879-668-11  |
| 24         | 6     | 100.0       | 6      | 10 | US-09-798-883B-55 |
| 25         | 6     | 100.0       | 6      | 10 | US-09-326-885-55  |
| 26         | 6     | 100.0       | 6      | 13 | US-10-026-389-4   |
| 27         | 6     | 100.0       | 6      | 13 | US-10-133-888-10  |

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| 83.3 | 5   | 9  | US-09-735-363A-9     | Sequence 9, Appli                 |
| 83.3 | 5   | 9  | US-09-735-363A-70    | Sequence 70, Appli                |
| 83.3 | 5   | 9  | US-09-879-668-1      | Sequence 1, Appli                 |
| 83.3 | 5   | 10 | US-09-958-221A-2     | Sequence 2, Appli                 |
| 83.3 | 5   | 11 | US-10-280-274-1      | Sequence 1, Appli                 |
| 83.3 | 5   | 12 | US-10-676-849-2      | Sequence 2, Appli                 |
| 83.3 | 5   | 13 | US-10-963-286-14     | Sequence 14, Appli                |
| 83.3 | 5   | 14 | US-10-190-312A-339   | Sequence 339, App                 |
| 73.3 | 4.4 | 16 | US-10-190-312A-344   | Sequence 344, App                 |
| 73.3 | 4.4 | 17 | US-09-735-363A-54    | Sequence 54, Appl                 |
| 66.7 | 4   | 4  | US-09-735-363A-59    | Sequence 59, Appli                |
| 66.7 | 4   | 5  | US-10-172-620-6      | Sequence 6, Appli                 |
| 66.7 | 4   | 6  | US-09-735-363A-39    | Sequence 39, Appli                |
| 66.7 | 4   | 6  | US-09-887-469-2      | Sequence 2, Appli                 |
| 66.7 | 4   | 6  | US-09-888-326-49     | Sequence 49, Appli                |
| 66.7 | 4   | 6  | US-09-776-479-645    | Sequence 645, App                 |
| 66.7 | 4   | 6  | US-09-776-479-645    | Sequence 645, App                 |
| 66.7 | 4   | 6  | US-09-887-469-2      | Sequence 2, Appli                 |
| 66.7 | 4   | 6  | US-10-112-653-619    | Sequence 619, App                 |
| 66.7 | 4   | 6  | US-10-017-995-645    | Sequence 645, App                 |
| 66.7 | 4   | 6  | US-10-336-265-2      | Sequence 2, Appli                 |
| 66.7 | 4   | 6  | US-10-336-265-5      | Sequence 5, Appli                 |
| 66.7 | 4   | 6  | US-10-091-281-27     | Sequence 27, Appli                |
| 66.7 | 4   | 6  | US-10-091-281-206    | Sequence 206, App                 |
| 66.7 | 4   | 6  | US-10-091-281-207    | Sequence 207, App                 |
| 66.7 | 4   | 6  | US-10-091-281-251    | Sequence 251, App                 |
| 66.7 | 4   | 6  | US-10-091-281-376    | Sequence 376, App                 |
| 66.7 | 4   | 6  | US-10-109-363-7      | Sequence 7, Appli                 |
| 66.7 | 4   | 6  | US-10-190-312A-311   | Sequence 311, App                 |
| 66.7 | 4   | 6  | US-10-314-578-645    | Sequence 645, App                 |
| 66.7 | 4   | 6  | US-10-413-357A-79    | Sequence 186, App                 |
| 66.7 | 4   | 6  | US-10-831-778-645    | Sequence 79, Appl                 |
| 66.7 | 4   | 6  | US-10-824-158A-79    | Sequence 645, App                 |
| 66.7 | 4   | 6  | US-10-912-932A-125   | Sequence 79, Appl                 |
| 56.7 | 3.4 | 5  | US-09-735-363A-61    | Sequence 125, App                 |
| 56.7 | 3.4 | 5  | US-10-027-632-177517 | Sequence 61, Appl                 |
| 56.7 | 3.4 | 5  | US-10-027-632-177522 | Sequence 177517, Sequence 177522, |
| 56.7 | 3.4 | 5  | US-10-027-632-177527 | Sequence 177527,                  |
| 56.7 | 3.4 | 5  | US-10-122-630-4      | Sequence 4, Appli                 |
| 56.7 | 3.4 | 5  | US-10-122-630-6      | Sequence 6, Appli                 |
| 56.7 | 3.4 | 5  | US-10-122-633-4      | Sequence 4, Appli                 |
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| 56.7 | 3.4 | 5  | US-10-172-620-4      | Sequence 4, Appli                 |
| 56.7 | 3.4 | 5  | US-10-185-363-2      | Sequence 2, Appli                 |
| 56.7 | 3.4 | 5  | US-10-027-632-177517 | Sequence 177517,                  |
| 56.7 | 3.4 | 5  | US-10-027-632-177522 | Sequence 177522,                  |
| 56.7 | 3.4 | 5  | US-10-027-632-177527 | Sequence 177527,                  |
| 56.7 | 3.4 | 5  | US-08-463-404-52     | Sequence 93, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-23    | Sequence 52, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-24    | Sequence 23, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-25    | Sequence 24, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-30    | Sequence 25, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-36    | Sequence 26, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-48    | Sequence 30, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-72    | Sequence 32, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-73    | Sequence 36, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-74    | Sequence 48, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-75    | Sequence 72, Appl                 |
| 56.7 | 3.4 | 6  | US-09-735-363A-79    | Sequence 73, Appl                 |
| 56.7 | 3.4 | 6  | US-09-879-668-3      | Sequence 74, Appl                 |
| 56.7 | 3.4 | 6  | US-09-879-668-4      | Sequence 75, Appl                 |
| 56.7 | 3.4 | 6  | US-09-879-668-5      | Sequence 79, Appl                 |
| 56.7 | 3.4 | 6  | US-09-879-668-6      | Sequence 3, Appli                 |
| 56.7 | 3.4 | 6  | US-09-879-668-11     | Sequence 4, Appli                 |
| 56.7 | 3.4 | 6  | US-09-879-668-11     | Sequence 5, Appli                 |
| 56.7 | 3.4 | 6  | US-09-879-668-11     | Sequence 10, Appl                 |
| 56.7 | 3.4 | 6  | US-09-798-883B-55    | Sequence 11, Appl                 |
| 56.7 | 3.4 | 6  | US-09-326-885-55     | Sequence 55, Appl                 |
| 56.7 | 3.4 | 6  | US-10-026-389-4      | Sequence 55, Appl                 |
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| 56.7 | 3.4 | 6  | US-10-133-888-10     | Sequence 10, Appl                 |

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c 82 3.4 56.7 6 13 US-10-027-632-53495 Sequence 53495, A  
c 83 3.4 56.7 6 13 US-10-027-632-178012 Sequence 178012,  
84 3.4 56.7 6 14 US-10-092-908-18 Sequence 18, Appl  
c 85 3.4 56.7 6 14 US-10-127-645-2 Sequence 2, Appl  
c 86 3.4 56.7 6 14 US-10-127-645-4 Sequence 4, Appl  
87 3.4 56.7 6 15 US-10-280-274-3 Sequence 3, Appl  
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91 3.4 56.7 6 15 US-10-280-274-10 Sequence 10, Appl  
92 3.4 56.7 6 15 US-10-280-274-11 Sequence 11, Appl  
93 3.4 56.7 6 15 US-10-264-280-1 Sequence 1, Appl  
c 94 3.4 56.7 6 15 US-10-264-280-3 Sequence 3, Appl  
95 3.4 56.7 6 15 US-10-264-280-5 Sequence 5, Appl  
c 96 3.4 56.7 6 15 US-10-264-280-7 Sequence 7, Appl  
97 3.4 56.7 6 15 US-10-255-535-12 Sequence 12, Appl  
c 98 3.4 56.7 6 16 US-10-041-860-101 Sequence 101, App  
c 99 3.4 56.7 6 16 US-10-041-860-112 Sequence 112, App  
c 100 3.4 56.7 6 16 US-10-041-860-131 Sequence 131, App

## ALIGNMENTS

## RESULT 1

US-09-735-363A-10  
; Sequence 10, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-10

Query Match 100.0%; Score 6; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
Db 1 GTGTGT 6

## RESULT 2

US-09-735-363A-71  
; Sequence 71, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925

; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 71  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-71  
Query Match 100.0%; Score 6; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGTGT 6  
Db 1 GTGTGT 6  
RESULT 3  
US-09-879-668-2  
; Sequence 2, Application US/09879668  
; Patent No. US20020091095A1  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0241 42368-256931  
; CURRENT APPLICATION NUMBER: US/09/879,668  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-09-879-668-2

Query Match 100.0%; Score 6; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
Db 1 GTGTGT 6

## RESULT 4

US-10-280-274-2  
; Sequence 2, Application US/10280274  
; Publication No. US2003011976A1  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0242 42368-279803  
; CURRENT APPLICATION NUMBER: US/10/280,274  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12



; PRIOR APPLICATION NUMBER: US 09/879,668  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-2

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
Db 1 GTGTGT 6

## RESULT 5

US-10-297-008-11/c  
; Sequence 11, Application US/10297008  
; Publication No. US20030211581A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Virginia Patent Foundation  
; APPLICANT: Herr, John  
; APPLICANT: Reddi, Prabhakara P  
; TITLE OF INVENTION: An Insulator Element having Enhancer-Blocking Properties  
; FILE REFERENCE: 00567-02  
; CURRENT APPLICATION NUMBER: US/10/297,008  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 60/208,371  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-297-008-11

Query Match 100.0%; Score 6; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
Db 6 GTGTGT 1

## RESULT 6

US-10-420-513A-1  
; Sequence 1, Application US/10420513A  
; Publication No. US20040058883A1  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Filion, Mario C.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of  
; FILE REFERENCE: 02811-0301 (42368-283135)  
; CURRENT APPLICATION NUMBER: US/10/420,513A  
; CURRENT FILING DATE: 2003-04-22  
; PRIOR APPLICATION NUMBER: US 60/374,540

; PRIOR FILING DATE: 2002-04-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-420-513A-1

Query Match 100.0%; Score 6; DB 18; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
Db 1 GTGTGT 6

## RESULT 7

US-10-963-286-15  
; Sequence 15, Application US/10963286  
; Publication No. US20050095634A1  
; GENERAL INFORMATION:  
; APPLICANT: BAKER, Joffre B.  
; APPLICANT: CRONIN, Maureen T.  
; APPLICANT: KIEFER, Michael C.  
; APPLICANT: LI, Xitong  
; APPLICANT: CLARK, Kim  
; TITLE OF INVENTION: QRT-PCR ASSAY SYSTEM FOR GENE EXPRESSION  
; FILE REFERENCE: 39740-0014A  
; CURRENT APPLICATION NUMBER: US/10/963,286  
; CURRENT FILING DATE: 2004-10-11  
; PRIOR APPLICATION NUMBER: US 60/512,556  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-963-286-15

Query Match 100.0%; Score 6; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
Db 1 GTGTGT 6

## RESULT 8

US-09-735-363A-9  
; Sequence 9, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Filion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0

```
; SEQ ID NO 9
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-9
```

```
Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGTG 5
 |||||
Db 2 GTGTG 6
```

## RESULT 9

```
US-09-735-363A-70
; Sequence 70, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-70
```

```
Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGTG 5
 |||||
Db 2 GTGTG 6
```

## RESULT 10

```
US-09-879-668-1
; Sequence 1, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-1
```

```
Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGTG 5
 |||||
Db 2 GTGTG 6
```

## RESULT 11

```
US-09-958-221A-2/c
; Sequence 2, Application US/09958221A
; Publication No. US20030017471A1
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-2
```

```
Query Match 83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGTG 5
 |||||
Db 5 GTGTG 1
```

## RESULT 12

```
US-10-280-274-1
; Sequence 1, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
```

; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1:  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-1

Query Match 83.3%; Score 5; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5  
|  
|  
|  
|  
Db 2 GTGTG 6

## RESULT 13

US-10-676-849-2/c

; Sequence 2, Application US/10676849

; Publication No. US200500938A1

; GENERAL INFORMATION:

; APPLICANT: Haeringen van, Willem A.

; APPLICANT: Haeringen van, Hendrik

; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS

; FILE REFERENCE: 92750/64

; CURRENT APPLICATION NUMBER: US/10/676,849

; CURRENT FILING DATE: 2003-09-30

; PRIOR APPLICATION NUMBER: US/09/958,221

; PRIOR FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: EP 00200757.3

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: PCT/NL01/00177

; PRIOR FILING DATE: 2001-03-05

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-10-676-849-2

Query Match 83.3%; Score 5; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5  
|  
|  
|  
|  
Db 5 GTGTG 1

## RESULT 14

US-10-963-286-14/c

; Sequence 14, Application US/10963286

; Publication No. US2005009563A1

; GENERAL INFORMATION:

; APPLICANT: BAKER, Joffre B.

; APPLICANT: CRONIN, Maureen T.

; APPLICANT: KIEFER, Michael C.

; APPLICANT: Li, Xitong

; APPLICANT: CLARK, Kim

; TITLE OF INVENTION: qRT-PCR ASSAY SYSTEM FOR GENE EXPRESSION

; FILE REFERENCE: 39740-0014A

; CURRENT APPLICATION NUMBER: US/10/963,286

; CURRENT FILING DATE: 2004-10-11

; PRIOR APPLICATION NUMBER: US 60/512,556

; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-963-286-14

Query Match 83.3%; Score 5; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5  
|  
|  
|  
|  
Db 5 GTGTG 1

## RESULT 15

US-10-190-312A-339/c

; Sequence 339, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; TITLE OF INVENTION: methods for detecting and using such DNA sequences

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 339

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-339

Query Match 73.3%; Score 4.4; DB 16; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGTGT 6  
|  
|  
|  
|  
Db 6 GTGGGT 1

## RESULT 16

US-10-190-312A-344/c

; Sequence 344, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; TITLE OF INVENTION: methods for detecting and using such DNA sequences

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 344

; LENGTH: 6

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-344

Query Match 73.3%; Score 4.4; DB 16; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6  
| | | | |  
Db 6 GGTGT 1

RESULT 17  
US-09-735-363A-54  
; Sequence 54, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 54  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-54

Query Match 66.7%; Score 4; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
| | | |  
Db 1 GTGT 4

RESULT 18  
US-09-735-363A-59  
; Sequence 59, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 59  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-59

Query Match 66.7%; Score 4; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5  
| | | | |  
Db 1 TGTG 4

RESULT 19  
US-10-172-620-6  
; Sequence 6, Application US/10172620  
; Publication No. US20030053995A1  
; GENERAL INFORMATION:  
; APPLICANT: Hung, Mien-Chie  
; APPLICANT: Lin, Shiao-Yih  
; TITLE OF INVENTION: Methods and Compositions for Inhibiting EGF Receptor  
; FILE REFERENCE: UTSC:720US  
; CURRENT APPLICATION NUMBER: US/10/172,620  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/298,579  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Muted ATRS Sequence  
US-10-172-620-6

Query Match 66.7%; Score 4; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4  
| | | | |  
Db 2 GTGT 5

RESULT 20  
US-09-735-363A-39  
; Sequence 39, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 39  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-39

Query Match 66.7%; Score 4; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5  
| | | | |

```
Db 2 TGTG 5

RESULT 21
US-09-887-469-2/c
; Sequence 2, Application US/09887469
; Patent No. US20020146433A1
; GENERAL INFORMATION:
; APPLICANT: Krempel, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-US
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-2

Query Match 66.7%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
 ||||
Db 4 TGTG 1

RESULT 22
US-09-888-326-49
; Sequence 49, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-49

Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
 ||||

Db 3 GTGT 6

RESULT 23
US-09-776-479-645
; Sequence 645, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 645
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-645

Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
 ||||
Db 3 GTGT 6

RESULT 24
US-09-776-479-645
; Sequence 645, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 645
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-645

Query Match 66.7%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
 ||||
Db 3 GTGT 6

RESULT 25
US-09-887-469-2/c
 ||||
```

; Sequence 2, Application US/09887469  
; Publication No. US20040258714A9  
; GENERAL INFORMATION:  
; APPLICANT: Krempf, Christine D.  
; APPLICANT: Collins, Peter L.  
; APPLICANT: Murphy, Brian R.  
; APPLICANT: Buchholz, Ursula  
; APPLICANT: Whitehead, Stephen S.  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING  
; TITLE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES  
; FILE REFERENCE: 15280-424-1US  
; CURRENT APPLICATION NUMBER: US/09/887,469  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,708  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Artificial  
; OTHER INFORMATION: Respiratory Syncytial Virus  
US-09-887-469-2

Query Match 66.7%; Score 4; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0

QY 2 TGTG 5  
|||  
Db 4 TGTG 1

RESULT 26  
US-10-112-653-619  
; Sequence 619, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Daniel J.  
; APPLICANT: Berg, Arthur M.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 619  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-619

Query Match 66.7%; Score 4; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0

QY 1 TGTG 4  
|||  
Db 3 GTGT 6

RESULT 27  
US-10-017-995-645  
; Sequence 645, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:

; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 645  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-645

Query Match 66.7%; Score 4; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0

QY 1 GTGT 4  
|||  
Db 3 GTGT 6

RESULT 28  
US-10-336-265-2  
; Sequence 2, Application US/10336265  
; Publication No. US20030148988A1  
; GENERAL INFORMATION:  
; APPLICANT: Kool, Eric T.  
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for  
; TITLE OF INVENTION: the Elongation of Telomere Repeats  
; FILE REFERENCE: 12665.0021.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/336,265  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 60/345,056  
; PRIOR FILING DATE: 2002-01-04  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-10-336-265-2

Query Match 66.7%; Score 4; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0

QY 2 TGTG 5  
|||  
Db 1 TGTG 4

RESULT 29  
US-10-336-265-5/c  
; Sequence 5, Application US/10336265  
; Publication No. US20030148988A1  
; GENERAL INFORMATION:  
; APPLICANT: Kool, Eric T.  
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for  
; TITLE OF INVENTION: the Elongation of Telomere Repeats  
; FILE REFERENCE: 12665.0021.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/336,265  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 60/345,056  
; PRIOR FILING DATE: 2002-01-04  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 6

```
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-10-336-265--5

Query Match 66.7%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
Db 6 TGTG 3

RESULT 30
US-10-091-281-27
; Sequence 27, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587,338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative HAML/AML1.01 motif
US-10-091-281-27

Query Match 66.7%; Score 4; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
Db 1 TGTG 4

Search completed: July 21, 2005, 07:13:12
Job time : 714.6 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds  
(without alignments)  
189.533 Million cell updates/sec

Title: US-09-735-363A-25  
Perfect score: 6  
Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| C 1        | 6     | 100.0       | 6      | 13 | Adr32691 Human nlc  |
| C 2        | 5     | 83.3        | 5      | 8  | Abz75664 Helicase-  |
| C 3        | 5     | 83.3        | 6      | 2  | Aat96305 Fungal te  |
| C 4        | 5     | 83.3        | 6      | 8  | Abx50029 Telomere   |
| C 5        | 5     | 83.3        | 6      | 12 | Adj35723 Stabilisi  |
| C 6        | 4.4   | 73.3        | 6      | 2  | Aat04935 Anti-HIV   |
| C 7        | 4.4   | 73.3        | 6      | 6  | Abz77547 Angiogene  |
| C 8        | 4.4   | 73.3        | 6      | 6  | Abx87320 Mammalian  |
| C 9        | 4.4   | 73.3        | 6      | 9  | Acad99345 Immunosti |
| C 10       | 4.4   | 73.3        | 6      | 10 | Acad88957 Selection |
| C 11       | 4.4   | 73.3        | 6      | 12 | Adj35665 Stabilisi  |
| C 12       | 4.4   | 73.3        | 6      | 12 | Adk14379 Candida p  |
| C 13       | 4.4   | 73.3        | 6      | 13 | Adr32931 Human nlc  |
| C 14       | 4     | 66.7        | 5      | 2  | Aat96299 Fungal te  |
| C 15       | 4     | 66.7        | 5      | 3  | Aaz93601 Transcrip  |
| C 16       | 4     | 66.7        | 5      | 8  | Abz75666 Helicase-  |
| C 17       | 4     | 66.7        | 5      | 8  | Abx49997 Telomere   |
| C 18       | 4     | 66.7        | 6      | 2  | Aaq50333 Ribozyme   |
| C 19       | 4     | 66.7        | 6      | 2  | Aat80319 Oligo HCV  |
| C 20       | 4     | 66.7        | 6      | 2  | Aat80320 Oligo HCV  |

|      |     |      |   |    |                     |
|------|-----|------|---|----|---------------------|
| C 21 | 4   | 66.7 | 6 | 2  | AAV61659 Fusarium   |
| C 22 | 4   | 66.7 | 6 | 3  | Aaz89322 Human UCP  |
| C 23 | 4   | 66.7 | 6 | 4  | AAS06241 PCR prime  |
| C 24 | 4   | 66.7 | 6 | 6  | Abk72534 Human OPA  |
| C 25 | 4   | 66.7 | 6 | 6  | Abz77550 Angiogene  |
| C 26 | 4   | 66.7 | 6 | 6  | Abz65903 Inhibitor  |
| C 27 | 4   | 66.7 | 6 | 6  | Abz65904 Inhibitor  |
| C 28 | 4   | 66.7 | 6 | 6  | Abk30087 Beta-lact  |
| C 29 | 4   | 66.7 | 6 | 9  | AcD99348 Immunosti  |
| C 30 | 4   | 66.7 | 6 | 10 | Adk14358 Human scl  |
| C 31 | 4   | 66.7 | 6 | 10 | Adk14140 Optineuri  |
| C 32 | 4   | 66.7 | 6 | 10 | Adk14096 Optineuri  |
| C 33 | 4   | 66.7 | 6 | 10 | Adk13916 Optineuri  |
| C 34 | 4   | 66.7 | 6 | 10 | Adk14095 Optineuri  |
| C 35 | 4   | 66.7 | 6 | 10 | Adk14265 Optineuri  |
| C 36 | 4   | 66.7 | 6 | 10 | Adk38298 Immune mo  |
| C 37 | 4   | 66.7 | 6 | 10 | Adk38299 Immune mo  |
| C 38 | 4   | 66.7 | 6 | 10 | Adk38306 Immune mo  |
| C 39 | 4   | 66.7 | 6 | 10 | Adk38277 Immune mo  |
| C 40 | 4   | 66.7 | 6 | 10 | Adk38273 Immune mo  |
| C 41 | 4   | 66.7 | 6 | 10 | Adk38281 Immune mo  |
| C 42 | 4   | 66.7 | 6 | 10 | Adk38307 Immune mo  |
| C 43 | 4   | 66.7 | 6 | 12 | Adk52744 Oligonucle |
| C 44 | 4   | 66.7 | 6 | 12 | Adj35342 Stabilisi  |
| C 45 | 4   | 66.7 | 6 | 12 | Adj35709 Stabilisi  |
| C 46 | 4   | 66.7 | 6 | 12 | Adj35456 Stabilisi  |
| C 47 | 4   | 66.7 | 6 | 12 | Adj35541 Stabilisi  |
| C 48 | 4   | 66.7 | 6 | 12 | Adk14301 Candida p  |
| C 49 | 4   | 66.7 | 6 | 12 | Adk14312 Candida p  |
| C 50 | 4   | 66.7 | 6 | 12 | Adk198067 Deleted s |
| C 51 | 4   | 66.7 | 6 | 12 | Ado05792 Telomere-  |
| C 52 | 4   | 66.7 | 6 | 13 | Adr37260 Human nlc  |
| C 53 | 4   | 66.7 | 6 | 13 | Adr32740 Human nlc  |
| C 54 | 4   | 66.7 | 6 | 13 | Adr32631 Human nlc  |
| C 55 | 4   | 66.7 | 6 | 13 | Adr32677 Human nlc  |
| C 56 | 4   | 66.7 | 6 | 13 | Adr32762 Human nlc  |
| C 57 | 4   | 66.7 | 6 | 13 | Adr32553 Human nlc  |
| C 58 | 4   | 66.7 | 6 | 13 | Adr32877 Human nlc  |
| C 59 | 4   | 66.7 | 6 | 13 | Adr37261 Human nlc  |
| C 60 | 4   | 66.7 | 6 | 13 | Adr37263 Human nlc  |
| C 61 | 4   | 66.7 | 6 | 13 | Adn33281 E. coli 2  |
| C 62 | 4   | 66.7 | 6 | 13 | Adn33272 E. coli 2  |
| C 63 | 3.6 | 60.0 | 6 | 13 | Adr37222 Human nlc  |
| C 64 | 3.6 | 60.0 | 6 | 13 | Adr37224 Human nlc  |
| C 65 | 3.6 | 60.0 | 6 | 13 | Adr37225 Human nlc  |
| C 66 | 3.6 | 60.0 | 6 | 13 | Adr37203 Human nlc  |
| C 67 | 3.6 | 60.0 | 6 | 13 | Adr37223 Human nlc  |
| C 68 | 3.6 | 60.0 | 6 | 13 | Adr37221 Human nlc  |
| C 69 | 3.6 | 60.0 | 6 | 13 | Adr37226 Human nlc  |
| C 70 | 3.6 | 60.0 | 6 | 13 | Adr37202 Human nlc  |
| C 71 | 3.4 | 56.7 | 5 | 2  | AAV72347 US5908745  |
| C 72 | 3.4 | 56.7 | 5 | 2  | AAV72349 US5908745  |
| C 73 | 3.4 | 56.7 | 5 | 8  | Abz75669 Helicase-  |
| C 74 | 3.4 | 56.7 | 5 | 10 | Adh0372 Myctophid   |
| C 75 | 3.4 | 56.7 | 6 | 2  | Aaq61541 TDI promo  |
| C 76 | 3.4 | 56.7 | 6 | 2  | Aat80318 Oligo HCV  |
| C 77 | 3.4 | 56.7 | 6 | 2  | Aaa45399 TDI promo  |
| C 78 | 3.4 | 56.7 | 6 | 3  | Aaa62709 PNA clamp  |
| C 79 | 3.4 | 56.7 | 6 | 4  | Aaf91656 Breast-ca  |
| C 80 | 3.4 | 56.7 | 6 | 4  | Aaf91686 Breast-ca  |
| C 81 | 3.4 | 56.7 | 6 | 4  | Aad17580 AC repeat  |
| C 82 | 3.4 | 56.7 | 6 | 6  | Abk65902 Inhibitor  |
| C 83 | 3.4 | 56.7 | 6 | 6  | Abk88579 Hepatitis  |
| C 84 | 3.4 | 56.7 | 6 | 6  | Abk87321 Mammalian  |
| C 85 | 3.4 | 56.7 | 6 | 8  | Abz75668 Helicase-  |
| C 86 | 3.4 | 56.7 | 6 | 12 | Adj35778 Stabilisi  |
| C 87 | 3.4 | 56.7 | 6 | 12 | Adj35353 Stabilisi  |
| C 88 | 3.4 | 56.7 | 6 | 12 | Adj35593 Stabilisi  |
| C 89 | 3.4 | 56.7 | 6 | 12 | Adj35427 Stabilisi  |
| C 90 | 3.4 | 56.7 | 6 | 12 | Adj35500 Stabilisi  |
| C 91 | 3.4 | 56.7 | 6 | 12 | Adj35463 Stabilisi  |
| C 92 | 3.4 | 56.7 | 6 | 12 | Adj35519 Stabilisi  |
| C 93 | 3.4 | 56.7 | 6 | 12 | Adj35391 Stabilisi  |

c 94 3.4 56.7 6 12 ADJ35621 Stabilisi  
c 95 3.4 56.7 6 12 ADO81155  
Ado81155 Prion pro  
c 96 3.4 56.7 6 13 ADR32491 Human nic  
Adr32491 Human nic  
c 97 3.4 56.7 6 13 ADR32878 Human nic  
Adr32878 Human nic  
c 98 3.4 56.7 6 13 ADR32508 Human nic  
Aan92488 Sequence  
c 99 3.2 53.3 6 1 AAN92488  
Aan92488 Sequence  
c 100 3.2 53.3 6 1 AAN92488

ALIGNMENTS

RESULT 1  
ADR32691/c  
ID ADR32691 standard; DNA; 6 BP.  
XX  
AC ADR32691;  
DT 04-NOV-2004 (first entry)  
DE Human nicking agent target DNA #232.  
XX  
DE ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
OS Homo sapiens.  
XX  
XX WO2004067765-A2.  
XX  
XX 12-AUG-2004.  
XX  
XX 29-JAN-2004; 2004WO-US002720.  
XX  
XX 29-JAN-2003; 2003US-0443811P.  
PR  
XX (KECK-) KECK GRADUATE INST.  
XX  
XX Van Ness J, Galas DJ, Van Ness LX;  
PI WPI; 2004-581010/56.  
XX  
XX Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
XX Example 1; Page 75; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with  
CC components under nicking conditions, where the components comprise a  
CC nicking agent, and the conditions cause the nicking agent to nick the  
CC nucleic acid sample to thus produce a family of initiating  
CC oligonucleotide fragments, and subjecting one or more members of the  
CC family of initiating oligonucleotide fragments to a characterization  
CC process to thus provide results. The method is useful for creating an  
CC assay panel of diagnostic oligonucleotides that can identify any organism  
CC or individual. The method is useful for characterizing other DNA  
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
CC The method, kit or composition is useful for identifying the source  
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
CC non-human animal or human. The method is particularly useful for rapidly  
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
CC subspecies, and especially strains or individuals of the subspecies. It  
CC is especially useful for identifying different bacterial strains involved  
CC in e.g., nosocomial infections. Furthermore, the method is useful for  
CC diagnosing bacterial disease in plants and humans, monitoring for  
CC bacterial content and/or contamination in the environment, monitoring  
CC food for bacterial contamination, monitoring manufacturing processes for  
CC bacterial contamination, monitoring quality assurance/quality control of  
CC laboratory tests involving microbiological assays, tracing bacterial  
CC contamination and/or outbreaks of bacterial infections, genome mapping,  
CC monitoring bioremediation sites, and for monitoring agricultural sites

CC for test crops, bacteria and recombinant molecules. This sequence  
CC corresponds to nucleic acid used in the method of the invention.  
XX  
SQ Sequence 6 BP; 1 A; 5 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 6; DB 13; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTGG 6  
DB 6 GGGTGG 1  
RESULT 2  
ABZ75664/c  
ID ABZ75664 standard; DNA; 5 BP.  
XX  
AC ABZ75664;  
DT 15-MAY-2003 (first entry)  
DE Helicase-like transcription factor (HLTF) binding oligonucleotide.  
XX  
XX HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;  
KW helicase-like transcription factor; telomerase reverse transcriptase;  
KW dermatological; gynaecological; TERT; gene therapy; cancer; ss.  
XX  
XX Synthetic.  
XX  
XX WO2003002068-A2.  
XX  
XX 09-JAN-2003.  
PD  
XX 27-JUN-2002; 2002WO-US020757.  
PF  
XX 27-JUN-2001; 2001US-0301384P.  
PR  
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
PA  
XX Androphy EJ, Doshi N, Delayew A;  
PI WPI; 2003-210197/20.  
XX  
XX Inhibiting carcinogenesis of a cell, especially useful for treating a  
PT human papilloma virus-mediated hyperproliferative lesion (warts) or  
PT cancer, by reducing the activity of helicase-like transcription factor in  
PT the cell.  
XX  
XX Claim 15; Page 24; 36pp; English.  
PS  
XX The invention relates to inhibiting carcinogenesis of a cell, or  
CC inhibiting growth of a cell in a human papillomavirus (HPV)-mediated  
CC hyperproliferative lesion. The method involves reducing the amount of  
CC helicase-like transcription factor (HLTF) in the cell or inhibiting the  
CC binding of endogenous HLTF to telomerase reverse transcriptase (TERT)  
CC promoter. The method is useful for inhibiting carcinogenesis of a cell,  
CC or inhibiting growth of a cell in an HPV-mediated hyperproliferative  
CC lesion. The method is particularly useful for treating cancer (especially  
CC cervical cancer), or hyperproliferative lesions (warts) caused by HPV.  
CC The method is also useful for diagnosing a neoplasm, or detecting the  
CC presence of a malignant tumour or a predisposition to developing the  
CC tumour. Sequences ABZ75663-669 represent specific examples of  
CC oligonucleotides that bind to endogenous HLTF, thereby preventing HLTF  
CC from binding to an intact TERT promoter region  
XX  
SQ Sequence 5 BP; 1 A; 4 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 83.3%; Score 5; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5

Db                   |||||  
                      5 GGCTG 1

RESULT 3  
AAT96305  
ID AAT96305 standard; DNA; 6 BP.  
XX  
AC AAT96305;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-APR-1998 (first entry)  
XX  
XX Fungal telomeric nucleic acid sequence.  
DE  
XX  
XX Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
KW telomerase activity; diagnosis; fungal infection; fungus; fungi;  
KW malarial infection; malaria; ss.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN US5695932-A.  
XX  
PD 09-DEC-1997.  
XX  
PF 13-MAY-1993; 93US-00060952.  
XX  
PR 13-MAY-1992; 92US-00882438.  
PR 24-MAR-1993; 93US-00038766.  
XX  
PA (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.  
PA (TEXA) UNIV TEXAS SYSTEM.  
XX  
PI Blackburn EH, Shay J, Mceachern MJ, West MD, Wright W;  
XX  
DR WPI; 1998-041292/04.  
XX  
PT Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -  
PT by detecting telomerase activity.  
XX  
PS Claim 5; Col 93-94; 82pp; English.  
XX  
CC The present sequence can be used in a novel method for detecting a  
CC eukaryotic pathogen in a patient. The method comprises obtaining a sample  
CC of somatic tissue or cells from the patient, determining if telomerase  
CC activity is present and correlating this with the presence of the  
CC pathogen. The method is useful for diagnosis of fungal infections,  
CC especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,  
CC Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides,  
CC Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,  
CC especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 6 BP; 0 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match           83.3%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 GGCTG 5  
              |||||  
Db           2 GGCTG 6

RESULT 4  
ABX50029  
ID ABX50029 standard; DNA; 6 BP.  
XX  
AC ABX50029;  
XX  
DT 12-FEB-2003 (first entry)  
XX  
DE Telomere length and/or telomerase activity related polynucleotide #52.

XX  
KW Cell proliferation; cell senescence; telomere length;  
KW telomerase activity; cell replication; neoplasia; cancer;  
KW age-related macular degeneration; Alzheimer's disease; atherosclerosis;  
KW telomerase; telomerase inhibitor; immortalised cell; ss.  
XX  
OS Synthetic.  
XX  
PN US2002127634-A1.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-JUN-1995; 95US-00463404.  
XX  
PR 13-MAY-1992; 92US-00882438.  
PR 24-MAR-1993; 93US-00038766.  
PR 13-MAY-1993; 93US-00060952.  
XX  
PA (WEST/) WEST M D.  
PA (SHAY/) SHAY J.  
PA (WRIG/) WRIGHT W.  
PA (BLAC/) BLACKBURN E H.  
XX  
PI West MD, Shay J, Wright W, Blackburn EH;  
XX  
DR WPI; 2003-066896/06.  
XX  
PT Treating condition associated with cell senescence or increased rate of  
PT cell proliferation, by administering to cell an agent that derepresses  
PT telomerase in the senescing cells or that reduces loss of telomere  
PT length.  
XX  
PS Disclosure; Page 50; 86pp; English.  
XX  
CC The invention describes a method use for treating increased rate of  
CC proliferation of a cell or extending the ability of a cell to replicate,  
CC or treating a disease associated with cell senescence. The method  
CC comprises administering an agent to reduce loss of telomere length within  
CC the cell during proliferation or replication, or to derepress telomerase  
CC in the senescing cells. The method is useful for treating a condition  
CC associated with an increased rate of proliferation of a cell extending  
CC the ability of a cell to replicate, or for treating a disease or  
CC condition associated with cell senescence e.g. neoplasia. A second method  
CC disclosed in the invention is useful for treating a condition associated  
CC with an elevated level of telomerase activity within a cell e.g. cancer.  
CC Also disclosed is a method useful for diagnosis of a condition associated  
CC with an increased rate of proliferation in a cell in an individual e.g.  
CC age-related macular degeneration, astrocytes associated with Alzheimer's  
CC disease and endothelial cells associated with atherosclerosis. This  
CC sequence represents a polynucleotide used in the study of telomere length  
CC and telomerase activity described in the invention  
XX  
SQ Sequence 6 BP; 0 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match           83.3%; Score 5; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 GGCTG 5  
              |||||  
Db           2 GGCTG 6

RESULT 5  
ADJ35723/c  
ID ADJ35723 standard; DNA; 6 BP.  
XX  
AC ADJ35723;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Stabilising anti-repression, STAR, element dyad sequence #389.

KW STAR affiliated proteinaceous molecule; post translational modification;  
 XX stabilising anti-repression; STAR; STAR element; ds; dyad.  
 OS Unidentified.  
 XX WO2003106674-A2.  
 XX 24-DEC-2003.  
 XX 30-MAY-2003; 2003WO-NL000410.  
 XX 14-JUN-2002; 2002EP-00077344.  
 XX (CHRO-) CHROMAGENICS BV.  
 XX  
 PI Otte AP, Kruckeberg AL, Satiijn DPE;  
 XX WPI; 2004-082195/08.  
 XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 XX  
 PS Disclosure; Page 103; 177pp; English.  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 XX  
 XX Sequence 6 BP; 1 A; 5 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 5; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB |||||  
 5 GGGTG 1  
 RESULT 6  
 AAT04935  
 ID AAT04935 standard; DNA; 6 BP.  
 XX  
 AC AAT04935;  
 XX  
 DT 10-MAY-1996 (first entry)  
 XX  
 DE Anti-HIV oligodeoxynucleotide.  
 XX  
 XX Anti-HIV; AIDS; ARC; treatment; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9526190-A1.  
 XX  
 XX 05-OCT-1995.  
 XX  
 XX 24-MAR-1995; 95WO-JP000543.  
 XX  
 XX 25-MAR-1994; 94JP-00092809.  
 XX 25-MAR-1994; 94JP-00092810.  
 XX  
 XX (KAJI/) KAJI A.  
 PA  
 XX

PI Kaji A;  
 XX WPI; 1995-351196/45.  
 XX  
 XX Anti HIV agents useful for the treatment of HIV, AIDS and ARC - comprise  
 PT a phosphodiester linked oligonucleotide deriv.  
 XX  
 PS Example 3; Page 11; 19pp; Japanese.  
 XX  
 CC The oligodeoxynucleotides AAT04934/35 are anti-HIV agents, useful for  
 CC treating HIV, AIDS and ARC. They are pref. given in a dosage of 1-100  
 CC mg/day parenterally, or 0.1- 6g/day orally  
 XX  
 XX Sequence 6 BP; 0 A; 0 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 4.4; DB 2; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGGTGG 6  
 DB |||||  
 1 GGGGGG 6  
 RESULT 7  
 ABS77547/c  
 ID ABS77547 standard; DNA; 6 BP.  
 XX  
 AC ABS77547;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #31.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; tetangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200253141-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 14-DEC-2001; 2001WO-US048458.  
 XX  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA  
 PI Bratzler RL;  
 XX  
 XX WPI; 2002-566690/60.  
 DR  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 PS Claim 2; Page 20; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
 |||||  
 Db 6 GGGGGG 1

RESULT 8  
 ABK87320  
 ID ABK87320 standard; DNA; 6 BP.

XX AC ABK87320;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE Mammalian SPI recognition sequence #1.

XX Nucleic acid detection; Spl; ss.

XX Mammalia.  
 XX WO200244326-A2.

PN 06-JUN-2002.

PD 26-NOV-2001; 2001WO-US044215.

PF 30-NOV-2000; 2000US-00728574.

XX (STRA-) STRATAGENE.

XX Sorge JA, Whalen AM;

XX WPI; 2002-508503/54.

XX Detecting/measuring target nucleic acid, by forming cleavage structure by  
 PT incubating target nucleic acid with probe having binding moiety, cleaving  
 PT structure to release nucleic acid and detecting released fragments.

XX Disclosure; Page 75; 157pp; English.

XX This invention relates to a novel method for detecting/measuring a target  
 CC nucleic acid. The method comprises forming a cleavage structure by  
 CC incubating the target sequence with a probe comprising a binding moiety  
 CC and a secondary structure that changes upon binding of the probe to the  
 CC target, cleaving the cleavage structure to release a nucleic acid  
 CC fragment, and detecting and/or measuring the fragment captured by binding  
 CC of the binding moiety to a capture element on a solid support. The method  
 CC of the invention is useful for detecting or measuring a target nucleic  
 CC acid and are useful for generating a signal indicative of the presence of  
 CC the target nucleic acid in a sample. Another method of the invention is  
 CC useful for simultaneously forming a cleavage structure, amplifying the  
 CC target nucleic acid in a sample and cleaving the cleavage structure. The  
 CC method does not require multiple steps, subsequent amplification process,  
 CC and allows for concurrent amplification and detection of target nucleic  
 CC acid in a sample. The present sequence represents the Mammalian SPI  
 CC recognition sequence shown in the specification  
 XX

SQ Sequence 6 BP; 0 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
 |||||  
 Db 1 GGGCGG 6

RESULT 9  
 ACD99345/C  
 ID ACD99345 standard; DNA; 6 BP.

XX AC ACD99345;

XX 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #31.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

XX (BERG/) BERG D J.

XX Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 9; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid

SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
 |||||  
 Db 6 GGGGGG 1

RESULT 10

ACA88957  
 ID ACA88957 standard; DNA; 6 BP.

XX AC ACA88957;

XX 08-JUL-2003 (first entry)

XX Selection and amplification of genetic markers PCR related primer #68.

|            |                                                                           |
|------------|---------------------------------------------------------------------------|
| XX         | Genetic marker selection; multiplex PCR amplification;                    |
| KW         | prenatal diagnostic testing; foetal sex determination;                    |
| KW         | genetic identification; DNA profiling; DNA fingerprinting;                |
| KW         | forensic analysis; PCR; primer; ss.                                       |
| OS         | Homo sapiens.                                                             |
| XX         |                                                                           |
| PN         | WO2003031646-A1.                                                          |
| XX         |                                                                           |
| PD         | 17-APR-2003.                                                              |
| XX         |                                                                           |
| PF         | 14-OCT-2002; 2002WO-AU001388.                                             |
| XX         |                                                                           |
| PR         | 12-OCT-2001; 2001AU-00008234.                                             |
| PR         | 12-OCT-2001; 2001AU-00008235.                                             |
| XX         |                                                                           |
| PA         | (UYQU ) UNIV QUEENSLAND.                                                  |
| XX         |                                                                           |
| PI         | Findlay I, Matthews PL, Mulcahy BK;                                       |
| XX         |                                                                           |
| DR         | WPI; 2003-381725/36.                                                      |
| XX         |                                                                           |
| PT         | Selecting genetic markers as targets for nucleic acid sequence            |
| PT         | amplification, useful for improving genetic testing, e.g. fetal sex       |
| PT         | determination, comprises selecting each of the genetic markers according  |
| PT         | to a heterozygosity index.                                                |
| XX         |                                                                           |
| PS         | Claim 36; Page 40; 64pp; English.                                         |
| XX         |                                                                           |
| CC         | The invention describes a method of selecting genetic markers as targets  |
| CC         | for nucleic acid sequence amplification comprising selecting each of the  |
| CC         | genetic markers according to a heterozygosity index of 0.5 or greater.    |
| CC         | Selecting and amplification of genetic markers are useful as targets for  |
| CC         | nucleic acid sequence amplification, for genetic testing or facilitating  |
| CC         | multiplex PCR amplification from limiting amounts of target nucleic acid. |
| CC         | The methods are also useful for improving genetic diagnostic and          |
| CC         | screening methods, such as prenatal diagnostic testing, foetal sex        |
| CC         | determination or genetic identification, e.g. DNA profiling or DNA        |
| CC         | fingerprinting. The nucleic acid sequence amplification is also useful in |
| CC         | forensic analysis of degraded, old, ancient and difficult samples that    |
| CC         | are difficult to amplify and identify. This sequence represents a PCR     |
| CC         | primer used in the selection and amplification of genetic markers         |
| XX         |                                                                           |
| SQ         | Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;                          |
|            |                                                                           |
|            | Query Match 73.3%; Score 4.4; DB 10; Length 6;                            |
|            | Best Local Similarity 83.3%; Pred. No. 9.7e+08;                           |
|            | Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0                 |
|            |                                                                           |
| QY         | 1 GGGTGG 6                                                                |
|            |                                                                           |
| Db         | 1 GGATGG 6                                                                |
|            |                                                                           |
| RESULT 11  |                                                                           |
| ADJ35665/c |                                                                           |
| ID         | ADJ35665 standard; DNA; 6 BP.                                             |
| XX         |                                                                           |
| AC         | ADJ35665;                                                                 |
| XX         |                                                                           |
| DT         | 22-APR-2004 (first entry)                                                 |
| XX         |                                                                           |
| DE         | Stabilising anti-repression, STAR, element dyad sequence #331.            |
| XX         |                                                                           |
| KW         | STAR affiliated proteinaceous molecule; post translational modification;  |
| KW         | stabilising anti-repression; STAR; STAR element; ds; dyad.                |
| XX         |                                                                           |
| OS         | Unidentified.                                                             |
| XX         |                                                                           |
| PN         | WO2003106674-A2.                                                          |
| XX         |                                                                           |
| PD         | 24-DEC-2003.                                                              |

[illegible]

PT protein of the beta or omega oxidation pathway in a yeast cell.  
 XX Example 2; SEQ ID NO 108; 99pp; English.  
 CC The present invention describes modified Candida tropicalis CYP gene  
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also  
 CC described: (1) a yeast host cell comprising the modified Candida  
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression  
 CC of a protein of the beta or omega oxidation pathway in a yeast cell  
 CC comprising: (a) isolating a CYP gene promoter from *C. tropicalis*; (b)  
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like  
 CC or URS2-like promoters; (c) operably linking the modified promoter with a  
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)  
 CC transforming a yeast cell with the modified promoter operably linked to  
 CC the coding sequence; and (e) growing the yeast under conditions  
 CC favourable for expression of the coding sequence under the control of the  
 CC modified promoter. The promoters are useful for modulating expression of  
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 BP; 0 A; 0 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 4.4; DB 12; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGGTGG 6  
 |||||  
 Db 1 GGGTTG 6  
 |||||  
 RESULT 13  
 ID ADR32931/C  
 AD ADR32931 standard; DNA; 6 BP.  
 AC ADR32931;  
 DT 04-NOV-2004 (first entry)  
 XX Human nicking agent target DNA #472.  
 DE ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004067765-A2.  
 XX  
 PD 12-AUG-2004.  
 XX  
 XX 29-JAN-2004; 2004WO-US002720.  
 XX  
 XX 29-JAN-2003; 2003US-0443811P.  
 XX  
 PA (KECK-) KECK GRADUATE INST.  
 XX  
 XX Van Ness J, Galas DJ, Van Ness LK;  
 PI WPI; 2004-581010/56.  
 DR  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX  
 XX Example 1; Page 79; 238pp; English.  
 PS  
 XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the

CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.  
 CC subpecies, and especially strains or individuals of the subpecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. This sequence  
 CC corresponds to nucleic acid used in the method of the invention.  
 XX  
 SQ Sequence 6 BP; 2 A; 4 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 4.4; DB 13; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGGTGG 6  
 |||||  
 Db 6 GGTGG 1  
 |||||  
 RESULT 14  
 AAT96299  
 ID AAT96299 standard; DNA; 5 BP.  
 XX  
 AC AAT96299;  
 DT 25-MAR-2003 (revised)  
 DT 08-APR-1998 (first entry)  
 XX  
 XX Fungal telomeric nucleic acid sequence.  
 DE  
 KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
 KW telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 KW malarial infection; malaria; ss.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 XX US5695932-A.  
 PN  
 XX 09-DEC-1997.  
 PD  
 XX 13-MAY-1993; 93US-00060952.  
 PF  
 XX 13-MAY-1992; 92US-00882438.  
 PR  
 PR 24-MAR-1993; 93US-00038766.  
 XX  
 XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 XX  
 XX Blackburn EH, Shay J, Mceachern MJ, West MD, Wright W;  
 PI WPI; 1998-041292/04.  
 DR  
 XX Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -  
 PT by detecting telomerase activity.  
 PT  
 XX Claim 5; Col 81-82; 82pp; English.  
 PS  
 XX The present sequence can be used in a novel method for detecting a sample  
 CC eukaryotic pathogen in a patient. The method comprises obtaining a sample

CC of somatic tissue or cells from the patient, determining if telomerase  
 CC activity is present and correlating this with the presence of the  
 CC pathogen. The method is useful for diagnosis of fungal infections,  
 CC especially a fungus of the genus *Candida*, *Cluyveromyces*, *Saccharomyces*,  
 CC *Sporothrix*, *Coccidioides*, *Histoplasma*, *Blastomyces*, *Paracoccidioides*,  
 CC *Cryptococcus*, *Aspergillus*, *Mucor* or *Rhizopus*, or malarial infections,  
 CC especially *Plasmodium vivax*, *P. ovale*, *P. malariae* or *P. falciparum*.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GTGG 5  
 Db ||||  
 2 GTGG 5  
 RESULT 15  
 AAZ93601/c  
 ID AAZ93601 standard; DNA; 5 BP.  
 XX  
 AC AAZ93601;  
 XX  
 DT 24-JUL-2000 (first entry)  
 XX  
 DE Transcription factor binding site of tobacco gene promoter sequence.  
 XX  
 KW Regulatory sequence; meristem; genetic engineering; gene expression;  
 KW crop protection; transgenic plant; resistance; tobacco;  
 KW transcription factor; alcohol dehydrogenase-1; Adhi; ss.  
 XX  
 OS Synthetic.  
 OS *Nicotiana acuminata*.  
 XX  
 PN WO200012713-A1.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 26-AUG-1999; 99WO-AU0000692.  
 XX  
 PR 26-AUG-1998; 98AU-00005498.  
 XX  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Mudge SR, Birch RG;  
 XX  
 DR WPI; 2000-237875/20.  
 XX  
 PT Meristem-expressible nucleic acid sequences, useful for producing  
 PT transgenic plants with improved characteristics such as resistance to  
 PT pathogens.  
 XX  
 PS Example 9; Page 51; 102pp; English.  
 XX  
 CC Isolated regulatory sequences of plants that are operable in dividing  
 CC cells, in particular the meristem cells of plants are useful in the  
 CC genetic engineering of plants. The regulatory sequences can be used to  
 CC control the expression of foreign genes placed under their control. Such  
 CC methods are useful for producing transgenic plants with altered shape  
 CC and/or size. The sequences are also useful for producing transgenic  
 CC plants capable of rapid regeneration following harvest or plants having  
 CC improved resistance to pathogens. This sequence has been shown to bind a  
 CC factor involved in the activation of the maize alcohol dehydrogenase-1  
 CC gene (adhi). It occurs three times in the meristem regulatory sequence of  
 CC Tobacco described in GENESEQ record AAZ93567  
 XX  
 SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GTGG 5  
 Db ||||  
 2 GTGG 5  
 RESULT 16  
 ABZ75666  
 ID ABZ75666 standard; DNA; 5 BP.  
 XX  
 AC ABZ75666;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE Helicase-like transcription factor (HLTF) binding oligonucleotide.  
 XX  
 KW HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;  
 KW helicase-like transcription factor; telomerase reverse transcriptase;  
 KW dermatological; gynaecological; TERT; gene therapy; cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003002068-A2.  
 XX  
 PD 09-JAN-2003.  
 XX  
 PF 27-JUN-2002; 2002WO-US020757.  
 XX  
 PR 27-JUN-2001; 2001US-0301384P.  
 XX  
 PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
 XX  
 PI Androphy EJ, Doshi N, Delayew A;  
 XX  
 DR WPI; 2003-210197/20.  
 XX  
 PT Inhibiting carcinogenesis of a cell, especially useful for treating a  
 PT human papilloma virus-mediated hyperproliferative lesion (warts) or  
 PT cancer, by reducing the activity of helicase-like transcription factor in  
 PT the cell.  
 XX  
 PS Claim 15; Page 24; 36pp; English.  
 XX  
 CC The invention relates to inhibiting carcinogenesis of a cell, or  
 CC inhibiting growth of a cell in a human papillomavirus (HPV)-mediated  
 CC hyperproliferative lesion. The method involves reducing the amount of  
 CC helicase-like transcription factor (HLTF) in the cell or inhibiting the  
 CC binding of endogenous HLTF to telomerase reverse transcriptase (TERT)  
 CC promoter. The method is useful for inhibiting carcinogenesis of a cell,  
 CC or inhibiting growth of a cell in an HPV-mediated hyperproliferative  
 CC lesion. The method is particularly useful for treating cancer (especially  
 CC cervical cancer), or hyperproliferative lesions (warts) caused by HPV.  
 CC The method is also useful for diagnosing a neoplasm, or detecting the  
 CC presence of a malignant tumour or a predisposition to developing the  
 CC tumour. Sequences ABZ75663-669 represent specific examples of  
 CC oligonucleotides that bind to endogenous HLTF, thereby preventing HLTF  
 CC from binding to an intact hTERT promoter region  
 XX  
 SQ Sequence 5 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTGG 6  
 Db ||||  
 2 GTGG 5  
 RESULT 17  
 ABX49997  
 ID ABX49997 standard; DNA; 5 BP.

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTGG 6  
 Db ||||  
 4 GTGG 1  
 RESULT 16  
 ABZ75666  
 ID ABZ75666 standard; DNA; 5 BP.  
 XX  
 AC ABZ75666;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE Helicase-like transcription factor (HLTF) binding oligonucleotide.  
 XX  
 KW HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;  
 KW helicase-like transcription factor; telomerase reverse transcriptase;  
 KW dermatological; gynaecological; TERT; gene therapy; cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003002068-A2.  
 XX  
 PD 09-JAN-2003.  
 XX  
 PF 27-JUN-2002; 2002WO-US020757.  
 XX  
 PR 27-JUN-2001; 2001US-0301384P.  
 XX  
 PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
 XX  
 PI Androphy EJ, Doshi N, Delayew A;  
 XX  
 DR WPI; 2003-210197/20.  
 XX  
 PT Inhibiting carcinogenesis of a cell, especially useful for treating a  
 PT human papilloma virus-mediated hyperproliferative lesion (warts) or  
 PT cancer, by reducing the activity of helicase-like transcription factor in  
 PT the cell.  
 XX  
 PS Claim 15; Page 24; 36pp; English.  
 XX  
 CC The invention relates to inhibiting carcinogenesis of a cell, or  
 CC inhibiting growth of a cell in a human papillomavirus (HPV)-mediated  
 CC hyperproliferative lesion. The method involves reducing the amount of  
 CC helicase-like transcription factor (HLTF) in the cell or inhibiting the  
 CC binding of endogenous HLTF to telomerase reverse transcriptase (TERT)  
 CC promoter. The method is useful for inhibiting carcinogenesis of a cell,  
 CC or inhibiting growth of a cell in an HPV-mediated hyperproliferative  
 CC lesion. The method is particularly useful for treating cancer (especially  
 CC cervical cancer), or hyperproliferative lesions (warts) caused by HPV.  
 CC The method is also useful for diagnosing a neoplasm, or detecting the  
 CC presence of a malignant tumour or a predisposition to developing the  
 CC tumour. Sequences ABZ75663-669 represent specific examples of  
 CC oligonucleotides that bind to endogenous HLTF, thereby preventing HLTF  
 CC from binding to an intact hTERT promoter region  
 XX  
 SQ Sequence 5 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTGG 6  
 Db ||||  
 2 GTGG 5  
 RESULT 17  
 ABX49997  
 ID ABX49997 standard; DNA; 5 BP.





```

XX FH Key Location/Qualifiers
XX FT modified_base 1..6
XX FT /*tag= a
XX FT /note= "Comprises phosphorothioate linkages"
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 1; Page 18; 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma
XX SQ Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
XX Query Match 66.7%; Score 4; DB 2; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGT 4
DB 4 GGGT 1
RESULT 20
AAT80320
ID AAT80320 standard; DNA; 6 BP.
XX AC AAT80320;
XX DT 16-OCT-1997 (first entry)
XX DE Oligo HCV-218, targeted to HCV mRNA position +240 to +245.
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KW inhibition; replication; expression; detection; chronic hepatitis;
XX KW acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..6
XX FT /*tag= a
XX FT /note= "Comprises phosphorothioate linkages"
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 1; Page 18; 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma
XX SQ Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
XX Query Match 66.7%; Score 4; DB 2; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGT 4
DB 4 GGGT 1
RESULT 21
AAV61659/c
ID AAV61659 standard; DNA; 6 BP.
XX AC AAV61659;
XX DT 03-DEC-1998 (first entry)
XX DE Fusarium sp. 18S rRNA DNA fragment #3.
XX KW 18S rRNA; detection; identification; fungus; ss.
XX OS Fusarium sp.
XX PN JP10234380-A.
XX PD 08-SEP-1998.
XX PF 28-FEB-1997; 97JP-00062104.
XX PR 28-FEB-1997; 97JP-00062104.
XX PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX WPI; 1998-535034/46.
XX PT Use of oligo:nucleotide for detecting and identification of fungus of
XX PT Fusarium genus - as primer or probe to detect of identify microbes
XX PT rapidly and exactly.
XX PS Claim 1; Page 6; 20pp; Japanese.
XX CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are

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CC used in a method for the detection and identification of a fungus of  
 CC Fusarium genus. The process can be used to detect or identify microbes  
 CC rapidly and exactly  
 XX  
 SQ Sequence 6 BP; 2 A; 4 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGT 4  
 Db ||||  
 4 GGGT 1

RESULT 22  
 AAZ89322/C  
 ID AAZ89322 standard; DNA; 6 BP.  
 XX  
 AC AAZ89322;  
 DT 13-JUN-2000 (first entry)  
 XX  
 DE Human UCP3 promoter fragment #2.  
 XX  
 XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
 KW fat metabolism; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19838837-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 27-AUG-1998; 98DE-01038837.  
 XX  
 PR 27-AUG-1998; 98DE-01038837.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 PI Esterbauer H, Oberkofler H, Patsch W;  
 XX  
 DR WPI; 2000-272214/24.  
 XX  
 PT Recombinant fat and muscle tissue specific uncoupling protein 3 promoters  
 PT useful for identifying UCP3 modulators.  
 XX  
 PS Claim 2; Page 10; 38pp; German.  
 XX  
 CC This invention describes novel recombinant DNA molecules containing an  
 CC uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat cells  
 CC but not functional in muscle cells or vice versa. The recombinant DNA  
 CC molecules are useful for transcription of genes and, with host cells, to  
 CC test for substances that can influence transcription. They can also be  
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
 CC metabolism and control of the promoter is useful in combating diseases  
 CC with inappropriate fat tissue metabolism. This sequence represents a  
 CC fragment of the human UCP-3 promoter which is used to illustrate the  
 CC method of the invention  
 XX  
 SQ Sequence 6 BP; 1 A; 4 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GGTC 5  
 Db ||||  
 4 GGTC 1

RESULT 23

AA506241  
 ID AAS06241 standard; DNA; 6 BP.  
 XX  
 AC AAS06241;  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE PCR primer 6B2-Hgb used to produce a population of hybrid DNA molecules.  
 KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;  
 KW lambda integrase; therapeutic; ss.  
 XX  
 OS Bacteriophage lambda.  
 OS Synthetic.  
 XX  
 PN WO200142509-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US033546.  
 XX  
 PR 10-DEC-1999; 99US-0169983P.  
 PR 09-MAR-2000; 2000US-0188020P.  
 XX  
 PA (CHEO/) CHEO D.  
 PA (BRAS/) BRASCH M A.  
 PA (TEMP/) TEMPLE G F.  
 PA (HART/) HARTLEY J L.  
 PA (BYRD/) BYRD D R N.  
 XX  
 PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;  
 XX  
 DR WPI; 2001-356174/37.  
 XX  
 PT Producing hybrid nucleic acids, useful for expressing novel therapeutic  
 PT polypeptides, by mixing the same or different nucleic acids having one or  
 PT more recombination sites in the presence of recombination proteins, e.g.  
 PT Cre.  
 XX  
 PS Example 8; Page 213; 357pp; English.  
 XX  
 CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination site  
 CC nucleic acid sequences, and PCR primers of the invention. The att  
 CC sequences are recognised by the recombination protein lambda integrase  
 CC (Int). The invention is a new method of producing a population of hybrid  
 CC nucleic acids comprising mixing at least a first population of nucleic  
 CC acids comprising one or more recombination sites with at least one target  
 CC nucleic acid comprising one or more recombination sites and causing some  
 CC or all of the nucleic acids to recombine with all or some of the target  
 CC nucleic acids. The method is useful for producing a population of hybrid  
 CC nucleic acids which may be the same or different. The nucleic acids may  
 CC be used to express therapeutic proteins or peptides and they may also be  
 CC used to create novel fusion proteins by expressing different sequences  
 CC linked to each other. The method allows simultaneous cloning of two or  
 CC more different nucleic acids  
 XX  
 SQ Sequence 6 BP; 0 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGT 4  
 Db ||||  
 3 GGGT 6

RESULT 24  
 ABK72534  
 ID ABK72534 standard; DNA; 6 BP.  
 XX  
 AC ABK72534;  
 XX

DT 13-AUG-2002 (first entry)  
 XX Human OPAL gene, exon/intron junction #1.  
 DE  
 XX  
 XX Human; ophthalmological; OPAL; autosomal dominant optic atrophy; ADOA;  
 KW gene; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200227022-A2.  
 PN  
 XX 04-APR-2002.  
 PD  
 XX 26-SEP-2001; 2001WO-GB004284.  
 XX  
 XX 26-SEP-2000; 2000GB-00023555.  
 PF  
 XX (UNLO ) UNIV COLLEGE LONDON.  
 PA (UYEY-) UNIV EYE HOSPITAL.  
 PA  
 XX Bhattacharya S, Wisinger B, Alexander C, Votruba M;  
 PI WPI; 2002-416484/44.  
 XX  
 XX Novel human normal or mutant OPAL (the predominant locus for autosomal  
 PT dominant optic atrophy (ADOA)) polypeptides and the OPAL gene, useful in  
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
 XX  
 XX Disclosure; Fig 12; 75pp; English.  
 PS  
 XX The invention relates to an isolated human normal or mutant OPAL (the  
 CC predominant locus for autosomal dominant optic atrophy (ADOA))  
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa,  
 CC and substantially free of other human proteins. Also described is the DNA  
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the  
 CC treatment of a medical condition resulting from a defect in the OPAL  
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid  
 CC and antibodies to (I) are useful in a variety of hybridisation and  
 CC immunological assays to screen for, and to detect the presence of, either  
 CC a normal or a defective OPAL gene or gene product. ABK72533-ABK72593  
 CC represent the human OPAL gene and intron/exon splice junctions  
 XX  
 XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 66.7%; Score 4; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTGG 6  
 Db |||||  
 3 GTGG 6  
 RESULT 25  
 ABS77550  
 ID ABS77550 standard; DNA; 6 BP.  
 XX  
 AC ABS77550;  
 XX  
 XX 13-DEC-2002 (first entry)  
 DT  
 XX Angiogenesis inhibitory oligonucleotide #34.  
 DE  
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200253141-A2.  
 PN  
 XX 11-JUL-2002.  
 PD  
 XX 14-DEC-2001; 2001WO-US048458.  
 PF  
 XX 14-DEC-2000; 2000US-0255534P.  
 PR  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA  
 XX Bratzler RL;  
 XX WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 PT  
 XX Claim 2; Page 20; 276pp; English.  
 PS  
 XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 XX Sequence 6 BP; 0 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 66.7%; Score 4; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTGG 6  
 Db |||||  
 3 GTGG 6  
 RESULT 26  
 ABS65903/c  
 ID ABS65903 standard; DNA; 6 BP.  
 XX  
 AC ABS65903;  
 XX  
 XX 15-NOV-2002 (first entry)  
 DT  
 XX Inhibitory oligonucleotide specific for hepatitis C virus #109.  
 DE  
 XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis; gene therapy; ss.  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW  
 XX  
 OS Synthetic.  
 XX  
 XX US2002081577-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 02-JUL-1997; 97US-00887505.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 XX (KILK/) KILKUSKIE R L.  
 PA

PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
PA (WALT/) WALTHER D M.  
XX  
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI; 2002-537132/57.  
XX  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX Claim 1; Page 6; 74pp; English.  
XX  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV  
XX  
XX Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 66.7%; Score 4; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGT 4  
Db ||||  
4 GGGT 1  
RESULT 27  
ABS65904  
ID ABS65904 standard; DNA; 6 BP.  
XX  
XX ABS65904;  
AC  
XX  
XX 15-NOV-2002 (first entry)  
DT  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #110.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KW gene therapy; ss.  
XX  
XX Synthetic.  
OS  
XX US2002081577-A1.  
PN  
XX 27-JUN-2002.  
PD  
XX 02-JUL-1997; 97US-00887505.  
PF  
XX 06-JUN-1995; 95US-00471968.  
PR  
XX 02-JUL-1996; 96US-0021104P.  
XX  
XX (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI; 2002-537132/57.  
XX  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX Claim 1; Page 6; 74pp; English.  
XX  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV  
XX  
XX Sequence 6 BP; 2 A; 0 C; 3 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 66.7%; Score 4; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGT 4  
Db ||||  
2 GGGT 5  
RESULT 28  
ABK30087/C  
ID ABK30087 standard; DNA; 6 BP.  
XX  
XX ABK30087;  
AC  
XX  
XX 23-APR-2002 (first entry)  
DT  
XX  
DE Beta-lactamase promoter, -35 to -30 region mutant M21.  
XX  
XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;  
KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;  
KW human epidermal growth factor receptor 2 promoter; AR promoter;  
KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;  
KW colon cancer; immunological disorder; prostate cancer; cytostatic;  
KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;  
KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;  
KW gene expression modulator; multiple sclerosis; MS;  
KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;  
KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;  
KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;  
KW mutant; transgenic; ds.  
XX  
XX Escherichia coli.  
OS  
XX WO200194600-A2.  
PN  
XX 13-DEC-2001.  
PD  
XX 06-JUN-2001; 2001WO-US018343.  
PF

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XX PR 06-JUN-2000; 2000US-0209549P.
XX PA (GENE-) GENELABS TECHNOLOGIES INC.
XX PA Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
PI Lim MY, Bruce TW;
XX WPI; 2002-130595/17.
XX
PT New nucleic acid regulatory sequences, which are able to regulate
PT expression of a gene operably linked to a promoter, useful for regulating
PT the expression of transgenes and for treating e.g., cancer and
PT immunological diseases.
XX
PS Example 7; Page 57; 95pp; English.
XX
CC The invention describes an isolated nucleic acid regulatory sequence for
CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
CC (Bla) promoter. Transcription regulatory sequences may be used to
CC regulate expression of the endogenous, autologous or heterologous genes
CC operably linked to the promoter, and may be incorporated into
CC heterologous nucleic acid constructs for use in regulated expression of
CC transgenes. Regulated expression of cyclin D1 can be used in cancer
CC therapies, such as breast, colon or pancreatic cancers and familial
CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
CC may be used in the treatment of immunological disorders, such as
CC autoimmune diseases e.g. multiple sclerosis (MS), systemic lupus
CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
CC arthritis. Regulated expression of genes under the control of the HBV
CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
CC hepatocellular carcinoma, and in the regulated expression of liver cell-
CC specific genes. Regulated expression of the vadh gene promoter can be
CC used in treatment of Enterococcus infection, while regulated expression
CC of the androgen receptor gene can be used in the treatment of prostate
CC cancer. This sequence represents a mutated promoter region used in the
CC invention to determine the regulatory regions involved in gene
CC expression, described in the method of the invention
XX
SQ Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGT 4
Db |||||
6 GGGT 3
RESULT 29
ACD99348
ID ACD99348 standard; DNA; 6 BP.
XX
AC ACD99348;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #34.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX

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PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
XX WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 9; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 6 BP; 0 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GTGG 6
Db |||||
3 GTGG 6
RESULT 30
ADD71358/c
ID ADD71358 standard; DNA; 6 BP.
XX
AC ADD71358;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human sclerosteosis (SOST) gene regulatory region downstream E box.
XX
KW ds; human; sclerosteosis; SOST; gene regulatory region;
KW bone degenerative diseases; bone formation; non-union fracture;
KW bone cavity; tumour resection; fresh fracture;
KW cranial/facial abnormality; spinal fusion; cancer; arthritis;
KW osteoarthritis; osteoporosis; bone/prosthesis in-growth;
KW dental implant/bone integration.
XX
OS Homo sapiens.
XX
XX US2003186915-A1.
XX
PD 02-OCT-2003.
XX
PF 11-FEB-2003; 2003US-00365737.
XX
PR 11-FEB-2002; 2002US-0356212P.
XX
PA (PANY/) PAN Y.
PA (SEVE/) SEVETSON B R.
PA (DERR/) DERRY J M J.
XX
PI Pan Y, Sevetsen BR, Derry JMJ;
XX
XX WPI; 2003-831265/77.
XX

```

XX New nucleic acid from a regulatory region of the SOST gene, useful for  
PT identifying agents which affect transcription of an operably linked gene,  
PT which are potentially useful for treating bone degenerative diseases such  
PT as osteoporosis.  
XX  
PS Example 3; SEQ ID NO 5; 20pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule comprising a  
CC regulatory polynucleotide. The method is useful for screening for agents  
CC that affect expression of a gene operably linked to the nucleic acid.  
CC Identified agents are potentially useful in treating bone degenerative  
CC diseases and in promoting bone formation. The bone degenerative disease  
CC or disorder is especially a non-union fracture, bone cavity, tumour  
CC resection, fresh fracture, cranial/facial abnormality, spinal fusion,  
CC cancer, arthritis, osteoarthritis and osteoporosis. The nucleic acid is  
CC useful in the methods. The treatment methods are also useful for  
CC promoting or inhibiting bone in-growth into a prosthesis, and for  
CC promoting the integration of dental implants into bone. The present  
CC sequence represents the human sclerosteosis (SOST) gene regulatory region  
CC downstream E box.  
XX  
SQ Sequence 6 BP; 1 A; 3 C; 1 G; 1 T; 0 U; 0 Other;  
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Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGTG 5  
Db ||||  
4 GGTG 1  
Search completed: July 20, 2005, 22:59:00  
Job time : 190.4 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds  
(without alignments)  
393.838 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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11: gb\_sts.\*  
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14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| C 3        | 6     | 100.0       | 6      | 6  | CQ757982 Sequence |
| C 4        | 6     | 100.0       | 6      | 6  | CQ758739 Sequence |
| C 5        | 6     | 100.0       | 6      | 6  | AX175261 Sequence |
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| C 7        | 6     | 100.0       | 6      | 6  | AX175315 Sequence |
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VERSION CQ755744.1 GI:44846549
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 245 24-DEC-2003;
 Chromagenics B.V. (NL)
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KEYWORDS .
SOURCE synthetic construct
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REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 1002 24-DEC-2003;
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VERSION CQ757982.1 GI:44848003
KEYWORDS .
SOURCE synthetic construct
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REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 286 24-DEC-2003;
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VERSION CQ758739.1 GI:44848760
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 1043 24-DEC-2003;
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REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 1043 24-DEC-2003;
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VERSION AX175261.1 GI:14598629
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ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 25 21-JUN-2001;
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ACCESSION AX175310
VERSION AX175310.1 GI:14598678
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 74 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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VERSION AX175315.1 GI:14598683
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ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.

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TITLE Therapeutically useful synthetic oligonucleotides
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VERSION AX189456.1 GI:15142968
KEYWORDS synthetic construct
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ORGANISM other sequences; artificial sequences.
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AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Hyaluronic acid in the treatment of cancer
JOURNAL Patent: WO 0147561-A 1 05-JUL-2001;
Bioniche Life Sciences Inc. (CA)
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ACCESSION AX743309
VERSION AX743309.1 GI:30577235
KEYWORDS synthetic construct
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE Therapeutically useful triethyleneglycol cholesteryl
oligonucleotides
JOURNAL Patent: WO 03028764-A 1 10-APR-2003;
Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)
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VERSION AX743311.1 GI:30577237
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SOURCE synthetic construct
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REFERENCE 1
AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE Therapeutically useful triethyleneglycol cholesteryl
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JOURNAL Patent: WO 03028764-A 3 10-APR-2003;
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SOURCE synthetic construct
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REFERENCE 1
AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE Therapeutically useful triethyleneglycol cholesteryl
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JOURNAL Patent: WO 03028764-A 5 10-APR-2003;
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)
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SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE Therapeutically useful triethyleneglycol cholesteryl
 oligonucleotides
JOURNAL Patent: WO 03028764-A 7 10-APR-2003;
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ACCESSION AX764782
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P. and Kruckeberg,A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 Patent: WO 03004704-A 252 16-JAN-2003;
 Chromagenics B.V. (NL)
JOURNAL Chromagenics B.V. (NL)
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 AUTHORS Otte, A.P. and Kruckeberg, A.L.  
 TITLE Dna sequences comprising gene transcription regulatory qualities  
 and methods for detecting and using such dna sequences  
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 DEFINITION Sequence 2 from Patent WO02085340.  
 ACCESSION AX816714  
 VERSION AX816714.1 GI:39647043  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Filion, M.C. and Phillips, N.C.  
 TITLE Oligonucleotide compositions and their use to induce  
 differentiation of cells  
 JOURNAL Patent: WO 02085340-A 2 31-OCT-2002;  
 Bioniche Life Sciences Inc. (CA)  
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 LOCUS CQ868990 5 bp DNA linear PAT 13-SEP-2004  
 DEFINITION Sequence 144 from Patent WO2004074429.  
 ACCESSION CQ868990  
 VERSION CQ868990.1 GI:51998917  
 KEYWORDS

SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS freskg Rd, P.O., Gouliaev, A.H., Thisted, T. and Olsen, E.K.  
 TITLE Method for producing second-generation library  
 JOURNAL Patent: WO 2004074429-A 144 02-SEP-2004;  
 Nuevolution A/S (DK)  
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 LOCUS CQ869027 5 bp DNA linear PAT 13-SEP-2004  
 DEFINITION Sequence 181 from Patent WO2004074429.  
 ACCESSION CQ869027  
 VERSION CQ869027.1 GI:51998954  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS freskg Rd, P.O., Gouliaev, A.H., Thisted, T. and Olsen, E.K.  
 TITLE Method for producing second-generation library  
 JOURNAL Patent: WO 2004074429-A 181 02-SEP-2004;  
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 LOCUS CQ869139 5 bp DNA linear PAT 13-SEP-2004  
 DEFINITION Sequence 293 from Patent WO2004074429.  
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 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS freskg Rd, P.O., Gouliaev, A.H., Thisted, T. and Olsen, E.K.  
 TITLE Method for producing second-generation library  
 JOURNAL Patent: WO 2004074429-A 293 02-SEP-2004;  
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RESULT 19
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CQ869176
VERSION
CQ869176.1 GI:51999103
KEYWORDS
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SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS
freskg Rd,P.O., Goulliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE
Method for producing second-generation library
JOURNAL
Patent: WO 2004074429-A 330 02-SEP-2004;
Nuevolution A/S (DK)
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Db 1 GGTGG 5

RESULT 20
AX046167/c
LOCUS
DEFINITION
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ACCESSION
AX046167
VERSION
AX046167.1 GI:11344250
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Lee,M.E. and Yet,S.F.
TITLE
Methods of treating hypertension
JOURNAL
Patent: WO 0066734-A 46 09-NOV-2000;
PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
FEATURES
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RESULT 21
AX175296
LOCUS
DEFINITION
Sequence 60 from Patent WO0144465. PAT 03-JUL-2001
ACCESSION
AX175296
VERSION
AX175296.1 GI:14598664
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Phillips,N.C. and Filion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 60 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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RESULT 22
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VERSION
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KEYWORDS
synthetic construct
SOURCE
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ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Phillips,N.C. and Filion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 61 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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RESULT 23
AX805865
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DEFINITION
Sequence 11 from Patent WO03060163. PAT 25-NOV-2003

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ACCESSION AX805865  
VERSION AX805865.1 GI:38522776  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS van Bijl, M.J. and van Schaik, C.  
TITLE Discrimination and detection of target nucleotide sequences using mass spectrometry  
JOURNAL Patent: WO 03060163-A 11 24-JUL-2003;  
Keygene N.V. (NL)  
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ACCESSION CQ755706  
VERSION CQ755706.1 GI:44846511  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte, A.P., Kruckeberg, A.L. and Satijn, D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 207 24-DEC-2003;  
Chromagenics B.V. (NL)  
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DEFINITION Sequence 227 from Patent WO2003106674.  
ACCESSION CQ755726  
VERSION CQ755726.1 GI:44846531  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1

AUTHORS Otte, A.P., Kruckeberg, A.L. and Satijn, D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 227 24-DEC-2003;  
Chromagenics B.V. (NL)  
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ACCESSION CQ755734  
VERSION CQ755734.1 GI:44846539  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte, A.P., Kruckeberg, A.L. and Satijn, D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 235 24-DEC-2003;  
Chromagenics B.V. (NL)  
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ACCESSION CQ755772  
VERSION CQ755772.1 GI:44846577  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte, A.P., Kruckeberg, A.L. and Satijn, D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 273 24-DEC-2003;  
Chromagenics B.V. (NL)  
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DEFINITION Sequence 327 from Patent WO2003106674.
ACCESSION CQ755826
VERSION CQ755826.1 GI:44846631
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 327 24-DEC-2003;
Chromagenics B.V. (NL)
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ACCESSION CQ755836
VERSION CQ755836.1 GI:44846641
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 337 24-DEC-2003;
Chromagenics B.V. (NL)
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ACCESSION CQ756230
VERSION CQ756230.1 GI:44847035
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 731 24-DEC-2003;
Chromagenics B.V. (NL)
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Search completed: July 21, 2005, 00:00:38
Job time : 741.2 secs
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds  
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Title: US-09-735-363A-25

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Scoring table: IDENTITY NUC

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Listing first 100 summaries

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# SUMMARIES

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| 5 | 1 | US-08-709-209-345  | Sequence 345, App |
| 5 | 1 | US-08-303-275-176  | Sequence 176, App |
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| 5 | 3 | US-08-855-372B-7   | Sequence 7, Appl  |
| 5 | 3 | US-08-855-372B-8   | Sequence 8, Appl  |
| 5 | 3 | US-09-180-903-5    | Sequence 5, Appl  |
| 5 | 3 | US-09-449-581-1    | Sequence 1, Appl  |
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| 5 | 4 | US-09-491-795-6    | Sequence 6, Appl  |
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| 6 | 1 | US-08-533-912-6    | Sequence 6, Appl  |
| 6 | 1 | US-08-465-590-140  | Sequence 140, App |
| 6 | 2 | US-08-471-994-8    | Sequence 8, Appl  |
| 6 | 2 | US-08-276-567A-7   | Sequence 7, Appl  |
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| 6 | 3 | US-08-711-417C-140 | Sequence 140, App |
| 6 | 3 | US-09-180-903-9    | Sequence 9, Appl  |
| 6 | 3 | US-09-638-509C-28  | Sequence 28, Appl |
| 6 | 3 | US-09-281-481A-22  | Sequence 22, Appl |
| 6 | 4 | US-09-830-401-3    | Sequence 3, Appl  |
| 6 | 4 | US-09-723-909-140  | Sequence 140, App |
| 6 | 4 | US-09-958-221A-2   | Sequence 2, Appl  |
| 6 | 4 | US-10-029-907-8    | Sequence 8, Appl  |
| 6 | 4 | US-09-686-631-12   | Sequence 12, Appl |
| 6 | 4 | US-09-521-11       | Sequence 11, Appl |
| 6 | 4 | US-09-657-289A-1   | Sequence 1, Appl  |
| 6 | 4 | US-09-288-719B-18  | Sequence 18, Appl |
| 6 | 4 | US-09-244-438-12   | Sequence 12, Appl |
| 6 | 4 | US-10-071-411A-61  | Sequence 61, Appl |

## ALIGNMENTS

## RESULT 1

US-09-305-839-46/c  
; Sequence 46, Application US/09305839  
; Patent No. 6514935  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Mu-En  
; APPLICANT: Yet, Shaw-Fang  
; TITLE OF INVENTION: Methods of Treating Hypertension  
; FILE REFERENCE: 21508-064  
; CURRENT APPLICATION NUMBER: US/09/305,839  
; CURRENT FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: 08/818,655  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: artif: peptide  
US-09-305-839-46

Query Match 83.3%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GGGTG 5  
|||  
Db 5 GGGTG 1

## RESULT 2

US-08-234-613-10  
; Sequence 10, Application US/08234613  
; Patent No. 5582981  
; GENERAL INFORMATION:  
; APPLICANT: TOOLE, JOHN J.  
; APPLICANT: LATHAM, JOHN  
; APPLICANT: BOCK, LOUIS C.  
; APPLICANT: GRIFFIN, LINDA C.  
; TITLE OF INVENTION: APTAMER TARGET ELUTION METHOD  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/234,613  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/744,870  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRACEY, NANCEY J.  
; REGISTRATION NUMBER: 28,216  
; REFERENCE/DOCKET NUMBER: 24610-20030.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-234-613-10

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||  
Db 1 GGGTGG 6

## RESULT 3

US-08-153-051B-53  
; Sequence 53, Application US/08153051B  
; Patent No. 5645986  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153,051B  
; FILING DATE: No. 5645986ember 12, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 204/195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-153-051B-53

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GGGTG 5  
| | | | |  
Db 2 GGGTG 6

## RESULT 4

US-08-060-952C-52  
; Sequence 52, Application US/08060952C

; Patent No. 5695932

; GENERAL INFORMATION:

; APPLICANT: Michael D. West

; APPLICANT: Jerry W. Shay

; APPLICANT: Woodring B. Wright

; APPLICANT: Elizabeth Blackburn

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS

; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR

; TITLE OF INVENTION: TELOMERASE ACTIVITY

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/060,952C

; FILING DATE: May 13, 1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/882,438

; FILING DATE: May 13, 1992

; APPLICATION NUMBER: 08/038,766

; FILING DATE: March 24, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 202/045

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-060-952C-52

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GGGTG 5  
| | | | |  
Db 2 GGGTG 6

## RESULT 5

US-08-151-477A-53

; Sequence 53, Application US/08151477A

; Patent No. 5830644

; GENERAL INFORMATION:

; APPLICANT: Michael D. West

; APPLICANT: Jerry W. Shay

; APPLICANT: Woodring B. Wright

; APPLICANT: Elizabeth Blackburn

; APPLICANT: Nam Woo Kim

; APPLICANT: Calvin B. Harley

; APPLICANT: Scott L. Weinrich

; APPLICANT: Catharine Strahl

; APPLICANT: Michael J. McEachern

; APPLICANT: Homayoun Vaziri

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE

; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/151,477A

; FILING DATE: No. 5830644ember 12, 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/038,766

; FILING DATE: March 24, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 202/189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-151-477A-53

Query Match 83.3%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
| | | | |  
Db 2 GGGTG 6

## RESULT 6

US-08-237-973-10

; Sequence 10, Application US/08237973

; Patent No. 5840867

; GENERAL INFORMATION:

; APPLICANT: TOOKE, JOHN J.

; APPLICANT: LATHAM, JOHN

; APPLICANT: BOCK, LOUIS C.

; APPLICANT: GRIFFIN, LINDA C.

; TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR

; TITLE OF INVENTION: BIOMOLECULES

```

; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,973
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,921
; FILING DATE: 06-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 24610-20032.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-237-973-10

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```

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GGGTGG 6
 |||||
Db 1 GGNTGG 6

```

```

RESULT 7
US-08-237-973-26
; Sequence 26, Application US/08237973
; Patent No. 5840867
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: LATHAM, JOHN
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: GRIFFIN, LINDA C.
; TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,973
; FILING DATE:
; CLASSIFICATION: 435

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,921
; FILING DATE: 06-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 24610-20032.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3
; OTHER INFORMATION: /note= "N is T, A, U, du (i.e., thymine in
; OTHER INFORMATION: uracil as a substitute base for thymine in
; OTHER INFORMATION: deoxyribonucleic acid) or G."
;
US-08-237-973-26

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```

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 GGGTGG 6
 |||||
Db 1 GGNTGG 6

```

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RESULT 8
US-08-819-867-70
; Sequence 70, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Fast-SEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

```
/ APPLICATION NUMBER: 08/153,051
/ FILING DATE: No. 6007989 September 12, 1993
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Chambers, Daniel M.
/ REGISTRATION NUMBER: 34,561
/ REFERENCE/DOCKET NUMBER: 224/232
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 70:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-819-867-70

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTG 5
DB 2 GGCTG 6

RESULT 9
US-08-464-011B-52
/ Sequence 52, Application US/08464011B
/ Patent No. 6368789
/ GENERAL INFORMATION:
/ APPLICANT: Michael D. West
/ Jerry W. Shay
/ Woodring E. Wright
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
/ RELATED TO TELOMERE LENGTH AND/OR
/ TELOMERASE ACTIVITY
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/464,011B
/ FILING DATE: 05-Jun-1995
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/882,438
/ FILING DATE: May 13, 1992
/ APPLICATION NUMBER: 08/038,766
/ FILING DATE: March 24, 1993
/ APPLICATION NUMBER: 08/060,952
/ FILING DATE: May 13, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 202/045
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440

/ APPLICATION NUMBER: 08/153,051
/ FILING DATE: No. 6007989 September 12, 1993
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Chambers, Daniel M.
/ REGISTRATION NUMBER: 34,561
/ REFERENCE/DOCKET NUMBER: 224/232
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 70:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-464-011B-52

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTG 5
DB 2 GGCTG 6

RESULT 10
US-09-196-099-17/c
/ Sequence 17, Application US/09196099
/ Patent No. 6465246
/ GENERAL INFORMATION:
/ APPLICANT: MUELLER, Rolf
/ APPLICANT: SEDLACEK, Hans-Harald
/ TITLE OF INVENTION: ONCOGENE- OR VIRUS-CONTROLLED EXPRESSION SYSTEM
/ FILE REFERENCE: 26083/190
/ CURRENT APPLICATION NUMBER: US/09/196,099
/ CURRENT FILING DATE: 1998-11-20
/ EARLIER APPLICATION NUMBER: DE 19751587.8
/ EARLIER FILING DATE: 1997-11-21
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
/ US-09-196-099-17

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTTG 6
DB 6 GGTTG 2

RESULT 11
US-09-378-535-70
/ Sequence 70, Application US/09378535
/ Patent No. 6551774
/ GENERAL INFORMATION:
/ APPLICANT: Michael D. West
/ Calvin B. Harley
/ Scott L. Weinrich
/ Catherine M. Strahl
/ Michael J. Mceachern
/ Jerry Shay
/ Woodring E. Wright
/ Elizabeth H. Blackburn
/ Nam Woo Kim
/ Homayoun Vaziri
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
/ CONDITIONS RELATED TO
/ TELOMERE LENGTH AND/OR
/ TELOMERASE ACTIVITY
/ NUMBER OF SEQUENCES: 80
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
```

STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-378-535-70  
Query Match 83.3%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;  
QY 1 GGTGG 5  
DB 2 GGTGG 6  
RESULT 12  
US-09-288-719B-17/c  
Sequence 17, Application US/09288719B  
Patent No. 6759518  
GENERAL INFORMATION:  
APPLICANT: KONTERMANN, Roland  
APPLICANT: SEDLACEK, Hans-Herald  
APPLICANT: MUELLER, Rolf  
TITLE OF INVENTION: SINGLE-CHAIN MULTIPLE ANTIGEN-BINDING MOLECULE, ITS PREPARATION  
FILE REFERENCE: 38005-0121  
CURRENT APPLICATION NUMBER: US/09/288,719B  
CURRENT FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: DE 198 27 239.1  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: DE 198 16 141.7  
PRIOR FILING DATE: 1998-04-09  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic nucleotide  
US-09-288-719B-17  
Query Match 83.3%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+08; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGTGG 6  
DB 6 GGTGG 2  
RESULT 13  
US-08-234-613-9  
Sequence 9, Application US/08234613  
Patent No. 5582981  
GENERAL INFORMATION:  
APPLICANT: TOOLE, JOHN J.  
APPLICANT: LATHAM, JOHN  
APPLICANT: BOCK, LOUIS C.  
APPLICANT: GRIFFIN, LINDA C.  
TITLE OF INVENTION: APTAMER TARGET ELUTION METHOD  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,613  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/744,870  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCEY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 24610-20030.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-234-613-9  
Query Match 73.3%; Score 4.4; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+08; Indels 1;  
Matches 5; Conservative 0; Mismatches 1; Gaps 0;  
QY 1 GGTGG 6  
DB 1 GGTGG 6  
RESULT 14  
US-08-237-973-9  
Sequence 9, Application US/08237973  
Patent No. 5840867  
GENERAL INFORMATION:  
APPLICANT: TOOLE, JOHN J.  
APPLICANT: LATHAM, JOHN  
APPLICANT: BOCK, LOUIS C.  
APPLICANT: GRIFFIN, LINDA C.  
TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR BIOMOLECULES

NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/237,973  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,921  
FILING DATE: 06-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 24610-20032.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-237-973-9

Query Match 73.3%; Score 4.4; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTGG 6  
|||  
Db 1 GGTGG 6

RESULT 15  
US-08-920-422-15  
; Sequence 15, Application US/08920422A  
; Patent No. 6255473  
; GENERAL INFORMATION:  
; APPLICANT: Vitek, Michael P.  
; APPLICANT: Mitsuda, No. 6255473iaki  
; APPLICANT: Roses, Allen D.  
; TITLE OF INVENTION: Presentin-1 Gene Promoter  
; FILE REFERENCE: VITEKPRESENTIN  
; CURRENT APPLICATION NUMBER: US/08/920,422A  
; CURRENT FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-920-422-15

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTGG 6  
|||  
Db 1 GGTGG 6

Db 1 GGGCGG 6

RESULT 16  
US-08-920-422-16/c  
; Sequence 16, Application US/08920422A  
; Patent No. 6255473  
; GENERAL INFORMATION:  
; APPLICANT: Vitek, Michael P.  
; APPLICANT: Mitsuda, No. 6255473iaki  
; APPLICANT: Roses, Allen D.  
; TITLE OF INVENTION: Presentin-1 Gene Promoter  
; FILE REFERENCE: VITEKPRESENTIN  
; CURRENT APPLICATION NUMBER: US/08/920,422A  
; CURRENT FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-920-422-16

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTGG 6  
|||  
Db 6 GGGCGG 1

RESULT 17  
US-09-593-323-29  
; Sequence 29, Application US/09593323  
; Patent No. 6265213  
; GENERAL INFORMATION:  
; APPLICANT: Morgan, Antony R.  
; APPLICANT: Severini, Alberto  
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity  
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of  
; TITLE OF INVENTION: Transcription  
; FILE REFERENCE: DNAB-02921  
; CURRENT APPLICATION NUMBER: US/09/593,323  
; CURRENT FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: 09/344,300  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-593-323-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTGG 6  
|||  
Db 1 GGGCGG 6

RESULT 18  
US-09-594-108-29  
; Sequence 29, Application US/09594108  
; Patent No. 6284468  
; GENERAL INFORMATION:

```
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
 ||||
Db 1 GGGCGG 6

RESULT 19
US-09-344-300-29
; Sequence 29, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/344,300B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-344-300-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
 ||||
Db 1 GGGCGG 6

RESULT 20
US-09-924-346-6
; Sequence 6, Application US/09924346
; Patent No. 6555674
; GENERAL INFORMATION:
; APPLICANT: Jens Tornoe
; TITLE OF INVENTION: The Jet Promoter
; FILE REFERENCE: 19313-005
; CURRENT APPLICATION NUMBER: US/09/924,346
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/224,087
; PRIOR FILING DATE: 2000-08-09
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chemically
; OTHER INFORMATION: Synthesized
US-09-924-346-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
 ||||
Db 1 GGGCGG 6

RESULT 21
US-09-483-184A-5/c
; Sequence 6, Application US/09483184A
; Patent No. 6800750
; GENERAL INFORMATION:
; APPLICANT: DARTMOUTH COLLEGE
; APPLICANT: CRAIG, Ruth W.
; APPLICANT: BINGLE, Colin D.
; APPLICANT: WHYTE, Moira
; TITLE OF INVENTION: Mcl-1 GENE REGULATORY ELEMENTS AND A PRO-APOPTOTIC Mcl-1 VARIANT
; FILE REFERENCE: DART1110-1
; CURRENT APPLICATION NUMBER: US/09/483,184A
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/166,113
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-483-184A-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
 ||||
Db 6 GGGCGG 1

RESULT 22
US-08-153-051B-47
; Sequence 47, Application US/08153051B
; Patent No. 5645986
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELEOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
```



```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 204/195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-153-051B-47

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTG 5
Db 2 GGTG 5

RESULT 23
US-08-060-952C-20
; Sequence 20, Application US/08060952C
; Patent No. 5695932
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring B. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 204/195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-153-051B-47

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTG 5
Db 2 GGTG 5

RESULT 24
US-08-151-477A-47
; Sequence 47, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring B. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US/08/060,952C
; FILING DATE: May 13, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-060-952C-20

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 202/189  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-151-477A-47

Query Match 66.7%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGG 5  
Db 2 GTGG 5

RESULT 25  
US-08-819-867-44  
; Sequence 44, Application US/08819867  
; Patent No. 6007989  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine M. Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Jerry Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth H. Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO  
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR  
; TITLE OF INVENTION: TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,867  
; FILING DATE: March 14, 1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/153,051  
; FILING DATE: NO. 6007989eember 12, 1993  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chambers, Daniel M.  
; REGISTRATION NUMBER: 34,561  
; REFERENCE/DOCKET NUMBER: 224/232  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-819-867-44

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGG 5  
Db 2 GTGG 5

RESULT 26  
US-08-973-068-59/c  
; Sequence 59, Application US/08973068  
; Patent No. 6127604  
; GENERAL INFORMATION:  
; APPLICANT: Dale, James Langham  
; APPLICANT: Harding, Robert Maxwell  
; APPLICANT: Dugdale, Benjamin  
; APPLICANT: Beetham, Peter Ronald  
; APPLICANT: Hainer, Gregory John  
; APPLICANT: Becker, Douglas Kenneth  
; TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS  
; FILE REFERENCE: 09657/002001  
; CURRENT APPLICATION NUMBER: US/08/973,068  
; CURRENT FILING DATE: 1998-03-12  
; EARLIER APPLICATION NUMBER: PCT/AU96/00335  
; EARLIER FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Banana Bunchy Top Virus (BBTV)  
US-08-973-068-59

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGG 6  
Db 4 GTGG 1

RESULT 27  
US-08-973-068-60  
; Sequence 60, Application US/08973068  
; Patent No. 6127604  
; GENERAL INFORMATION:  
; APPLICANT: Dale, James Langham  
; APPLICANT: Harding, Robert Maxwell  
; APPLICANT: Dugdale, Benjamin  
; APPLICANT: Beetham, Peter Ronald  
; APPLICANT: Hainer, Gregory John  
; APPLICANT: Becker, Douglas Kenneth  
; TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS  
; FILE REFERENCE: 09657/002001  
; CURRENT APPLICATION NUMBER: US/08/973,068  
; CURRENT FILING DATE: 1998-03-12  
; EARLIER APPLICATION NUMBER: PCT/AU96/00335  
; EARLIER FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 60

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; LENGTH: 5
; TYPE: DNA
; ORGANISM: Banana Bunchy Top Virus (BBTV)
US-08-973-068-60

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 GTGG 6
Db 2 GTGG 5
 |||||

RESULT 28
US-08-464-011B-20
; Sequence 20, Application US/08464011B
; Patent No. 6368789
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Jerry W. Shay
; Woodring E. Wright
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; RELATED TO TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,011B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-464-011B-20

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 GTGG 5
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; LENGTH: 5
; TYPE: DNA
; ORGANISM: Banana Bunchy Top Virus (BBTV)
US-09-735-363a-25.szlm6.rni

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 GTGG 6
Db 2 GTGG 5
 |||||

RESULT 29
US-09-638-509C-22/c
; Sequence 22, Application US/09638509C
; Patent No. 6372435
; GENERAL INFORMATION:
; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; TITLE OF INVENTION: Methods of Surveying For CC (Beta) Chemokine
; TITLE OF INVENTION: Receptor Variants and Their Association With HIV-1
; TITLE OF INVENTION: Transmission and/or Disease Progression
; FILE REFERENCE: D6217
; CURRENT APPLICATION NUMBER: US/09/638,509C
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,530
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 22
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: allele
; OTHER INFORMATION: CCR5 promoter allele P*0201
US-09-638-509C-22

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 GTGG 6
Db 5 GTGG 2
 |||||

RESULT 30
US-09-378-535-44
; Sequence 44, Application US/09378535
; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. McEachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-378-535-44

Query Match 66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTG 5
DB 2 GGTG 5

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Search completed: July 21, 2005, 04:29:19  
Job time : 60 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds

(without alignments)

169.325 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description        |
|------------|-------|---------------|--------|-------|--------------------|
| 1          | 5     | 83.3          | 6      | 7     | CF312755 ABP--08-K |
| 2          | 3.4   | 56.7          | 5      | 7     | CF327761 NACL--02  |
| 3          | 3.4   | 56.7          | 5      | 7     | CF339974 RCL1--06  |
| 4          | 3.4   | 56.7          | 5      | 7     | CF340386 RCL1--07  |
| 5          | 3.4   | 56.7          | 5      | 7     | CF340514 RCL1--08  |
| 6          | 3.4   | 56.7          | 5      | 7     | CF920850 gmtrRwv3- |
| 7          | 3.4   | 56.7          | 5      | 9     | CL423849 OIS0750-0 |
| 8          | 3.4   | 56.7          | 5      | 9     | CL664862 PRI0148A- |
| 9          | 3.4   | 56.7          | 5      | 9     | CL685110 PRI0140b- |
| 10         | 3.4   | 56.7          | 6      | 6     | CA851633 DI5H03 OI |
| 11         | 3.4   | 56.7          | 6      | 6     | CA851767 D17C12 E2 |
| 12         | 3.4   | 56.7          | 6      | 7     | CF339116 RCL1--03  |
| 13         | 3.4   | 56.7          | 6      | 7     | CF340012 RCL1--06  |
| 14         | 3.4   | 56.7          | 6      | 7     | CF340239 RCL1--07  |
| 15         | 3.4   | 56.7          | 6      | 9     | CL689395 PRI0151a  |
| 16         | 3     | 50.0          | 3      | 6     | CA850938 D08D06 H1 |
| 17         | 3     | 50.0          | 3      | 6     | CA851961 D19E06 I1 |
| 18         | 3     | 50.0          | 3      | 7     | CF315089 HD--03-N2 |
| 19         | 3     | 50.0          | 3      | 7     | CF338538 RCL1--01  |
| 20         | 3     | 50.0          | 3      | 7     | CF339357 RCL1--04  |
| 21         | 3     | 50.0          | 3      | 7     | CF339421 RCL1--04  |
| 22         | 3     | 50.0          | 3      | 7     | CF339646 RCL1--05  |
| 23         | 3     | 50.0          | 3      | 7     | CF339761 RCL1--05  |
| 24         | 3     | 50.0          | 3      | 9     | CL423861 OIS0750-0 |

|          |            |   |      |   |   |          |
|----------|------------|---|------|---|---|----------|
| CL655746 | PRI0127b-  | 3 | 50.0 | 3 | 9 | CL655746 |
| CL668376 | PRI0157c-  | 3 | 50.0 | 3 | 9 | CL668376 |
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| CA853352 | B07C08..se | 4 | 50.0 | 4 | 6 | CA853352 |
| CF300913 | 7LEAF--05  | 4 | 50.0 | 4 | 7 | CF300913 |
| CF306914 | HDAl--05   | 4 | 50.0 | 4 | 7 | CF306914 |
| CF324158 | HDN--05-M  | 4 | 50.0 | 4 | 7 | CF324158 |
| CF324308 | HDN--06-D  | 4 | 50.0 | 4 | 7 | CF324308 |
| CF336880 | JMT--07-B  | 4 | 50.0 | 4 | 7 | CF336880 |
| CF338536 | RCL1--01   | 4 | 50.0 | 4 | 7 | CF338536 |
| CF340391 | RCL1--07   | 4 | 50.0 | 4 | 7 | CF340391 |
| CF340642 | RCL1--08   | 4 | 50.0 | 4 | 7 | CF340642 |
| CF340653 | RCL1--08   | 4 | 50.0 | 4 | 7 | CF340653 |
| CF323326 | HDN--03-I  | 5 | 50.0 | 5 | 7 | CF323326 |
| CF930992 | CF--05-R   | 5 | 50.0 | 5 | 7 | CF930992 |
| CL661701 | PRI013c-C  | 5 | 50.0 | 5 | 9 | CL661701 |
| CL688637 | PRI014a-B  | 5 | 50.0 | 5 | 9 | CL688637 |
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| CA850905 | D07H12 O2  | 6 | 50.0 | 6 | 6 | CA850905 |
| CF302557 | 7LEAF--08  | 6 | 50.0 | 6 | 7 | CF302557 |
| CF307125 | HDAl--05   | 6 | 50.0 | 6 | 7 | CF307125 |
| CF310635 | ABP--05-G  | 6 | 50.0 | 6 | 7 | CF310635 |
| CF323984 | HDN--05-E  | 6 | 50.0 | 6 | 7 | CF323984 |
| CF921483 | gmtrRwv3-  | 6 | 50.0 | 6 | 7 | CF921483 |
| CF787556 | DKF2p469C  | 6 | 50.0 | 6 | 7 | CF787556 |
| CF333346 | JMT--04-P  | 4 | 40.0 | 4 | 7 | CF333346 |
| CK582549 | IST W15 4  | 4 | 40.0 | 4 | 7 | CK582549 |
| CL655267 | PRI0122d   | 4 | 40.0 | 4 | 7 | CL655267 |
| CA853329 | B07A01..se | 5 | 40.0 | 5 | 6 | CA853329 |
| CF282401 | 14ETL--09  | 5 | 40.0 | 5 | 7 | CF282401 |
| CF297897 | 7LEAF--01  | 5 | 40.0 | 5 | 7 | CF297897 |
| CF300956 | 7LEAF--05  | 5 | 40.0 | 5 | 7 | CF300956 |
| CF302927 | 7LEAF--08  | 5 | 40.0 | 5 | 7 | CF302927 |
| CF307095 | HDAl--05   | 5 | 40.0 | 5 | 7 | CF307095 |
| CF307842 | ABP--01-G  | 5 | 40.0 | 5 | 7 | CF307842 |
| CF318944 | HD--09-E0  | 5 | 40.0 | 5 | 7 | CF318944 |
| CF320271 | HD--11-B1  | 5 | 40.0 | 5 | 7 | CF320271 |
| CF327578 | NACL--02   | 5 | 40.0 | 5 | 7 | CF327578 |
| CL423373 | OIS0554-0  | 5 | 40.0 | 5 | 9 | CL423373 |
| AL043164 | DKF2p434F  | 6 | 40.0 | 6 | 1 | AL043164 |
| CF314367 | HD--02-N2  | 6 | 40.0 | 6 | 1 | CF314367 |
| CF329138 | NACL--04   | 6 | 40.0 | 6 | 7 | CF329138 |
| CF338772 | RCL1--02   | 6 | 40.0 | 6 | 7 | CF338772 |
| CL665420 | PRI0149C   | 6 | 40.0 | 6 | 9 | CL665420 |
| CL665420 | PRI0149C   | 6 | 40.0 | 6 | 9 | CL665420 |
| CL680271 | PRI0128c   | 6 | 40.0 | 6 | 9 | CL680271 |
| CL682618 | PRI0134c-  | 6 | 40.0 | 6 | 9 | CL682618 |
| BX266185 | BX266185   | 2 | 33.3 | 2 | 5 | BX266185 |
| BX266563 | BX266563   | 2 | 33.3 | 2 | 5 | BX266563 |
| BX267118 | BX267118   | 2 | 33.3 | 2 | 5 | BX267118 |
| CA850842 | D07B06 C1  | 2 | 33.3 | 2 | 6 | CA850842 |
| CF291112 | 14ROOF--0  | 2 | 33.3 | 2 | 7 | CF291112 |
| CF299820 | 7LEAF--03  | 2 | 33.3 | 2 | 7 | CF299820 |
| CF301411 | 7LEAF--06  | 2 | 33.3 | 2 | 7 | CF301411 |
| CF306288 | HDAl--03   | 2 | 33.3 | 2 | 7 | CF306288 |
| CF307123 | HDAl--05   | 2 | 33.3 | 2 | 7 | CF307123 |
| CF311851 | ABP--07-E  | 2 | 33.3 | 2 | 7 | CF311851 |
| CF315237 | HD--04-B0  | 2 | 33.3 | 2 | 7 | CF315237 |
| CF331310 | NACL--07   | 2 | 33.3 | 2 | 7 | CF331310 |
| CF333014 | JMT--01-L  | 2 | 33.3 | 2 | 7 | CF333014 |
| CN411958 | 170005322  | 2 | 33.3 | 2 | 7 | CN411958 |
| CO792627 | NT015C D1  | 2 | 33.3 | 2 | 7 | CO792627 |
| CR774574 | DKF2p469G  | 2 | 33.3 | 2 | 7 | CR774574 |
| CR787484 | DKF2p469H  | 2 | 33.3 | 2 | 7 | CR787484 |
| CL661289 | PRI0139b-  | 2 | 33.3 | 2 | 9 | CL661289 |
| CL670560 | PRI0162b-  | 2 | 33.3 | 2 | 9 | CL670560 |
| CL682684 | PRI0134c-  | 2 | 33.3 | 2 | 9 | CL682684 |
| CL688205 | PRI0148d   | 2 | 33.3 | 2 | 9 | CL688205 |
| CL688890 | PRI0148A   | 2 | 33.3 | 2 | 9 | CL688890 |
| CL688912 | PRI014d C  | 2 | 33.3 | 2 | 9 | CL688912 |
| CL690186 | PRI0153a-  | 2 | 33.3 | 2 | 9 | CL690186 |
| CL694963 | PRI0165c-  | 2 | 33.3 | 2 | 9 | CL694963 |
| CL872635 | ab883910.  | 2 | 33.3 | 2 | 9 | CL872635 |

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98 2 33.3 2 9 CL874640 CL874640 abe96h02.
99 2 33.3 2 9 CL876415 CL876415 abf13c11.
100 2 33.3 2 9 CL883717 CL883717 abf63c08.

ALIGNMENTS

RESULT 1
CF312755 6 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--08-K07.b1 ABP3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-K07, mRNA sequence.
ACCESSION CF312755
VERSION CF312755.1 GI:33684516
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 6)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="ABF--08-K07"
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/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABP3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 83.3%; Score 5; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db |||||
2 GGGTG 6

RESULT 2
CF327761/c 5 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--02-G02.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--02-G02, mRNA
sequence.
ACCESSION CF327761
VERSION CF327761.1 GI:33803773
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db |||||
5 GGGCG 1

RESULT 3
CF339974 5 bp mRNA linear EST 18-AUG-2003
LOCUS RCL1--06-118.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-118,
mRNA sequence.
ACCESSION CF339974
VERSION CF339974.1 GI:33828316
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="RCL1--06-118"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..5
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--06-118"

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/tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site.1: SstI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

## ORIGIN

Query Match 56.7%; Score 3.4; DB 7; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+09;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6  
 | | | |  
 Db 1 GCTGG 5

## RESULT 4

CF340386 5 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--07-N21.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-N21,  
 mRNA sequence.

ACCESSION CF340386.1 GI:33829128

VERSION CF340386

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 5)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source Location/Qualifiers  
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 /organism="Oryza sativa (japonica cultivar-group)"  
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 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site.1: SstI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

## ORIGIN

Query Match 56.7%; Score 3.4; DB 7; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+09;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6  
 | | | |  
 Db 1 GCTGG 5

## RESULT 5

LOCUS CF340514

DEFINITION

CF340514 5 bp mRNA linear EST 18-AUG-2003  
 RCL1--08-E10.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--08-E10,  
 mRNA sequence.

ACCESSION CF340514

VERSION CF340514

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 5)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers  
 1..5  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="RCL1--08-E10"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site.1: SstI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

## ORIGIN

Query Match 56.7%; Score 3.4; DB 7; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+09;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6  
 | | | |  
 Db 1 GCTGG 5

## RESULT 6

LOCUS CF920850/c

DEFINITION

CF920850 5 bp mRNA linear EST 05-NOV-2003  
 smrhrw3-02\_E07\_1\_055 Soybean root hair subtracted cDNA library  
 DEFINITION Glycine max cDNA, mRNA sequence.

ACCESSION CF920850

VERSION CF920850.1 GI:38191644

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 5)

AUTHORS Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.  
 TITLE Expressed sequence tags from soybean root hair subtractive cDNA





```

ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE
AppADB: an AcedB database for the nematode satelilite organism
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
source
Location/Qualifiers
1..5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
ORIGIN
Query Match 56.7%; Score 3.4; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCGTG 5
| | | |
Db 1 GCGTG 5

RESULT 10
CA851633/c
LOCUS
D15H03_015_16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION
cDNA clone D15H03 5', mRNA sequence.
ACCESSION
CA851633
VERSION
CA851633.1 GI:33388426
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
FEATURES
source
Location/Qualifiers
1..6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone_lib="D17C12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
ORIGIN
Query Match 56.7%; Score 3.4; DB 6; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCGTG 5
| | | |
Db 6 GTGTG 2

RESULT 11
CA851767/c
LOCUS
D17C12_E24_06.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION
cDNA clone D17C12 5', mRNA sequence.
ACCESSION
CA851767
VERSION
CA851767.1 GI:33388560
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
FEATURES
source
Location/Qualifiers
1..6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone_lib="D17C12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
ORIGIN
Query Match 56.7%; Score 3.4; DB 6; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCGTG 5
| | | |
Db 6 GTGTG 2

RESULT 12
CF339116
LOCUS
RCL1--03-N11.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION
Oryza sativa [japonica cultivar-group] cDNA clone RCL1--03-N11,
mRNA sequence.
ACCESSION
CF339116

```

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VERSION CF339116.1 GI:33826619
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1..6
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--03-N11"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 ||||
Db 2 GCTGG 6

RESULT 13
CF340012
LOCUS CF340012
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-K19,
 mRNA sequence.
ACCESSION CF340012
VERSION CF340012.1 GI:33828387
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..6
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /db_xref="taxon:39947"
 /clone="RCL1--06-K19"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 ||||
Db 2 GCTGG 6

RESULT 13
CF340012
LOCUS CF340012
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-K19,
 mRNA sequence.
ACCESSION CF340012
VERSION CF340012.1 GI:33828387
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1..6
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
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 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 ||||
Db 2 GCTGG 6

RESULT 14
CF340239
LOCUS CF340239
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-G09,
 mRNA sequence.
ACCESSION CF340239
VERSION CF340239.1 GI:33828836
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1..6
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--07-G09"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN

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```

Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 | |||
DB 2 GCTGG 6

RESULT 15
CL689395/c
LOCUS
DEFINITION
Pristionchus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL689395
CL689395.1 GI:50211303
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
APPABD: an AcedB database for the nematode satellite organism
TITLE
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
source
Location/Qualifiers
1..6
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 | |||
DB 6 GATGG 2

RESULT 16
CL6850938
LOCUS
DEFINITION
D08D06_H18_07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08D06 5', mRNA sequence.
CL6850938
CL6850938.1 GI:33387731
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)

Query Match 56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 | |||
DB 6 GATGG 2

RESULT 16
CL6850938
LOCUS
DEFINITION
D08D06_H18_07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08D06 5', mRNA sequence.
CL6850938
CL6850938.1 GI:33387731
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)

```

```

AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
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Location/Qualifiers
1..3
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D08D06"
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/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
 |||
DB 1 TGG 3

RESULT 17
CL6851961
LOCUS
DEFINITION
CA851961
D19E06_H18_09.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D19E06 5', mRNA sequence.
CA851961
CA851961.1 GI:33388754
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)
AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
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Location/Qualifiers
1..3
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D19E06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA

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FEATURES
source
1. .3
/Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-K02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
|||
Db 1 TGG 3

RESULT 21
LOCUS CF339421 3 bp mRNA linear EST 18-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-N02, mRNA sequence.
ACCESSION CF339421
VERSION CF339421.1 GI:33827229
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-N02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
|||
Db 1 TGG 3

RESULT 23
LOCUS CF339761 3 bp mRNA linear EST 18-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-N20, mRNA sequence.
ACCESSION CF339761
VERSION CF339761.1 GI:33827892
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

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Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
|||
Db 1 TGG 3

RESULT 22
LOCUS CF339646 3 bp mRNA linear EST 18-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-I07, mRNA sequence.
ACCESSION CF339646
VERSION CF339646.1 GI:33827664
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--05-I07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
|||
Db 1 TGG 3

RESULT 23
LOCUS CF339761 3 bp mRNA linear EST 18-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-N20, mRNA sequence.
ACCESSION CF339761
VERSION CF339761.1 GI:33827892
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

```

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ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1..3
 /location=Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1-05-N20"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3
 |||
Db 1 GGG 3

RESULT 24
LOCUS CL423861
DEFINITION CL423861 3 bp DNA linear GSS 16-MAR-2004
O1S0750-04C1-C02 UniformMu MutAIL Library Zea mays genomic clone
O1S0750-04C1-C02, genomic survey sequence.
ACCESSION CL423861
VERSION CL423861.1 GI:45501905
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 3)
AUTHORS Lathwaj,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE Population tagged transposon insertions from the UniformMu maize
 sequence
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
 Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA
 Tel: 352-392-1928 x322
 Email: drmc@ufl.edu
 Sequence flanking probable Mu insertion site in UniformMu
 line: O1S0750-04, Primer set: C
 Class: transposon insertion site.
 Location/Qualifiers
 1..3

FEATURES
source
 1..3
 /location=Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="O1S0750-04C1-C02"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTG 5
 |||
Db 3 GTG 1

RESULT 25
LOCUS CL656746
DEFINITION CL656746 3 bp DNA linear GSS 09-JUL-2004
PRI0127b_H01 - PRI0127b.B21 (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL656746
VERSION CL656746.1 GI:50137492
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 3)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
 Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: 77
 Class: fosmid ends.
 Location/Qualifiers
 1..3
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
 |||
Db 1 TGG 3

```

```

USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
1. .4
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B06A04"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."

ORIGIN
Query Match 50.0%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3
 |||
DB 1 GGG 3

RESULT 28
CA853352/c
LOCUS
DEFINITION CA853352 seq CDNA Peking library 12hr SCN3 Glycine max cDNA clone
 B07C08 5', mRNA sequence.
ACCESSION CA853352
VERSION CA853352.1 GI:33390145
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
REFERENCE 1 (bases 1 to 4)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
 infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
 USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
1. .4
/organism="Glycine max"
/mol_type="mRNA"
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/db_xref="taxon:3847"
/clone="B07C08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."

ORIGIN
Query Match 50.0%; Score 3; DB 6; Length 4;

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Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGG 3
Db |||
4 GGG 2

RESULT 29
CF300913/c
LOCUS
DEFINITION
7LEAF--05-J02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J02, mRNA
sequence.
ACCESSION
CF300913
VERSION
CF300913.1 GI:33672674
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGG 3
Db |||
3 GGG 1

RESULT 30
CF306914
LOCUS
DEFINITION
HDAL--05-D09.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--05-D09, mRNA sequence.
ACCESSION
CF306914
VERSION
CF306914.1 GI:33678675
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

---

```

REFERENCE
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAL--05-D09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOUR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TGG 6
Db |||
1 TGG 3

Search completed: July 21, 2005, 01:54:32
Job time : 1351.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 00:00:54 ; Search time 710.6 Seconds  
(without alignments)

53.568 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 6704

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:\*

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| 3:  | /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*  |
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| 7:  | /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*  |
| 8:  | /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*  |
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| 23: | /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq* |
| 24: | /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*  |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No.        | Score | Query Match | Length | ID | Description       |
|-------------------|-------|-------------|--------|----|-------------------|
| 1                 | 6     | 100.0       | 6      | 9  | US-09-735-363A-45 |
| 2                 | 6     | 100.0       | 6      | 9  | US-09-879-668-17  |
| 3                 | 6     | 100.0       | 6      | 14 | US-10-127-645-3   |
| 4                 | 6     | 100.0       | 6      | 15 | US-10-280-274-17  |
| 5                 | 6     | 100.0       | 6      | 15 | US-10-264-280-2   |
| 6                 | 6     | 100.0       | 6      | 15 | US-10-264-280-6   |
| 7                 | 6     | 100.0       | 6      | 18 | US-10-420-513A-6  |
| Sequence 45, Appl |       |             |        |    |                   |
| Sequence 17, Appl |       |             |        |    |                   |
| Sequence 3, Appl  |       |             |        |    |                   |
| Sequence 17, Appl |       |             |        |    |                   |
| Sequence 2, Appl  |       |             |        |    |                   |
| Sequence 6, Appl  |       |             |        |    |                   |
| Sequence 6, Appl  |       |             |        |    |                   |

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|---|----|----------------------|------|---|------|-----------------------|
| 5 | 15 | US-10-055-732-14     | 83.3 | 5 | 83.3 | Sequence 14, Appl     |
| 5 | 19 | US-10-658-093-55     | 83.3 | 5 | 83.3 | Sequence 55, Appl     |
| 5 | 20 | US-10-658-093-55     | 83.3 | 5 | 83.3 | Sequence 55, Appl     |
| 5 | 21 | US-10-664-835-97     | 83.3 | 5 | 83.3 | Sequence 97, Appl     |
| 6 | 9  | US-09-735-363A-47    | 83.3 | 5 | 83.3 | Sequence 47, Appl     |
| 6 | 9  | US-09-942-487-1      | 83.3 | 5 | 83.3 | Sequence 1, Appl      |
| 6 | 9  | US-09-888-049-1      | 83.3 | 5 | 83.3 | Sequence 1, Appl      |
| 6 | 16 | US-10-041-860-191    | 83.3 | 5 | 83.3 | Sequence 191, Appl    |
| 6 | 16 | US-10-190-312A-212   | 83.3 | 5 | 83.3 | Sequence 212, Appl    |
| 6 | 16 | US-10-190-312A-274   | 83.3 | 5 | 83.3 | Sequence 274, Appl    |
| 6 | 16 | US-10-190-312A-321   | 83.3 | 5 | 83.3 | Sequence 321, Appl    |
| 6 | 16 | US-10-190-312A-326   | 83.3 | 5 | 83.3 | Sequence 326, Appl    |
| 6 | 16 | US-10-190-312A-636   | 83.3 | 5 | 83.3 | Sequence 636, Appl    |
| 6 | 18 | US-10-420-513A-9     | 83.3 | 5 | 83.3 | Sequence 9, Appl      |
| 6 | 19 | US-10-645-181-12     | 83.3 | 5 | 83.3 | Sequence 12, Appl     |
| 6 | 21 | US-10-656-450-12     | 83.3 | 5 | 83.3 | Sequence 12, Appl     |
| 6 | 22 | US-10-948-872-12     | 83.3 | 5 | 83.3 | Sequence 12, Appl     |
| 6 | 9  | US-09-735-363A-25    | 73.3 | 4 | 73.3 | Sequence 25, Appl     |
| 6 | 9  | US-09-735-363A-42    | 73.3 | 4 | 73.3 | Sequence 42, Appl     |
| 6 | 9  | US-09-735-363A-44    | 73.3 | 4 | 73.3 | Sequence 44, Appl     |
| 6 | 9  | US-09-735-363A-46    | 73.3 | 4 | 73.3 | Sequence 46, Appl     |
| 6 | 9  | US-09-735-363A-74    | 73.3 | 4 | 73.3 | Sequence 74, Appl     |
| 6 | 9  | US-09-735-363A-79    | 73.3 | 4 | 73.3 | Sequence 79, Appl     |
| 6 | 9  | US-09-879-668-5      | 73.3 | 4 | 73.3 | Sequence 5, Appl      |
| 6 | 9  | US-09-879-668-14     | 73.3 | 4 | 73.3 | Sequence 14, Appl     |
| 6 | 9  | US-09-879-668-16     | 73.3 | 4 | 73.3 | Sequence 16, Appl     |
| 6 | 9  | US-09-879-668-18     | 73.3 | 4 | 73.3 | Sequence 18, Appl     |
| 6 | 9  | US-09-924-346-6      | 73.3 | 4 | 73.3 | Sequence 6, Appl      |
| 6 | 9  | US-09-728-574-20     | 73.3 | 4 | 73.3 | Sequence 20, Appl     |
| 6 | 10 | US-09-888-326-165    | 73.3 | 4 | 73.3 | Sequence 165, Appl    |
| 6 | 10 | US-09-776-479-31     | 73.3 | 4 | 73.3 | Sequence 31, Appl     |
| 6 | 11 | US-09-776-479-31     | 73.3 | 4 | 73.3 | Sequence 31, Appl     |
| 6 | 14 | US-10-179-053-3      | 73.3 | 4 | 73.3 | Sequence 3, Appl      |
| 6 | 14 | US-10-127-645-2      | 73.3 | 4 | 73.3 | Sequence 2, Appl      |
| 6 | 14 | US-10-127-645-4      | 73.3 | 4 | 73.3 | Sequence 4, Appl      |
| 6 | 14 | US-10-112-653-31     | 73.3 | 4 | 73.3 | Sequence 31, Appl     |
| 6 | 14 | US-10-017-995-31     | 73.3 | 4 | 73.3 | Sequence 31, Appl     |
| 6 | 15 | US-10-280-274-5      | 73.3 | 4 | 73.3 | Sequence 5, Appl      |
| 6 | 15 | US-10-280-274-14     | 73.3 | 4 | 73.3 | Sequence 14, Appl     |
| 6 | 15 | US-10-280-274-16     | 73.3 | 4 | 73.3 | Sequence 16, Appl     |
| 6 | 15 | US-10-280-274-18     | 73.3 | 4 | 73.3 | Sequence 18, Appl     |
| 6 | 15 | US-10-264-280-1      | 73.3 | 4 | 73.3 | Sequence 1, Appl      |
| 6 | 15 | US-10-264-280-3      | 73.3 | 4 | 73.3 | Sequence 3, Appl      |
| 6 | 15 | US-10-264-280-5      | 73.3 | 4 | 73.3 | Sequence 5, Appl      |
| 6 | 15 | US-10-264-280-7      | 73.3 | 4 | 73.3 | Sequence 7, Appl      |
| 6 | 16 | US-10-041-860-95     | 73.3 | 4 | 73.3 | Sequence 95, Appl     |
| 6 | 16 | US-10-041-860-154    | 73.3 | 4 | 73.3 | Sequence 154, Appl    |
| 6 | 16 | US-10-240-305-12     | 73.3 | 4 | 73.3 | Sequence 12, Appl     |
| 6 | 16 | US-10-168-327-1      | 73.3 | 4 | 73.3 | Sequence 1, Appl      |
| 6 | 16 | US-10-109-363-5      | 73.3 | 4 | 73.3 | Sequence 5, Appl      |
| 6 | 16 | US-10-190-312A-201   | 73.3 | 4 | 73.3 | Sequence 201, Appl    |
| 6 | 16 | US-10-190-312A-252   | 73.3 | 4 | 73.3 | Sequence 252, Appl    |
| 6 | 16 | US-10-190-312A-253   | 73.3 | 4 | 73.3 | Sequence 253, Appl    |
| 6 | 16 | US-10-190-312A-680   | 73.3 | 4 | 73.3 | Sequence 680, Appl    |
| 6 | 16 | US-10-190-312A-1009  | 73.3 | 4 | 73.3 | Sequence 1009, Appl   |
| 6 | 17 | US-10-314-578-31     | 73.3 | 4 | 73.3 | Sequence 31, Appl     |
| 6 | 17 | US-10-182-329-4      | 73.3 | 4 | 73.3 | Sequence 4, Appl      |
| 6 | 18 | US-10-420-513A-3     | 73.3 | 4 | 73.3 | Sequence 3, Appl      |
| 6 | 18 | US-10-420-513A-5     | 73.3 | 4 | 73.3 | Sequence 5, Appl      |
| 6 | 18 | US-10-420-513A-7     | 73.3 | 4 | 73.3 | Sequence 7, Appl      |
| 6 | 19 | US-10-716-029-165    | 73.3 | 4 | 73.3 | Sequence 165, Appl    |
| 6 | 19 | US-10-716-029-168    | 73.3 | 4 | 73.3 | Sequence 168, Appl    |
| 6 | 19 | US-10-831-778-31     | 73.3 | 4 | 73.3 | Sequence 31, Appl     |
| 6 | 19 | US-10-433-258-13     | 70.0 | 4 | 70.0 | Sequence 13, Appl     |
| 6 | 20 | US-10-486-865-24     | 70.0 | 4 | 70.0 | Sequence 24, Appl     |
| 4 | 10 | US-09-929-507-15     | 66.7 | 4 | 66.7 | Sequence 15, Appl     |
| 4 | 13 | US-10-027-632-177911 | 66.7 | 4 | 66.7 | Sequence 177911, Appl |
| 4 | 17 | US-10-027-632-177911 | 66.7 | 4 | 66.7 | Sequence 177911, Appl |
| 4 | 17 | US-10-378-558A-14    | 66.7 | 4 | 66.7 | Sequence 14, Appl     |
| 4 | 19 | US-10-686-317-4      | 66.7 | 4 | 66.7 | Sequence 4, Appl      |
| 4 | 19 | US-10-686-317-37     | 66.7 | 4 | 66.7 | Sequence 37, Appl     |
| 4 | 19 | US-10-686-317-41     | 66.7 | 4 | 66.7 | Sequence 41, Appl     |
| 4 | 19 | US-10-686-317-64     | 66.7 | 4 | 66.7 | Sequence 64, Appl     |

c 81 4 66.7 5 9 US-09-912-680-12 Sequence 12, Appl  
c 82 4 66.7 5 9 US-09-912-680-14 Sequence 14, Appl  
c 83 4 66.7 5 9 US-09-816-763-21 Sequence 21, Appl  
c 84 4 66.7 5 10 US-09-731-289B-3 Sequence 3, Appl  
c 85 4 66.7 5 10 US-09-798-883B-54 Sequence 54, Appl  
c 86 4 66.7 5 10 US-09-326-885-54 Sequence 54, Appl  
c 87 4 66.7 5 13 US-10-027-632-51789 Sequence 51789, A  
c 88 4 66.7 5 13 US-10-027-632-53175 Sequence 53175, A  
c 89 4 66.7 5 13 US-10-027-632-176308 Sequence 176308,  
c 90 4 66.7 5 16 US-10-109-789-12 Sequence 12, Appl  
c 91 4 66.7 5 16 US-10-109-799-14 Sequence 14, Appl  
c 92 4 66.7 5 17 US-10-027-632-51789 Sequence 51789, A  
c 93 4 66.7 5 17 US-10-027-632-53175 Sequence 53175, A  
c 94 4 66.7 5 17 US-10-027-632-176308 Sequence 176308,  
c 95 4 66.7 5 17 US-10-395-709-24 Sequence 24, Appl  
c 96 4 66.7 5 18 US-10-315-907A-24 Sequence 24, Appl  
c 97 4 66.7 5 18 US-10-619-939-13 Sequence 13, Appl  
c 98 4 66.7 5 19 US-10-281-067B-24 Sequence 24, Appl  
c 99 4 66.7 5 19 US-10-681-818-215 Sequence 215, App  
c 100 4 66.7 5 19 US-10-681-818-216 Sequence 216, App

## ALIGNMENTS

RESULT 1  
US-09-735-363A-45  
; Sequence 45, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-45

Query Match 100.0%; Score 6; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||||  
Db 1 GGGAGG 6

RESULT 2  
US-09-879-668-17  
; Sequence 17, Application US/09879668  
; Patent No. US20020091095A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0241 42368-256931  
; CURRENT APPLICATION NUMBER: US/09/879,668  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/228,925

; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-09-879-668-17

Query Match 100.0%; Score 6; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||||  
Db 1 GGGAGG 6

RESULT 3  
US-10-127-645-3  
; Sequence 3, Application US/10127645  
; Publication No. US20030045493A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiation  
; FILE REFERENCE: 02811-0261 (42368-273010)  
; CURRENT APPLICATION NUMBER: US/10/127,645  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US 60/286,158  
; PRIOR FILING DATE: 2001-04-24  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-10-127-645-3

Query Match 100.0%; Score 6; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||||  
Db 1 GGGAGG 6

RESULT 4  
US-10-280-274-17  
; Sequence 17, Application US/10280274  
; Publication No. US2003011976A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0242 42368-279803  
; CURRENT APPLICATION NUMBER: US/10/280,274  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 09/879,668  
; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-17

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 1 GGGAGG 6

RESULT 5  
US-10-264-280-2  
; Sequence 2, Application US/10264280  
; Publication No. US20030125290A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; APPLICANT: Phillips, Nigel C.  
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleob  
; FILE REFERENCE: 02811-0271 42368-277492  
; CURRENT APPLICATION NUMBER: US/10/264,280  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 60/326,884  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-264-280-2

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 1 GGGAGG 6

RESULT 6  
US-10-264-280-6  
; Sequence 6, Application US/10264280  
; Publication No. US20030125290A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Herrera-Gayol, Andrea C.  
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleob  
; FILE REFERENCE: 02811-0271 42368-277492  
; CURRENT APPLICATION NUMBER: US/10/264,280  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 60/326,884

; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide  
US-10-264-280-6

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 1 GGGAGG 6

RESULT 7  
US-10-420-513A-6  
; Sequence 6, Application US/10420513A  
; Publication No. US20040058883A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; APPLICANT: Phillips, Nigel C.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of  
; TITLE OF INVENTION: Immune Response  
; FILE REFERENCE: 02811-0301 (42368-283135)  
; CURRENT APPLICATION NUMBER: US/10/420,513A  
; CURRENT FILING DATE: 2003-04-22  
; PRIOR APPLICATION NUMBER: US 60/374,540  
; PRIOR FILING DATE: 2002-04-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-420-513A-6

Query Match 100.0%; Score 6; DB 18; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 1 GGGAGG 6

RESULT 8  
US-10-055-732-14  
; Sequence 14, Application US/10055732  
; Publication No. US20030135040A1  
; GENERAL INFORMATION:  
; APPLICANT: Eritja, Ramon  
; APPLICANT: Garcia, Ramon Guimil  
; APPLICANT: Oste, Christian C.  
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US2003013504  
; TITLE OF INVENTION: Structures  
; FILE REFERENCE: 03038-0202 42892-265833  
; CURRENT APPLICATION NUMBER: US/10/055,732  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/162,627  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/702,066  
; PRIOR FILING DATE: 2000-10-30

; PRIOR APPLICATION NUMBER: US 60/197,559  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-055-732-14

Query Match 83.3%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 1 GGAGG 5

RESULT 9  
US-10-658-093-55/c  
; Sequence 55, Application US/10658093  
; Publication No. US20040115704A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, John Michael  
; TITLE OF INVENTION: Constructs for Gene Expression Analysis  
; FILE REFERENCE: 12177722  
; CURRENT APPLICATION NUMBER: US/10/658,093  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: USSN 60/274770  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: PCT/AU02/00351  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: mammalian  
US-10-658-093-55

Query Match 83.3%; Score 5; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 5 GGAGG 1

RESULT 10  
US-10-658-093-55/c  
; Sequence 55, Application US/10658093  
; Publication No. US20040209274A2  
; GENERAL INFORMATION:  
; APPLICANT: Daly, John Michael  
; TITLE OF INVENTION: Constructs for Gene Expression Analysis  
; FILE REFERENCE: 12177722  
; CURRENT APPLICATION NUMBER: US/10/658,093  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: USSN 60/274770  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: PCT/AU02/00351  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: mammalian  
US-10-658-093-55

Query Match 83.3%; Score 5; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 5 GGAGG 1

RESULT 11  
US-10-664-835-97/c  
; Sequence 97, Application US/10664835  
; Publication No. US20050042620A1  
; GENERAL INFORMATION:  
; APPLICANT: Hampel, Arnold  
; APPLICANT: Tritz, Richard  
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES  
; FILE REFERENCE: 43863-C1YA  
; CURRENT APPLICATION NUMBER: US/10/664,835  
; CURRENT FILING DATE: 2003-09-15  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 97  
; LENGTH: 5  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Ribozyme, portion of ribozyme or ribozyme target substrate  
US-10-664-835-97

Query Match 83.3%; Score 5; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 5 GGAGG 1

RESULT 12  
US-09-735-363A-47  
; Sequence 47, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-47

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 1 GGAGG 5

## RESULT 13

US-09-942-487-1  
; Sequence 1, Application US/09942487  
; Publication No. US20020086310A1  
; GENERAL INFORMATION:  
; APPLICANT: FAN, FRANK  
; APPLICANT: HE, YIPING  
; APPLICANT: HUANG, JIANZHONG  
; APPLICANT: JIANG, XINHE  
; APPLICANT: MCDEVITT, DAMIEN  
; APPLICANT: ROSENBERG, MARTIN  
; APPLICANT: ST. JOHN, ANNEMARIE  
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF  
; TITLE OF INVENTION: ANTIMICROBIAL COMPOUNDS  
; FILE REFERENCE: P51167  
; CURRENT APPLICATION NUMBER: US/09/942,487  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/229,965  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-942-487-1

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
Db 2 GGAGG 6

## RESULT 14

US-09-888-049-1  
; Sequence 1, Application US/09888049  
; Patent No. US20020137215A1  
; GENERAL INFORMATION:  
; APPLICANT: Francis, Kevin P.  
; APPLICANT: Purchio, Anthony F.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE THEREOF IN MODIFYING  
; TITLE OF INVENTION: THE GENOMES OF MICROORGANISMS  
; FILE REFERENCE: PXE-013 USP / 9400-0013  
; CURRENT APPLICATION NUMBER: US/09/888,049  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/216,257  
; PRIOR FILING DATE: 2000-07-06  
; PRIOR APPLICATION NUMBER: 60/274,105  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Gram-positive  
; OTHER INFORMATION: ribosome binding site  
US-09-888-049-1

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
Db 2 GGAGG 6

## RESULT 15

US-10-041-860-191/c  
; Sequence 191, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Peng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 191  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-041-860-191

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
Db 6 GGAGG 2

## RESULT 16

US-10-190-312A-212/c  
; Sequence 212, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 212  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-212

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
Db 6 GGAGG 2

## RESULT 17

US-10-190-312A-274/c  
; Sequence 274, Application US/10190312A  
; Publication No. US20030199468A1

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; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 274
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-274

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 5 GGGAG 1

RESULT 18
US-10-190-312A-321/c
; Sequence 321, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 321
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-321

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6
Db 5 GGGAG 1

RESULT 19
US-10-190-312A-326/c
; Sequence 326, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
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; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 326
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-326

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 6 GGGAG 2

RESULT 20
US-10-190-312A-636/c
; Sequence 636, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 636
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-636

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6
Db 6 GGGAG 2

RESULT 21
US-10-420-513A-9
; Sequence 9, Application US/10420513A
; Publication No. US20040058883A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Filion, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
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; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: "n" = G, C, A or T  
US-10-420-513a-9

Query Match 83.3%; Score 5; DB 18; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
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Db 1 GGGNGG 6

RESULT 22  
US-10-645-187-12  
; Sequence 12, Application US/10645187  
; Publication No. US20040191222A1  
; GENERAL INFORMATION:  
; APPLICANT: Emimi, Emilio A.  
; APPLICANT: Shiver, John W.  
; APPLICANT: Bett, Andrew J.  
; APPLICANT: Casimiro, Danilo R.  
; APPLICANT: Kaslow, David C.  
; APPLICANT: Chastain, Michael  
; TITLE OF INVENTION: ADENOVIRUS SEROTYPE 34 VECTORS, NUCLEIC  
; FILE REFERENCE: 21390  
; CURRENT APPLICATION NUMBER: US/10/645,187  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: 60/458,825  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: adenovirus serotype 34  
US-10-645-187-12

Query Match 83.3%; Score 5; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6  
|||||  
Db 1 GGGAG 5

RESULT 23  
US-10-656-450-12/c  
; Sequence 12, Application US/10656450  
; Publication No. US20050059620A1  
; GENERAL INFORMATION:  
; APPLICANT: Brunicardi, F. C.  
; TITLE OF INVENTION: Promoter Driven Tissue Specific Cytotoxic Agents  
; FILE REFERENCE: A146.0136  
; CURRENT APPLICATION NUMBER: US/10/656,450  
; CURRENT FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: US/09/686,631  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 60/161,109

; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: UNKNOWN  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-656-450-12

Query Match 83.3%; Score 5; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 5 GGGAG 1

RESULT 24  
US-10-948-872-12/c  
; Sequence 12, Application US/10948872  
; Publication No. US20050137157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brunicardi, F. Charles  
; TITLE OF INVENTION: Promoter Driven Tissue Specific Cytotoxic Agents and Method of  
; FILE REFERENCE: 607110-00002USC2  
; CURRENT APPLICATION NUMBER: US/10/948,872  
; CURRENT FILING DATE: 2004-09-24  
; PRIOR APPLICATION NUMBER: US 10/656,450  
; PRIOR FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US 09/686,631  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: US 60/161,109  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: US 60/224,382  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-948-872-12

Query Match 83.3%; Score 5; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 5 GGGAG 1

RESULT 25  
US-09-735-363A-25  
; Sequence 25, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Filion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13

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; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-25

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 9; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGTGG 6

RESULT 26
US-09-735-363A-42
; Sequence 42, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-42

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 9; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGAAGG 6

RESULT 27
US-09-735-363A-44
; Sequence 44, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-44

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 9; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGGGG 6

RESULT 28
US-09-735-363A-46
; Sequence 46, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-46

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 9; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGGGG 6

RESULT 29
US-09-735-363A-74
; Sequence 74, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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US-09-735-363A-74

Query Match 73.3%; Score 4.4; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||  
Db 1 GGGTGG 6

RESULT 30

US-09-735-363A-79/c  
; Sequence 79, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 79  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-79

Query Match 73.3%; Score 4.4; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||  
Db 6 GGGTGG 1

Search completed: July 21, 2005, 07:13:23  
Job time : 712.6 secs

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds  
(without alignments)  
172.240 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*
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- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
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- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| C 1        | 5     | 83.3        | 5      | 4  | US-09-153-242-31   |
| C 2        | 5     | 83.3        | 5      | 4  | US-09-491-795-6    |
| C 3        | 5     | 83.3        | 5      | 4  | US-10-055-732-14   |
| C 4        | 5     | 83.3        | 6      | 1  | US-08-533-912-6    |
| C 5        | 5     | 83.3        | 6      | 1  | US-08-465-590-140  |
| C 6        | 5     | 83.3        | 6      | 3  | US-08-711-417C-140 |
| C 7        | 5     | 83.3        | 6      | 4  | US-09-723-909-140  |
| C 8        | 5     | 83.3        | 6      | 4  | US-09-686-631-12   |
| C 9        | 5     | 83.3        | 6      | 4  | US-09-557-289A-1   |
| C 10       | 5     | 83.3        | 6      | 4  | US-08-453-485B-17  |
| C 11       | 5     | 83.3        | 6      | 5  | PCT-US93-08743-140 |
| C 12       | 4.4   | 73.3        | 6      | 3  | US-08-920-422-15   |
| C 13       | 4.4   | 73.3        | 6      | 3  | US-08-920-422-16   |
| C 14       | 4.4   | 73.3        | 6      | 3  | US-08-920-422-17   |
| C 15       | 4.4   | 73.3        | 6      | 3  | US-09-593-323-29   |
| C 16       | 4.4   | 73.3        | 6      | 3  | US-09-594-108-29   |
| C 17       | 4.4   | 73.3        | 6      | 4  | US-09-344-300-29   |
| C 18       | 4.4   | 73.3        | 6      | 4  | US-09-924-346-6    |
| C 19       | 4.4   | 73.3        | 6      | 4  | US-09-483-184A-6   |
| C 20       | 4     | 66.7        | 4      | 5  | PCT-US94-06456-38  |
| C 21       | 4     | 66.7        | 5      | 1  | US-08-247-809A-15  |
| C 22       | 4     | 66.7        | 5      | 1  | US-08-381-097A-14  |
| C 23       | 4     | 66.7        | 5      | 2  | US-08-597-948A-6   |
| C 24       | 4     | 66.7        | 5      | 2  | US-08-711-728-15   |
| C 25       | 4     | 66.7        | 5      | 3  | US-08-873-709-8    |
| C 26       | 4     | 66.7        | 5      | 4  | US-08-921-497-12   |
| C 27       | 4     | 66.7        | 5      | 4  | US-08-921-497-14   |

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| 5 | 5 | 66.7 | 4   | 28  | PCT-US93-03027-7  | Sequence 7, Appli |
| 6 | 1 | 66.7 | 4   | 29  | US-08-242-402-20  | Sequence 20, Appl |
| 6 | 1 | 66.7 | 4   | 30  | US-08-270-180-19  | Sequence 19, Appl |
| 6 | 1 | 66.7 | 4   | 31  | US-07-724-500B-13 | Sequence 13, Appl |
| 6 | 1 | 66.7 | 4   | 32  | US-08-611-510-15  | Sequence 15, Appl |
| 6 | 2 | 66.7 | 4   | 33  | US-08-442-809A-1  | Sequence 1, Appli |
| 6 | 2 | 66.7 | 4   | 34  | US-08-442-809A-6  | Sequence 6, Appli |
| 6 | 3 | 66.7 | 4   | 35  | US-08-682-423-19  | Sequence 19, Appl |
| 6 | 3 | 66.7 | 4   | 36  | US-09-056-868B-14 | Sequence 14, Appl |
| 6 | 3 | 66.7 | 4   | 37  | US-09-632-538C-10 | Sequence 10, Appl |
| 6 | 4 | 66.7 | 4   | 38  | US-09-608-958-50  | Sequence 50, Appl |
| 6 | 4 | 66.7 | 4   | 39  | US-09-608-958-51  | Sequence 51, Appl |
| 6 | 4 | 66.7 | 4   | 40  | US-09-435-327A-1  | Sequence 1, Appli |
| 6 | 4 | 66.7 | 4   | 41  | US-09-975-413A-1  | Sequence 2, Appli |
| 6 | 4 | 66.7 | 4   | 42  | US-09-575-413A-2  | Sequence 14, Appl |
| 6 | 4 | 66.7 | 4   | 43  | US-09-851-271A-14 | Sequence 13, Appl |
| 6 | 4 | 66.7 | 4   | 44  | US-10-134-188-13  | Sequence 13, Appl |
| 6 | 5 | 66.7 | 4   | 45  | PCT-US92-08094-63 | Sequence 63, Appl |
| 6 | 5 | 66.7 | 4   | 46  | PCT-US95-05141-19 | Sequence 19, Appl |
| 5 | 5 | 63.3 | 4   | 47  | PCT-US91-03680-78 | Sequence 78, Appl |
| 5 | 1 | 56.7 | 3.4 | 48  | US-07-862-831A-1  | Sequence 1, Appli |
| 5 | 1 | 56.7 | 3.4 | 49  | US-07-862-831A-2  | Sequence 2, Appli |
| 5 | 1 | 56.7 | 3.4 | 50  | US-08-126-564A-1  | Sequence 1, Appli |
| 5 | 1 | 56.7 | 3.4 | 51  | US-08-126-564A-2  | Sequence 2, Appli |
| 5 | 1 | 56.7 | 3.4 | 52  | US-08-717-526-53  | Sequence 53, Appl |
| 5 | 2 | 56.7 | 3.4 | 53  | US-08-950-709-1   | Sequence 1, Appli |
| 5 | 3 | 56.7 | 3.4 | 54  | US-09-107-708-1   | Sequence 1, Appli |
| 5 | 3 | 56.7 | 3.4 | 55  | US-09-449-581-1   | Sequence 1, Appli |
| 5 | 4 | 56.7 | 3.4 | 56  | US-09-305-839-46  | Sequence 46, Appl |
| 5 | 5 | 56.7 | 3.4 | 57  | PCT-US91-03680-76 | Sequence 76, Appl |
| 5 | 5 | 56.7 | 3.4 | 58  | PCT-US94-09143-1  | Sequence 1, Appli |
| 5 | 5 | 56.7 | 3.4 | 59  | PCT-US94-09143-2  | Sequence 2, Appli |
| 6 | 1 | 56.7 | 3.4 | 60  | US-07-791-2130-45 | Sequence 45, Appl |
| 6 | 1 | 56.7 | 3.4 | 61  | US-08-234-613-10  | Sequence 10, Appl |
| 6 | 1 | 56.7 | 3.4 | 62  | US-08-488-672-1   | Sequence 1, Appli |
| 6 | 1 | 56.7 | 3.4 | 63  | US-08-381-097A-12 | Sequence 12, Appl |
| 6 | 1 | 56.7 | 3.4 | 64  | US-08-153-051B-53 | Sequence 53, Appl |
| 6 | 1 | 56.7 | 3.4 | 65  | US-08-060-952C-52 | Sequence 52, Appl |
| 6 | 1 | 56.7 | 3.4 | 66  | US-08-533-912-7   | Sequence 7, Appli |
| 6 | 1 | 56.7 | 3.4 | 67  | US-08-533-912-8   | Sequence 8, Appli |
| 6 | 1 | 56.7 | 3.4 | 68  | US-08-293-150A-45 | Sequence 45, Appl |
| 6 | 2 | 56.7 | 3.4 | 69  | US-08-151-477A-53 | Sequence 53, Appl |
| 6 | 2 | 56.7 | 3.4 | 70  | US-08-237-973-10  | Sequence 10, Appl |
| 6 | 2 | 56.7 | 3.4 | 71  | US-08-237-973-26  | Sequence 26, Appl |
| 6 | 3 | 56.7 | 3.4 | 72  | US-08-819-867-70  | Sequence 70, Appl |
| 6 | 3 | 56.7 | 3.4 | 73  | US-08-464-011B-52 | Sequence 52, Appl |
| 6 | 3 | 56.7 | 3.4 | 74  | US-09-196-099-17  | Sequence 17, Appl |
| 6 | 4 | 56.7 | 3.4 | 75  | US-09-378-535-70  | Sequence 70, Appl |
| 6 | 4 | 56.7 | 3.4 | 76  | US-09-220-794-10  | Sequence 10, Appl |
| 6 | 4 | 56.7 | 3.4 | 77  | US-08-708-354-1   | Sequence 1, Appli |
| 6 | 4 | 56.7 | 3.4 | 78  | US-09-288-719B-17 | Sequence 17, Appl |
| 6 | 4 | 56.7 | 3.4 | 79  | US-09-288-719B-18 | Sequence 18, Appl |
| 6 | 4 | 56.7 | 3.4 | 80  | US-10-071-411A-61 | Sequence 61, Appl |
| 6 | 5 | 56.7 | 3.4 | 81  | PCT-US93-05331-1  | Sequence 1, Appli |
| 6 | 5 | 53.3 | 3.2 | 82  | US-08-646-301A-13 | Sequence 13, Appl |
| 3 | 3 | 50.0 | 3   | 83  | US-08-268-679B-7  | Sequence 7, Appli |
| 3 | 3 | 50.0 | 3   | 84  | US-08-873-709-9   | Sequence 9, Appli |
| 3 | 3 | 50.0 | 3   | 85  | US-09-032-365A-36 | Sequence 36, Appl |
| 3 | 3 | 50.0 | 3   | 86  | US-07-630-288A-13 | Sequence 13, Appl |
| 4 | 1 | 50.0 | 3   | 87  | US-08-393-219-11  | Sequence 11, Appl |
| 4 | 1 | 50.0 | 3   | 88  | US-08-468-049-13  | Sequence 13, Appl |
| 4 | 1 | 50.0 | 3   | 89  | US-08-463-288A-62 | Sequence 62, Appl |
| 4 | 1 | 50.0 | 3   | 90  | US-08-463-288A-63 | Sequence 63, Appl |
| 4 | 2 | 50.0 | 3   | 91  | US-08-470-445A-62 | Sequence 62, Appl |
| 4 | 2 | 50.0 | 3   | 92  | US-08-470-445A-63 | Sequence 63, Appl |
| 4 | 2 | 50.0 | 3   | 93  | US-08-462-679-62  | Sequence 62, Appl |
| 4 | 2 | 50.0 | 3   | 94  | US-08-462-679-63  | Sequence 63, Appl |
| 4 | 2 | 50.0 | 3   | 95  | US-08-466-210A-62 | Sequence 62, Appl |
| 4 | 2 | 50.0 | 3   | 96  | US-08-466-210A-63 | Sequence 63, Appl |
| 4 | 2 | 50.0 | 3   | 97  | US-08-467-147A-62 | Sequence 62, Appl |
| 4 | 2 | 50.0 | 3   | 98  | US-08-467-147A-63 | Sequence 63, Appl |
| 4 | 2 | 50.0 | 3   | 99  | US-08-469-014-62  | Sequence 62, Appl |
| 4 | 2 | 50.0 | 3   | 100 | US-08-469-014-63  | Sequence 63, Appl |

## ALIGNMENTS

## RESULT 1

US-09-153-242-31/c  
; Sequence 31, Application US/09153242  
; Patent No. 6482592  
; GENERAL INFORMATION:  
; APPLICANT: Lundberg, Joakim  
; APPLICANT: Uhlen, Mathias  
; TITLE OF INVENTION: MODULAR PROBES II  
; FILE REFERENCE: 1181-242  
; CURRENT APPLICATION NUMBER: US/09/153,242  
; CURRENT FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: H2  
US-09-153-242-31

Query Match 83.3%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 5 GGAGG 1

## RESULT 2

US-09-491-795-6  
; Sequence 6, Application US/09491795  
; Patent No. 6596281  
; GENERAL INFORMATION:  
; APPLICANT: Gennaro, Maria L.  
; APPLICANT: Lyashchenko, Konstantin P.  
; APPLICANT: Manca, Claudia M.A.  
; TITLE OF INVENTION: MIXOCACTERIUM TUBERCULOSIS SPECIFIC PROTEINS AND GENES,  
; TITLE OF INVENTION: MIXTURES OF ANTIGENS AND USES THEREOF  
; FILE REFERENCE: 07763/028002  
; CURRENT APPLICATION NUMBER: US/09/491,795  
; CURRENT FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: US 08/796,792  
; PRIOR FILING DATE: 1997-02-06  
; PRIOR APPLICATION NUMBER: US 60/011,364  
; PRIOR FILING DATE: 1996-02-09  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-491-795-6

Query Match 83.3%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 1 GGAGG 5

## RESULT 3

US-10-055-732-14

; Sequence 14, Application US/10055732  
; Patent No. 6831072  
; GENERAL INFORMATION:  
; APPLICANT: Eritja, Ramon  
; APPLICANT: Garcia, Ramon Guimil  
; APPLICANT: Oste, Christian C.  
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. 6831072el N  
; TITLE OF INVENTION: Structures  
; FILE REFERENCE: 03038-0202 42892-265833  
; CURRENT APPLICATION NUMBER: US/10/055,732  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/162,627  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/702,066  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 60/197,559  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-055-732-14

Query Match 83.3%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||  
Db 1 GGAGG 5

## RESULT 4

US-08-533-912-6  
; Sequence 6, Application US/08533912  
; Patent No. 574308  
; GENERAL INFORMATION:  
; APPLICANT: GUILLOU-BONNICI, Francoise  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: MALLET, Francois  
; APPLICANT: LEVASSEUR, Pierre  
; APPLICANT: MCALLISTER, William  
; TITLE OF INVENTION: CHIMERA OLIGONUCLEOTIDE AND ITS  
; TITLE OF INVENTION: UTILIZATION FOR OBTAINING TRANSCRIPTS OF A NUCLEIC ACID  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oliff & Berridge  
; STREET: 700 South Washington Street, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/533,912  
; FILING DATE: 26-SEP-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94011455  
; FILING DATE: 26-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 36613  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-533-912-6

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GGGAG 5  
Db 1 GGGAG 5

RESULT 5  
US-08-465-590-140  
Sequence 140, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,590  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/238,212  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,438  
FILING DATE: 14-SEP-1993  
APPLICATION NUMBER: US 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,695  
REFERENCE/DOCKET NUMBER: MPF-006C2DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-465-590-140

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GGGAG 5  
Db 2 GGGAG 6

RESULT 6  
US-08-711-417C-140  
Sequence 140, Application US/08711417C  
Patent No. 6228611  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 202  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/711,417C  
FILING DATE: 05-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/238,212  
FILING DATE: 02-MAY-1994  
APPLICATION NUMBER: 08/121,438  
FILING DATE: 14-SEP-1993  
APPLICATION NUMBER: 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis P.  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10287/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-08-711-417C-140

Query Match 83.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GGGAG 5  
Db 2 GGGAG 6

RESULT 7  
US-09-723-909-140  
Sequence 140, Application US/09723909  
Patent No. 6630141  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 202  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street

/ CITY: Boston  
/ STATE: MA  
/ COUNTRY: USA  
/ ZIP: 02110-2804  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: Windows 95  
/ SOFTWARE: FastSeq for Windows Version 2.0b  
/ CURRENT APPLICATION DATA: US/09/723,909  
/ FILING DATE: 28-NO. 6630141-2000  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/711,417  
/ FILING DATE: 05-Sep-1996  
/ APPLICATION NUMBER: 08/238,212  
/ FILING DATE: 02-MAY-1994  
/ APPLICATION NUMBER: 08/121,438  
/ FILING DATE: 14-SEP-1993  
/ APPLICATION NUMBER: 07/946,233  
/ FILING DATE: 14-SEP-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Myers, Louis P.  
/ REGISTRATION NUMBER: 35,965  
/ REFERENCE/DOCKET NUMBER: 10287/007001  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 617/542-5070  
/ TELEFAX: 617/542-8906  
/ TELEX: 200154  
/ INFORMATION FOR SEQ ID NO: 140:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-723-909-140

Query Match 83.3%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 2 GGGAG 6

RESULT 8  
US-09-686-631-12/c  
/ Sequence 12, Application US/09686631  
/ Patent No. 6716824  
/ GENERAL INFORMATION:  
/ APPLICANT: Brunicardi, F. C.  
/ TITLE OF INVENTION: Promoter Driven Tissue Specific Cytotoxic Agents  
/ FILE REFERENCE: A146.0136  
/ CURRENT APPLICATION NUMBER: US/09/686,631  
/ CURRENT FILING DATE: 2000-10-11  
/ PRIOR APPLICATION NUMBER: 60/161,109  
/ PRIOR FILING DATE: 1999-10-22  
/ PRIOR APPLICATION NUMBER: UNKNOWN  
/ PRIOR FILING DATE: 2000-08-09  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 12  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-686-631-12

Query Match 83.3%; Score 5; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
DB 5 GGGAG 1

RESULT 9  
US-09-657-289A-1  
/ Sequence 1, Application US/09657289A  
/ Patent No. 6737245  
/ GENERAL INFORMATION:  
/ APPLICANT: Francis, Kevin P.  
/ APPLICANT: Contag, Pamela R.  
/ APPLICANT: Joh, Danny J.  
/ TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE  
/ FILE REFERENCE: 9400-0006  
/ CURRENT APPLICATION NUMBER: US/09/657,289A  
/ CURRENT FILING DATE: 2000-09-07  
/ NUMBER OF SEQ ID NOS: 26  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 1  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Gram-positive  
/ OTHER INFORMATION: ribosome binding site  
US-09-657-289A-1

Query Match 83.3%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6  
DB 2 GGGAG 6

RESULT 10  
US-08-453-485E-17  
/ Sequence 17, Application US/08453485E  
/ Patent No. 6828125  
/ GENERAL INFORMATION:  
/ APPLICANT: Baxter Biotech Technology Sarl  
/ TITLE OF INVENTION: DNA ENCODING FUSED DI-ALPHA GLOBINS AND USE THEREOF  
/ FILE REFERENCE: BXTB 1885  
/ CURRENT APPLICATION NUMBER: US/08/453,485E  
/ CURRENT FILING DATE: 1995-05-30  
/ PRIOR APPLICATION NUMBER: 07/789,179  
/ PRIOR FILING DATE: 1991-11-08  
/ PRIOR APPLICATION NUMBER: 07/671,707  
/ PRIOR FILING DATE: 1991-04-01  
/ NUMBER OF SEQ ID NOS: 114  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 17  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: spacer region  
US-08-453-485E-17

Query Match 83.3%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6  
DB 2 GGGAG 6

RESULT 11  
PCT-US93-08743-140  
; Sequence 140, Application PC/TUS9308743  
; GENERAL INFORMATION:  
; APPLICANT: IKAROS: A T CELL PATHWAY REGULATORY GENE  
; TITLE OF INVENTION: 152  
; NUMBER OF SEQUENCES: 152  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08743  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 946,233  
; FILING DATE: 14-SEP-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 140:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US93-08743-140

Query Match 83.3%; Score 5; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 2 GGGAG 6

RESULT 12  
US-08-920-422-15  
; Sequence 15, Application US/08920422A  
; Patent No. 6255473  
; GENERAL INFORMATION:  
; APPLICANT: Vitek, Michael P.  
; APPLICANT: Mitsuda, No. 6255473iaki  
; APPLICANT: Roses, Allen D.  
; TITLE OF INVENTION: Presenilin-1 Gene Promoter  
; FILE REFERENCE: VITEKPRESENTILIN  
; CURRENT APPLICATION NUMBER: US/08/920,422A  
; CURRENT FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-920-422-15

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 1 GGGCGG 6

RESULT 13  
US-08-920-422-16/c  
; Sequence 16, Application US/08920422A  
; Patent No. 6255473

; GENERAL INFORMATION:  
; APPLICANT: Vitek, Michael P.  
; APPLICANT: Mitsuda, No. 6255473iaki  
; APPLICANT: Roses, Allen D.  
; TITLE OF INVENTION: Presenilin-1 Gene Promoter  
; FILE REFERENCE: VITEKPRESENTILIN  
; CURRENT APPLICATION NUMBER: US/08/920,422A  
; CURRENT FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-920-422-16

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 6 GGGCGG 1

RESULT 14  
US-09-593-323-29  
; Sequence 29, Application US/09593323  
; Patent No. 6265213  
; GENERAL INFORMATION:  
; APPLICANT: Morgan, Antony R.  
; APPLICANT: Severini, Alberto  
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity  
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of  
; TITLE OF INVENTION: Transcription  
; FILE REFERENCE: DNAB-02921  
; CURRENT APPLICATION NUMBER: US/09/593,323  
; CURRENT FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: 09/344,300  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-593-323-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
Db 1 GGGCGG 6

RESULT 15  
US-09-594-108-29  
; Sequence 29, Application US/09594108  
; Patent No. 6284468  
; GENERAL INFORMATION:  
; APPLICANT: Morgan, Antony R.  
; APPLICANT: Severini, Alberto  
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity  
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of  
; TITLE OF INVENTION: Transcription  
; FILE REFERENCE: DNAB-02921  
; CURRENT APPLICATION NUMBER: US/09/594,108

/ CURRENT FILING DATE: 2000-06-13  
/ PRIOR APPLICATION NUMBER: 09/344,300  
/ PRIOR FILING DATE: 1999-06-24  
/ NUMBER OF SEQ ID NOS: 72  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 29  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||  
Db 1 GGGCGG 6

## RESULT 16

US-09-344-300-29  
/ Sequence 29, Application US/09344300B  
/ Patent No. 6297013  
/ GENERAL INFORMATION:  
/ APPLICANT: Morgan, Antony R.  
/ APPLICANT: Severini, Alberto  
/ TITLE OF INVENTION: Compositions and Methods for Determining the Activity  
/ TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of  
/ TITLE OF INVENTION: Transcription  
/ FILE REFERENCE: DNAB-02921  
/ CURRENT APPLICATION NUMBER: US/09/344,300B  
/ CURRENT FILING DATE: 1999-06-24  
/ NUMBER OF SEQ ID NOS: 72  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 29  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-344-300-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||  
Db 1 GGGCGG 6

## RESULT 17

US-09-924-346-6  
/ Sequence 6, Application US/09924346  
/ Patent No. 6555674  
/ GENERAL INFORMATION:  
/ APPLICANT: Jens Tornoe  
/ TITLE OF INVENTION: The Jet Promoter  
/ FILE REFERENCE: 19313-005  
/ CURRENT APPLICATION NUMBER: US/09/924,346  
/ CURRENT FILING DATE: 2001-08-08  
/ PRIOR APPLICATION NUMBER: 60/224,087  
/ PRIOR FILING DATE: 2000-08-09  
/ NUMBER OF SEQ ID NOS: 8  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 6  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Chemically  
/ OTHER INFORMATION: Synthesized  
US-09-924-346-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||  
Db 1 GGGCGG 6

## RESULT 18

US-09-483-184A-6/c  
/ Sequence 6, Application US/09483184A  
/ Patent No. 6800750  
/ GENERAL INFORMATION:  
/ APPLICANT: DARTMOUTH COLLEGE  
/ APPLICANT: CRAIG, Ruth W.  
/ APPLICANT: BINGLE, Colin D.  
/ APPLICANT: WHYTE, Moira  
/ TITLE OF INVENTION: Mcl-1 GENE REGULATORY ELEMENTS AND A PRO-APOPTOTIC Mcl-1 VARIANT  
/ FILE REFERENCE: DART1110-1  
/ CURRENT APPLICATION NUMBER: US/09/483,184A  
/ CURRENT FILING DATE: 2000-01-14  
/ PRIOR APPLICATION NUMBER: US 60/166,113  
/ PRIOR FILING DATE: 1999-11-16  
/ NUMBER OF SEQ ID NOS: 31  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 6  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial sequence  
/ FEATURE:  
/ OTHER INFORMATION: oligonucleotide for PCR  
US-09-483-184A-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.6e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6  
|||  
Db 6 GGGCGG 1

## RESULT 19

PCT-US94-06456-9/c  
/ Sequence 9, Application PC/TUS9406456  
/ GENERAL INFORMATION:  
/ APPLICANT: Beutel, Bruce A.  
/ APPLICANT: Coppola, George R.  
/ APPLICANT: Sherman, Michael I.  
/ TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function  
/ NUMBER OF SEQUENCES: 60  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein  
/ STREET: 6 Becker Farm Road  
/ CITY: Roseland  
/ STATE: New Jersey  
/ COUNTRY: USA  
/ ZIP: 07068  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5 inch diskette  
/ COMPUTER: IBM PS/2  
/ OPERATING SYSTEM: PC - DOS  
/ SOFTWARE: DW4.V2  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US94/06456  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:



APPLICATION NUMBER: 08/073,873  
FILING DATE: 09-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliott M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 23550-89  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide  
PCT-US94-06456-9

Query Match 66.7%; Score 4; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6  
DB 4 GAGG 1

RESULT 20  
PCT-US94-06456-38/c  
Sequence 38, Application PC/TUS9406456  
GENERAL INFORMATION:  
APPLICANT: Beutel, Bruce A.  
APPLICANT: Coppola, George R.  
APPLICANT: Sherman, Michael I.  
TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC - DOS  
SOFTWARE: DW4.V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06456  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/073,873  
FILING DATE: 09-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliott M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 23550-89  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide  
PCT-US94-06456-38

Query Match 66.7%; Score 4; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.9e+08;

APPLICATION NUMBER: 08/247,809A-15  
Sequence 15, Application US/08247809A  
Patent No. 5569823  
GENERAL INFORMATION:  
APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;  
APPLICANT: Edgar Maiss  
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
STREET: 660 White Plains Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-5144  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
MEDIUM TYPE: storage  
COMPUTER: NEC Powermate 1 Plus  
OPERATING SYSTEM: DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/247,809A  
FILING DATE: May 23, 1994  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P 43 178 45.6 (Germany)  
FILING DATE: May 28, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurt G. Briscoe  
REGISTRATION NUMBER: 33,141  
REFERENCE/DOCKET NUMBER: Bayer 9049-KGB  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-247-809A-15

Query Match 66.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6  
DB 2 GAGG 5

RESULT 22  
US-08-381-097A-14  
Sequence 14, Application US/08381097A  
Patent No. 5643890  
GENERAL INFORMATION:  
APPLICANT: Iverson, Patrick L.  
APPLICANT: Mata, John E.  
TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides  
TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment  
TITLE OF INVENTION: of Cancer and Other Diseases  
NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease  
 ; STREET: 801 Grand Suite 3200  
 ; CITY: Des Moines  
 ; STATE: Iowa  
 ; COUNTRY: United States  
 ; ZIP: 50309  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/381,097A  
 ; FILING DATE: 31-JAN-1995  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Nebel, Heidi S  
 ; REGISTRATION NUMBER: 37,719  
 ; REFERENCE/DOCKET NUMBER: unmc 63092  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 515-288-3667  
 ; TELEFAX: 515-288-1338  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-08-381-097A-14

Query Match 66.7%; Score 4; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAGG 6  
 Db 2 GAGG 5

RESULT 23  
 US-08-597-948A-6/c  
 ; Sequence 6, Application US/08597948A  
 ; Patent No. 595322  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guarnieri, Frank  
 ; APPLICANT: Bancroft, Frank Carter  
 ; TITLE OF INVENTION: A DNA-BASED COMPUTER  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Baker & Botts  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: Fast SEQ VERSION 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/597,948A  
 ; FILING DATE: 7 February 1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION NUMBER:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kole, Lisa B.

; REGISTRATION NUMBER: 35,225  
 ; REFERENCE/DOCKET NUMBER: 30372 070165.0385  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-408-2500  
 ; TELEFAX: 212-765-2519  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; HYPOTHETICAL:  
 ; ANTI-SENSE:  
 ; FRAGMENT TYPE:  
 ; ORIGINAL SOURCE:  
 ; US-08-597-948A-6  
 ; Query Match 66.7%; Score 4; DB 2; Length 5;  
 ; Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
 ; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Qy 2 GGAG 5  
 ; Db 5 GGAG 2  
 ; RESULT 24  
 ; US-08-711-728-15  
 ; Sequence 15, Application US/08711728  
 ; Patent No. 5973135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;  
 ; APPLICANT: Edgar Maiss  
 ; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
 ; STREET: 660 White Plains Road  
 ; CITY: Tarrytown  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10591-5144  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: NEC Powermate 1 Plus  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/711,728  
 ; FILING DATE: 03-SEPT-1996  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/247,809  
 ; FILING DATE: 23-MAY-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE 43178456  
 ; FILING DATE: 28-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kurt G. Briescoe  
 ; REGISTRATION NUMBER: 33,141  
 ; REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (914) 332-1700  
 ; TELEFAX: (914) 332-1844  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-711-728-15

Query Match
Best Local Similarity 66.7%; Score 4; DB 2; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6
DB 2 GAGG 5

RESULT 25
US-08-873-709-8
; Sequence 8, Application US/08873709
; Patent No. 6037126
; GENERAL INFORMATION:
; APPLICANT: Grossman, Abraham
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
; TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
; TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abraham Grossman
; STREET: 666 Washington Avenue
; CITY: Pleasantville
; STATE: NY
; COUNTRY: USA
; ZIP: 10570
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,709
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: Q001/002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-747-9108
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-873-709-8

Query Match
Best Local Similarity 66.7%; Score 4; DB 3; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
DB 1 GGGA 4

RESULT 26
US-08-921-497-12/c
; Sequence 12, Application US/08921497
; Patent No. 6521225
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Arun
; APPLICANT: Ponnazhagan, Selvarangan
; APPLICANT: Chloemer, Robert H.
; APPLICANT: Wang, Xu-Shan
; APPLICANT: Yoder, Mervin C.
; APPLICANT: Zhou, Shang-Zhen
; APPLICANT: Escobedo, Jaime
; APPLICANT: Variavani, Dwaraki
; TITLE OF INVENTION: An AAV Vector Having Two Modified D-Sequences (As Amended)
; FILE REFERENCE: 1242.003
; CURRENT APPLICATION NUMBER: US 60/025,616
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US 60/025,649
; PRIOR FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: DNA
; ORGANISM: adenoassociated virus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: D-sequence in ITRs
; OTHER INFORMATION: Antisense strand
US-08-921-497-14

Query Match
Best Local Similarity 66.7%; Score 4; DB 4; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5
DB 2 GGAG 5

RESULT 27
US-08-921-497-14
; Sequence 14, Application US/08921497
; Patent No. 6521225
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Arun
; APPLICANT: Ponnazhagan, Selvarangan
; APPLICANT: Chloemer, Robert H.
; APPLICANT: Wang, Xu-Shan
; APPLICANT: Yoder, Mervin C.
; APPLICANT: Zhou, Shang-Zhen
; APPLICANT: Escobedo, Jaime
; APPLICANT: Variavani, Dwaraki
; TITLE OF INVENTION: An AAV Vector Having Two Modified D-Sequences (As Amended)
; FILE REFERENCE: 1242.003
; CURRENT APPLICATION NUMBER: US/08/921,497
; CURRENT FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 60/025,616
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US 60/025,649
; PRIOR FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: DNA
; ORGANISM: adenoassociated virus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: D-sequence in ITRs
; OTHER INFORMATION: Antisense strand
US-08-921-497-14

Query Match
Best Local Similarity 66.7%; Score 4; DB 4; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5
DB 2 GGAG 5
```

RESULT 28  
PCT-US93-03027-7  
; Sequence 7, Application PC/TUS9303027  
; GENERAL INFORMATION:  
; APPLICANT: LEONARD, WARREN; TOLEDANO,  
; APPLICANT: MICHEL  
; TITLE OF INVENTION: CONTROL AND/OR  
; PREVENTION OF BINDING OF NF- B/REL/DORSAL  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/03027  
; FILING DATE: 19930401  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/862,987  
; FILING DATE: 06-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOROTHY R. AUTH  
; REGISTRATION NUMBER: P-36,434  
; REFERENCE/DOCKET NUMBER: 2026-4010 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: oligonucleotide  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: "A" half of Ig- B binding  
; NAME/KEY: site  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
PCT-US93-03027-7  
Query Match 66.7%; Score 4; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.1e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGA 4  
DB 1 GGGA 4  
RESULT 29  
US-08-242-402-20/c  
; Sequence 20, Application US/08242402  
; Patent No. 5580967  
; GENERAL INFORMATION:  
; APPLICANT: JOYCE, GERALD F  
; TITLE OF INVENTION: OPTIMIZED CATALYTIC DNA-CLEAVING  
; TITLE OF INVENTION: RIBOZYMES  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE, OFFICE OF  
; ADDRESSEE: PATENT COUNSEL  
; STREET: 10666 NORTH TORREY PINES ROAD, TPC 8

; CITY: LA JOLLA  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/242,402  
; FILING DATE: 13-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LOGAN, APRIL C  
; REGISTRATION NUMBER: 33,950  
; REFERENCE/DOCKET NUMBER: TSRI 412.0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-242-402-20  
Query Match 66.7%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GAGG 6  
DB 5 GAGG 2  
RESULT 30  
US-08-270-180-19/c  
; Sequence 19, Application US/08270180  
; Patent No. 5595873  
; GENERAL INFORMATION:  
; APPLICANT: JOYCE, Gerald F.  
; TITLE OF INVENTION: ENZYMIC RNA MOLECULES THAT CLEAVE  
; TITLE OF INVENTION: AMIDE BONDS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5595873th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/270,180  
; FILING DATE: 01-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/242,402  
; FILING DATE: 13-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Logan, April C.  
; REGISTRATION NUMBER: 33,950  
; REFERENCE/DOCKET NUMBER: TSRI 412.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937

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; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6
; OTHER INFORMATION: /label= N
; OTHER INFORMATION: /note= "N SIGNIFIES A NUCLEOTIDE ANALOG"
;
US-08-270-180-19

Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAGG 6
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Db 5 GAGG 2
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Search completed: July 21, 2005, 04:29:26  
Job time : 58 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds  
(without alignments)  
169.325 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| C 2        | 4     | 66.7        | 4      | 7     | CK582549    |
| C 3        | 4     | 66.7        | 5      | 7     | CF327578    |
| C 4        | 4     | 66.7        | 6      | 7     | CF314367    |
| C 5        | 4     | 66.7        | 6      | 7     | CF338772    |
| C 6        | 3.4   | 56.7        | 5      | 7     | CF327761    |
| C 7        | 3.4   | 56.7        | 5      | 7     | CF920850    |
| C 8        | 3.4   | 56.7        | 5      | 9     | CL658581    |
| C 9        | 3.4   | 56.7        | 6      | 7     | CF312755    |
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| C 12       | 3     | 50.0        | 3      | 7     | CF300120    |
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| C 14       | 3     | 50.0        | 3      | 7     | CF315183    |
| C 15       | 3     | 50.0        | 3      | 7     | CF339761    |
| C 16       | 3     | 50.0        | 3      | 7     | CO790264    |
| C 17       | 3     | 50.0        | 3      | 9     | CL674562    |
| C 18       | 3     | 50.0        | 3      | 9     | CL679821    |
| C 19       | 3     | 50.0        | 4      | 1     | AL045617    |
| C 20       | 3     | 50.0        | 4      | 6     | CA853244    |
| C 21       | 3     | 50.0        | 4      | 6     | CA853352    |
| C 22       | 3     | 50.0        | 4      | 7     | CF300913    |
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| AL042484 | DXFZp434F | 6 | 1 | AL042833 |
| AL042833 | DXFZp434G | 6 | 1 | CA850792 |
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| CA850861 | D07D05_G1 | 6 | 6 | CF302557 |
| CF302557 | 7LEAF--08 | 6 | 7 | CF310635 |
| CF310635 | ABF--05-G | 6 | 7 | CF322957 |
| CF322957 | JMT--01-K | 6 | 7 | CF920971 |
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| CF317391 | HD--07-B0 | 4 | 7 | CL655267 |
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| CF280384 | 14ETL--07 | 2 | 7 | CF280511 |
| CF280511 | 14ETL--07 | 2 | 7 | CF291112 |
| CF291112 | 14ROOF--0 | 2 | 7 | CF299820 |
| CF299820 | 7LEAF--03 | 2 | 7 | CF307123 |
| CF307123 | H0A1--05- | 2 | 7 | CF307878 |
| CF307878 | ABF--01-H | 2 | 7 | CF311389 |
| CF311389 | ABF--06-J | 2 | 7 | CF311851 |
| CF311851 | ABF--07-E | 2 | 7 | CF315237 |
| CF315237 | HD--04-B0 | 2 | 7 | CF329006 |
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| CL688912 | PR1014d_C | 2 | 9 | CL690186 |
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| CL694963 | PR10165C  | 2 | 9 |          |

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c 100 2 33.3 3 6 CA850938 CA850938

## ALIGNMENTS

RESULT 1  
LOCUS CL664862  
DEFINITION PRI0148a H04 - PRI0148a.B21 (5) Mixed stage fosmid library of *P. pacificus* var. California *Pristionchus pacificus* genomic, genomic survey sequence.  
ACCESSION CL664862  
VERSION CL664862.1 GI:50155779  
KEYWORDS GSS.  
SOURCE *Pristionchus pacificus*  
ORGANISM *Pristionchus pacificus*  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; *Pristionchus*.  
REFERENCE 1 (bases 1 to 5)  
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
TITLE AppADB: an AcedB database for the nematode satellite organism *Pristionchus pacificus*  
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: raif.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES  
source

1..5 Location/Qualifiers  
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## ORIGIN

Query Match 83.3%; Score 5; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.6e+09; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6  
|||||  
Db 1 GGAGG 5

RESULT 2  
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LOCUS CK582549  
DEFINITION IST W15 41282 AD-wrmcDNA library *Caenorhabditis elegans* cDNA 5' similar to K07A12.3, mRNA sequence.  
ACCESSION CK582549  
VERSION CK582549.1 GI:40966478  
KEYWORDS EST.  
SOURCE *Caenorhabditis elegans*

ORGANISM *Caenorhabditis elegans*  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabdicoidea; Rhabditidae; Pelodierinae; *Caenorhabditis*.

REFERENCE 1 (bases 1 to 4)  
AUTHORS Li,S., Armstrong,C.M., Bertin,N., Ge,H., Milstein,S., Boxem,M., Vidalain,P.O., Han,J.D., Chesneau,A., Hao,T., Goldberg,D.S., Li,N., Martinez,M., Rual,J.F., Lamesch,P., Xu,L., Tewari,M., Wong,S.L.,

TITLE  
JOURNAL  
COMMENT

A Map of the Interactome Network of the Metazoan *C. elegans*  
Science (2004) In press  
Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu

For the purpose of protein interaction mapping, we generated a *C. elegans* cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. cDNAs were generated and cloned into the two hybrid vector pPC86 This interacting Sequence Tag IST\_W15\_41282 (K07A12.3) interacts as a prey with the bait E02H1.7

## PCR Primers

FORWARD: CGCGTTGGAACTCACTACAGG  
BACKWARD: GGAGCTTGACCAACCTCTGGCG  
Insert Length: 4 Std Error: 3.00  
Plate: 540 row: 07 column: A  
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POLYA=No.

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Location/Qualifiers

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/note="Vector: pPC86; For the purpose of protein interaction mapping, we generated a *C. elegans* cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. This library was made with poly(A)+ RNA isolated from mated populations of wild-type (N2 strain) animals of all stages of development including embryonic, larval (L1 to L4 stages), adults and dauer. Approximately equal quantities of RNA from different populations were acquired. cDNAs were generated and cloned into the two hybrid vector pPC86. The library contains ~3\*10e7 clones. Reference - GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFomes - Walhout AJ, Temple GF, Brasch MA, Hartley JL, Iorson MA, van den Heuvel S, Vidal M - Methods Enzymol. 2000;328:575-92"

## ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.5e+09; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5  
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Db 4 GGAG 1

## RESULT 3

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LOCUS CF327578  
DEFINITION NACL-02-B23.b1 Rice callus plasmid cDNA library (NACL) *Oryza sativa* (japonica cultivar-group) cDNA clone NACL-02-B23, mRNA sequence.  
ACCESSION CF327578



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VERSION CF327578.1 GI:33803408
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 /cultivar="Nackdong"
 /db_xref="taxon:39947"
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 RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5
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Db 5 GGAG 2

RESULT 4
CF314367
LOCUS HD--02-N20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--02-N20, mRNA sequence.
ACCESSION CF314367
VERSION CF314367.1 GI:33686128
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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ORIGIN
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DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--02-L14,
 mRNA sequence.
ACCESSION CF338772
VERSION CF338772.1 GI:33825924
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 /clone_lib="Regenerated callus lambda phage cDNA library
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 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 66.7%; Score 4; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db ||||
 6 GGAG 3

RESULT 6
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LOCUS CF327761
DEFINITION
NACL--02-G02.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--02-G02, mRNA
sequence.
ACCESSION
CF327761
VERSION CF327761.1 GI:33803773
KEYWORDS
SOURCE EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

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Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAG 5
Db ||||
 5 GGCG 1

RESULT 7
CF920850/c
LOCUS CF920850
DEFINITION
gmrhRw3-02 E07_1 055 Soybean root hair subtracted cDNA library
gmrhRw3 Glycine max cDNA, mRNA sequence.
ACCESSION
CF920850
VERSION CF920850.1 GI:38191644
KEYWORDS
SOURCE EST.
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 5)
AUTHORS Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

Expressed sequence tags from soybean root hair subtractive cDNA
library
Unpublished (2003)
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7.

FEATURES source
 source
 1..5
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /tissue_type="root hairs"
 /clone_lib="Soybean root hair subtracted cDNA library
 gmrhRw3"
 /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
 generated from soybean root hair tissue treated with
 Bradyrhizobium japonicum for 3 hours."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAG 5
Db ||||
 5 GGCG 1

RESULT 8
CL658581
LOCUS CL658581
DEFINITION
PRI0131d_E08 - PRI0131d.B21 (5) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
CL658581
VERSION CL658581.1 GI:50141602
KEYWORDS
SOURCE GSS.
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 5)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL Contact: Sommer RJ
COMMENT Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: raif.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES source
 source
 1..5
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strains="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

```



```

DEFINITION HD--03-N24_g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--03-N24, mRNA sequence.

ACCESSION CF315089.1 GI:33686850
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahmeggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
 ..3
 /location=Oryza sativa (japonica cultivar-group) "
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39347"
 /clone="HD--03-N24"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /notes="Vector: pCR4-TOPO; Site1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGG 3
 |||
Db 1 GGG 3

RESULT 14
CF315183
LOCUS
DEFINITION HD--04-A04_b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-A04, mRNA sequence.

ACCESSION CF315183 GI:33686944
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .3  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HD-04-A04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN  
Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4  
|||  
Db 1 GGA 3

RESULT 15  
CF339761  
LOCUS  
DEFINITION  
RCL1--05-N20.g1 Regenerated callus lambda phage cDNA library (RCL1)  
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-N20,  
mRNA sequence.  
CF339761  
VERSION  
CF339761.1 GI:33827892  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 3)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .3  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="RCL1-05-N20"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .3  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HD-04-A04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN  
Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4  
|||  
Db 1 GGA 3

RESULT 15  
CF339761  
LOCUS  
DEFINITION  
RCL1--05-N20.g1 Regenerated callus lambda phage cDNA library (RCL1)  
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-N20,  
mRNA sequence.  
CF339761  
VERSION  
CF339761.1 GI:33827892  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 3)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .3  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="RCL1-05-N20"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN  
Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3  
|||  
Db 1 GGG 3

RESULT 16  
CO790264  
LOCUS  
DEFINITION  
NT009A.H05 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5',  
similar to hypothetical protein, mRNA sequence.  
CO790264  
ACCESSION  
CO790264.1 GI:51006235  
VERSION  
CO790264.1  
KEYWORDS  
EST.  
SOURCE  
Ambystoma mexicanum (axolotl)  
ORGANISM  
Ambystoma mexicanum  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;  
Ambystoma.  
1 (bases 1 to 3)  
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,  
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.  
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352  
expressed sequence tags from embryonic and regenerating blastema  
cDNA libraries  
Genome Biol. (2004) In press  
Contact: Ely M. Tanaka  
Tanaka Lab  
Max Planck Institute of Molecular Cell Biology and Genetics,  
Dresden  
Protenhauerstrasse 108, 01307 Dresden, Germany  
Tel: 0049 351 210 2620  
Fax: 0049 351 210 1489  
Email: tanaka@mpi-cbg.de  
Plate: NT009A row: 05 column: H  
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.  
Location/Qualifiers  
1. .3  
/organism="Ambystoma mexicanum"  
/mol\_type="mRNA"  
/db\_xref="taxon:8296"  
/tissue\_type="Neural Tube, Notochord, Somites"  
/cell\_type="Includes Neural tube, notochord, somites"  
/dev\_stage="Stage 18-22"  
/clone\_lib="St18-22 Neural tube (NT)"  
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;  
Unnormalized cDNA plasmid library prepared by Invitrogen.  
Size fractionated mRNA was polydri primed and cloned into  
NotI-SalI site of pCMVSPORT6. Bacterial host is  
EMDH103-TONA. Average insert size is 1.5 KB.  
TAG\_LTB=NT"

ORIGIN  
Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6  
|||  
Db 1 AGG 3

RESULT 17  
CL674562/c  
LOCUS  
DEFINITION  
PRI0112c\_A06\_2 - PRI0112c.BR (3) Mixed stage foemid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL674562  
VERSION CL674562.1 GI:50177804

GSS.

Pristionchus pacificus

Pristionchus pacificus

EuKaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 3)

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..3

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 50.0%; Score 3; DB 9; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4

Db |||

3 GGA 1

RESULT 18

CL679821/c

LOCUS

DEFINITION

Pristionchus pacificus

EuKaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 3)

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..3

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 19

AL045617/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..4

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp4340245"

/tissue\_type="testis"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 20

CA853244

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..4

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp4340245"

/tissue\_type="testis"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 20

CA853244

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Class: fosmid ends.

Location/Qualifiers

1..3

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 20

CA853244

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..4

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp4340245"

/tissue\_type="testis"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 20

CA853244

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..4

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp4340245"

/tissue\_type="testis"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 20

CA853244

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 4)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

#### FEATURES

1..4

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Peking"

/db\_xref="taxon:3847"

/clone="B06A04"

/tissue\_type="Roots"

/dev\_stage="Seedlings"

/clone\_lib="cDNA Peking library 12hr SCN3"

/notes="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

#### ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

|||

Db 1 GGG 3

#### RESULT 21

CA853352/c

LOCUS

DEFINITION B07C08.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone

B07C08 5', mRNA sequence.

CA853352

VERSION 1 GI:33390145

KEYWORDS

SOURCE

Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 4)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

#### FEATURES

1..4

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Peking"

/db\_xref="taxon:3847"

/clone="B07C08"

/tissue\_type="Roots"

/dev\_stage="Seedlings"

/clone\_lib="cDNA Peking library 12hr SCN3"

/notes="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

#### ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

|||

Db 4 GGG 2

#### RESULT 22

CF300913/c

LOCUS

DEFINITION

7LEAF--05-J02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J02, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..4

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--05-J02"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

#### ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

|||

Db 3 GGG 1

#### RESULT 23

```

CF307853/c
LOCUS CF307853 4 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-G24.b1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CF307853
VERSION HD--01-G24, mRNA sequence.
KEYWORDS ABF--01-G24, mRNA sequence.
SOURCE CF307853.1 GI:33679614
 EST.
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 4)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES 1..4
 Location/Qualifiers
 1..4
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--01-G24"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."
ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
 |||
Db 3 AGG 1

RESULT 24
CF317789/c
LOCUS CF317789 4 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J18.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CF317789
VERSION HD--07-J18, mRNA sequence.
KEYWORDS HD--07-J18, mRNA sequence.
SOURCE CF317789.1 GI:33689550
 EST.
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 4)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
FEATURES 1..4
 Location/Qualifiers
 1..4
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--01-G24"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."
ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
 |||
Db 3 AGG 1

RESULT 24
CF317789/c
LOCUS CF317789 4 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J18.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CF317789
VERSION HD--07-J18, mRNA sequence.
KEYWORDS HD--07-J18, mRNA sequence.
SOURCE CF317789.1 GI:33689550
 EST.
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 4)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
FEATURES 1..4
 Location/Qualifiers
 1..4
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--01-P22"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES 1..4
 Location/Qualifiers
 1..4
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--07-J18"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."
ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
 |||
Db 3 GGA 1

RESULT 25
CF338536
LOCUS CF338536 4 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--01-P22.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P22,
 mRNA sequence.
ACCESSION CF338536
VERSION CF338536.1 GI:33825460
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 4)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL of Bioscience and Bioinformatics, Myongji University
COMMENT Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES 1..4
 Location/Qualifiers
 1..4
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--01-P22"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:

```



XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

## ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.5e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4  
|||  
Db 2 GGA 4

## RESULT 26

CN755098/c

## LOCUS

DEFINITION CN755098 4 bp mRNA linear EST 19-MAY-2004  
ID0AA14DE08R1 ApMS Acyrthosiphon pisum cDNA clone ID0AA14DE08

5', mRNA sequence.

## ACCESSION

VERSION CN755098

## KEYWORDS

SOURCE EST.

## ORGANISM

Acyrthosiphon pisum (pea aphid)  
Acyrthosiphon pisum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

## REFERENCE

1 (bases 1 to 4)

## AUTHORS

Hunter, W., Martinez-Torres, D., Rabbe, Y., Sabater-Munoz, B.,  
Stern, D., Tagu, D. and Winkler, P.

## TITLE

An expressed sequence tags database for the pea aphid Acyrthosiphon

## JOURNAL

COMMENT

## UNPUBLISHED (2004)

Contact: D. Tagu

## INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts. These sequences were

obtained in the frame of the International Consortium of Aphid

Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 14 row: E column: 8.

Location/Qualifiers

1. .4

/organism="Acyrthosiphon pisum"

/mol\_type="mRNA"

/cultivar="developmentstage"

/db\_xref="taxon:7029"

/clone="ID0AA14DE08"

/tissue\_type="whole insect"

/dev\_stage="nymphs and adults (parthenogenetic females)"

/lab\_host="XLI-Blue"

/clone\_lib="ApMs"

/notes="Vector: PBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA; Plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University;

Soil conditions: Soil; Sowing date: 01/06/1999;

Harvesting date: 01/06/1999; Stress date: no stress;

Description: Aphids inoculated on one-week old *Vicia faba*

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

## ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 7; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

## RESULT 27

CL651736/c

## LOCUS

DEFINITION

CL651736

4 bp DNA linear GSS 09-JUL-2004

PR10112d H07 - PR10112d.B21 (4) Note: Recurring String Mixed stage

fosmid library of *P. pacificus* var. California Pristionchus

*pacificus* genomic, genomic survey sequence.

ACCESSION CL651736

VERSION CL651736.1

GI:50130363

GSS.

Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 4)

Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1. .4

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of *P. pacificus*

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

## ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 9; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

## RESULT 28

CK584110/c

## LOCUS

DEFINITION

CK584110

5 bp mRNA linear EST 16-JAN-2004

1ST W15.1687 AD-ORFeome1.0 library Caenorhabditis elegans cDNA 5'

similar to F44G3.9, mRNA sequence.

ACCESSION CK584110

VERSION CK584110.1

GI:40968039

EST.

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditioidea; Rhabditidae; Feloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 5)

Li, S., Armstrong, C.M., Bertin, N., Ge, H., Milstein, S., Boxem, M.,

Vidalain, P.O., Han, J.D., Chesneau, A., Hao, T., Goldberg, D.S., Li, N.,

Martinez, M., Rual, J.F., Lamesch, P., Xu, L., Tewari, M., Wong, S.L.,

Zhang, L.V., Beriz, G.F., Jacotot, L., Vaglio, P., Reboul, J.,

Hirozane-Kishikawa, T., Li, Q., Gabel, H.W., Elewa, A., Baumgartner, B.,

Rose, D.J., Yu, H., Bosak, S., Sequerra, R., Fraser, A., Mango, S.E.,

Saxton, W.M., Strome, S., Van Den Heuvel, S., Piano, F., Vandenhaute, J., Sardet, C., Gerstein, M., Doucette-Stamm, L., Gunsalus, K.C., Harper, J.W., Cusick, M.E., Roth, F.P., Hill, D.E. and Vidal, M.

A Map of the Interactome Network of the Metazoan C. elegans Science (2004) In press

Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu

For the purpose of protein interaction mapping, we generated a C. elegans a normalized library of ORF fused to the AD-encoding sequence of the yeast transcription factor GAL4. Those ORFs derive from the PCR amplification between the predicted (WS9) initiation and termination codons, using the cDNA library AD-wrmcDNA as template. This Interacting Sequence Tag IST\_W15\_1687 (F44G3.9) interacts as a prey with the bait F37B1.8

PCR Primers  
FORWARD: CGCGTTTGGAATCACTACAGGG  
BACKWARD: GGAGACTTGACCAACTCTGGCG  
Insert Length: 5 Std Error: 4.00  
Plate: 22 row: 02 column: G  
Seq primer: CGCGTTTGGAATCACTACAGGG  
High quality sequence stop: 4  
POLYA=No.

Location/Qualifiers  
1. 5  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/sex="male, hermaphrodite"  
/dev\_stage="embryos, L1, L2, L3, L4, adult, dauer"  
/clone\_lib="AD-ORFeome1.0 library"  
/note="Vector: pDestPC86/CyB; For the purpose of protein interaction mapping, predicted protein-encoding ORFs were amplified by PCR precisely between the predicted (WS9 version of WormPeP) initiation and termination codons, using a cDNA library (AD-wrmcDNA library - Walhout et al. Methods Enzymol. 2000;328:575-92) as template. The resulting 11,984 Gateway cloned ORFs along with the attempted ones were transferred into a two-hybrid destination vector downstream of the vector sequence encoding the activation domain (AD) of the yeast GAL4 transcription factor. Those constructs were pooled together to constitute a 'normalized' AD-ORFeome1.1 library. Reference - Reboul J, Vaglio P et al. C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. Nat Genet. 2003 May;34(1):35-41. PMID: 12679813"

ORIGIN  
Query Match 50.0%; Score 3; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6  
|||  
DB 5 AGG 3

RESULT 29  
CL423849/c  
LOCUS  
DEFINITION  
CL423849  
VERSION  
KEYWORDS  
GSS.

CL423849 5 bp DNA linear GSS 16-MAR-2004  
01S0750-04Cl-Al2 UniformMu MUTAIL Library Zea mays genomic clone  
01S0750-04Cl-Al2, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
GSS.

CL423849.1 GI:45501893

Ze mays  
Ze mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 5)  
Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.  
Sequence tagged transposon insertions from the UniformMu maize population  
Unpublished (2003)  
Contact: Donald R. McCarty  
Plant Molecular and Cellular Biology Program  
University of Florida  
PO 110690 Gainesville, FL 32611-0690, USA  
Tel: 352-392-1928 x322  
Email: drmc@ufl.edu  
Sequence Sequence flanking probable Mu insertion site in UniformMu line: 01S0750-04, Primer set: C  
Class: transposon insertion site.  
Location/Qualifiers  
1. 5  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="W22 (ACR, bz1-m9)"  
/cultivar="UniformMu"  
/db\_xref="taxon:4577"  
/clone="01S0750-04Cl-Al2"  
/clone\_lib="UniformMu MUTAIL Library"  
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN  
Query Match 50.0%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAG 5  
|||  
DB 5 GAG 3

RESULT 30  
CL661701/c  
LOCUS  
DEFINITION  
CL661701  
VERSION  
KEYWORDS  
GSS.

CL661701 5 bp DNA linear GSS 09-JUL-2004  
PRI013c.C05 - PRI013c.B21 (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
CL661701 GI:50148524  
CL661701.1 GI:50148524  
GSS.  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 5)  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: raif.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

ORIGIN  
Query Match 50.0%; Score 3; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.6e+09;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6  
|||  
DB 5 AGG 3

RESULT 29  
CL423849/c  
LOCUS  
DEFINITION  
CL423849  
VERSION  
KEYWORDS  
GSS.

CL423849 5 bp DNA linear GSS 16-MAR-2004  
01S0750-04Cl-Al2 UniformMu MUTAIL Library Zea mays genomic clone  
01S0750-04Cl-Al2, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
GSS.

CL423849.1 GI:45501893

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Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .5
/organism="Pristionchus pacificus"
/mol type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
 |||
Db 3 GGA 1

Search completed: July 21, 2005, 01:54:38
Job time : 1349.8 secs
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**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds  
(without alignments)  
189.533 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 999agg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description        |
|------------|-------|---------------|--------|----|--------------------|
| 1          | 5     | 83.3          | 6      | 2  | AAQ61541 TDT promo |
| 2          | 5     | 83.3          | 6      | 2  | AAV45399 TDT promo |
| 3          | 5     | 83.3          | 6      | 3  | AAAG2709 PNA clamp |
| 4          | 5     | 83.3          | 6      | 12 | ADJ35621 Stabilisi |
| 5          | 4.4   | 73.3          | 6      | 2  | AAT04935 Anti-HIV  |
| 6          | 4.4   | 73.3          | 6      | 6  | ABK87320 Mammalian |
| 7          | 4.4   | 73.3          | 6      | 6  | ABK87320 Mammalian |
| 8          | 4.4   | 73.3          | 6      | 9  | ACD99345 Immunosti |
| 9          | 4.4   | 73.3          | 6      | 12 | ADJ35665 Stabilisi |
| 10         | 4.4   | 73.3          | 6      | 13 | ADR32691 Human nic |
| 11         | 4     | 66.7          | 5      | 1  | AAH56407 Escherich |
| 12         | 4     | 66.7          | 5      | 4  | AAH56407 Escherich |
| 13         | 4     | 66.7          | 5      | 12 | ADP90315 NEO ribos |
| 14         | 4     | 66.7          | 5      | 12 | ADJ61783 NEO ribos |
| 15         | 4     | 66.7          | 6      | 2  | AAQ38797 PCR prime |
| 16         | 4     | 66.7          | 6      | 2  | AAV61657 Fusarium  |
| 17         | 4     | 66.7          | 6      | 3  | AAZ89322 Human UCP |
| 18         | 4     | 66.7          | 6      | 4  | AAZ89322 Human UCP |
| 19         | 4     | 66.7          | 6      | 8  | AAZ89322 Human UCP |
| 20         | 4     | 66.7          | 6      | 10 | AAZ89322 Human UCP |

|    |   |      |   |    |                    |
|----|---|------|---|----|--------------------|
| 21 | 4 | 66.7 | 6 | 10 | ADJ35808           |
| 22 | 4 | 66.7 | 6 | 10 | ADJ35808           |
| 23 | 4 | 66.7 | 6 | 12 | ADJ35691 Stabilisi |
| 24 | 4 | 66.7 | 6 | 12 | ADJ35735           |
| 25 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 26 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 27 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 28 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 29 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 30 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 31 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 32 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 33 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 34 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 35 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 36 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 37 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 38 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 39 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 40 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 41 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 42 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 43 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 44 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 45 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 46 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 47 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 48 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 49 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 50 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 51 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 52 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 53 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 54 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 55 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 56 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 57 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 58 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 59 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 60 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 61 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 62 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 63 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 64 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 65 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 66 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 67 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 68 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 69 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 70 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 71 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 72 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 73 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 74 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 75 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 76 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 77 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 78 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 79 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 80 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 81 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 82 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 83 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 84 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 85 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 86 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 87 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 88 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 89 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 90 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 91 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 92 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |
| 93 | 4 | 66.7 | 6 | 12 | ADJ35654 Stabilisi |

c 94 3 50.0 6 2 AAQ85606 Aaq85606 T-DNA Vir  
 c 95 3 50.0 6 2 AAQ86731 Aaq86731 Mung bean  
 c 96 3 50.0 6 2 AAQ86731 Aaq86731 Mung bean  
 c 97 3 50.0 6 2 AAQ86737 Aaq86737 Mung bean  
 c 98 3 50.0 6 2 AAQ86737 Aaq86737 Mung bean  
 c 99 3 50.0 6 2 AAQ86741 Aaq86741 Mung bean  
 c 100 3 50.0 6 2 AAQ86741 Aaq86741 Mung bean

## ALIGNMENTS

RESULT 1  
 AAQ61541  
 ID AAQ61541 standard; cDNA; 6 BP.  
 XX  
 AC AAQ61541;  
 XX 25-MAR-2003 (revised)  
 DT 10-MAR-2003 (revised)  
 DT 21-OCT-1994 (first entry)  
 XX  
 DE TDT promoter/LYF sequence comprising Ikaros binding site.  
 XX  
 KW Ikaros; zinc finger; protein; immune disorder; therapy; treatment;  
 KW corpus striatum; regulatory gene; enhancer; regulatory element;  
 KW gene expression; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9406814-A1.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 14-SEP-1993; 93WO-US008743.  
 XX  
 PR 14-SEP-1992; 92US-00946233.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Georgopoulos K;  
 XX  
 DR WPI; 1994-118387/14.  
 XX  
 PT I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc  
 PT finger proteins, useful for treating immune system disorders.  
 XX  
 PS Disclosure; Page 28; 112pp; English.  
 XX  
 CC The Ikaros gene encodes a zinc finger protein which can be used in a  
 CC therapeutic composition to treat animals with an immune system disorder.  
 CC It may also be used for assessing whether a subject is at risk for an  
 CC immune disorder. It is of particular use in treating a disorder of the  
 CC corpus striatum. Heterologous genes may be expressed by placing them  
 CC under the control of an Ikaros responsive control element and contacting  
 CC the element with an Ikaros protein. Potential high affinity binding sites  
 CC for the Ikaros proteins were found in the enhancer and promoter regions  
 CC of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma  
 CC genes, the SL3 and HIV long terminal repeat and in the regulatory domains  
 CC of other T cell restricted antigens. Related sequences to the Ikaros  
 CC motif were also found in the purine boxes of the IL2 gene in the  
 CC LYF site of the TDT promoter as well as in the NFkB variant sites of the  
 CC HIV long terminal repeat. See also AAQ61504-Q61543. (Updated on 10-MAR-  
 CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 83.3%; Score 5; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5

RESULT 3  
 AAA62709/c  
 ID AAA62709 standard; DNA; 6 BP.  
 XX

Db 2 GGGAG 6  
 RESULT 2  
 AAV45399  
 ID AAV45399 standard; DNA; 6 BP.  
 XX  
 AC AAV45399;  
 XX 11-JAN-1999 (first entry)  
 DT  
 DE TDT promoter/LYF binding site for Ikaros.  
 XX  
 KW Ikaros; mIK; transcription factor; mouse; lymphocyte;  
 KW cell differentiation; T cell; cancer; immunodeficiency;  
 KW Alzheimer's disease; therapy; diagnosis; TDT; promoter; LYF; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2194256-A.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 02-JAN-1997; 97CA-02194256.  
 XX  
 PR 05-SEP-1996; 96US-00711417.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Georgopoulos K;  
 XX  
 DR WPI; 1998-378292/33.  
 XX  
 PT New nucleic acid encoding Ikaros protein involved in early  
 PT differentiation of lymphocytes - existing in several isoforms, and  
 PT related products, used to treat e.g. immune diseases or cancer and to  
 PT control cell differentiation.  
 XX  
 PS Disclosure; Page 38; 158pp; English.  
 XX  
 CC This oligonucleotide from the TDT pomoter/LYF site was identified as a  
 CC potential high affinity binding site for Ikaros proteins (see AAW70963-  
 CC 71). It partially includes the core motif GGGAA found in consensus  
 CC recognition sequences for murine Ikaros protein isoforms mIk-1, mIk-2 and  
 CC mIk-3 (see AAV52830-32). High affinity binding sites for Ikaros have been  
 CC found in enhancer and promoter regions of the regulatory domains of the  
 CC TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal repeat  
 CC and in the regulatory domains of other T cell restricted antigens (see  
 CC AAV45358-402) by gel retardation assay. Ikaros is involved in early  
 CC differentiation of lymphocytes. The invention provides Ikaros nucleic  
 CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host  
 CC cells. These are used to treat T and B cell diseases, to control  
 CC expression of heterologous genes placed under control of an Ikaros-  
 CC responsive element, to treat nervous system diseases and to modulate cell  
 CC division, amplification or differentiation, especially in haematopoietic  
 CC cells  
 XX  
 SQ Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 83.3%; Score 5; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db 2 GGGAG 6  
 RESULT 3  
 AAA62709/c  
 ID AAA62709 standard; DNA; 6 BP.  
 XX







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Db |||||
 1 GGGCGG 6

RESULT 8
ACD99345/c
ID ACD99345 standard; DNA; 6 BP.
XX
AC ACD99345;
XX
XX 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #31.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
XX US2003050268-A1.
XX
PN 13-MAR-2003.
XX
PD
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 9; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 73.3%; Score 4.4; DB 9; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGG 6
Db |||||
 6 GGGCGG 1

RESULT 10
ADR32691/c
ID ADR32691 standard; DNA; 6 BP.
XX
XX ADR32691;
XX
AC ADR32691;
XX
DT 04-NOV-2004 (first entry);
XX
XX Human nicking agent target DNA #232.
DE
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
XX
XX WO2004067765-A2.
XX
PN 12-AUG-2004.
PD
XX
XX 29-JAN-2004; 2004WO-US0002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
KW

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---

```

Db |||||
 1 GGGCGG 6

RESULT 8
ACD99345/c
ID ACD99345 standard; DNA; 6 BP.
XX
AC ACD99345;
XX
XX 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #31.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
XX US2003050268-A1.
XX
PN 13-MAR-2003.
XX
PD
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 9; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 73.3%; Score 4.4; DB 9; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGG 6
Db |||||
 6 GGGCGG 1

RESULT 9
ADJ35665/c
ID ADJ35665 standard; DNA; 6 BP.
XX
AC ADJ35665;
XX
XX 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #331.
XX
KW STAR affiliated proteinaceous molecule; post translational modification;

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KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX
OS Unidentified.
XX
PN WO2003106674-A2.
XX
PD 24-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-NL000410.
XX
PR 14-JUN-2002; 2002EP-00077344.
XX
PA (CHRO-) CHROMAGENICS BV.
XX
PI Otte AP, Kruckeberg AL, Satiijn DPE;
XX
DR WPI; 2004-082195/08.
XX
PT Producing proteinaceous molecules in cells by selecting a cell, providing
PT a nucleic acid encoding a proteinaceous molecule with an Stabilising Anti
PT -Repression sequence and expressing proteinaceous molecule.
XX
XX Disclosure; Page 101; 177pp; English.
XX
XX The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
CC comprising a Stabilising Anti-repression (STAR) sequence, expressing the
CC resulting nucleic acid in the cell and collecting (I). The method is
CC useful for producing (I). A cell line (II) provided with a nucleic acid
CC comprising a STAR sequence is useful for producing (I). (II) Enables
CC production of affiliated proteinaceous molecule, as cell carries out
CC proper post-translational modifications of produced proteins. The present
CC sequence represents a stabilising anti-repression, STAR, element primer
CC dyad sequence.
XX
SQ Sequence 6 BP; 0 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 73.3%; Score 4.4; DB 12; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGG 6
Db |||||
 6 GGGCGG 1

RESULT 10
ADR32691/c
ID ADR32691 standard; DNA; 6 BP.
XX
XX ADR32691;
XX
AC ADR32691;
XX
DT 04-NOV-2004 (first entry);
XX
XX Human nicking agent target DNA #232.
DE
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
XX
XX WO2004067765-A2.
XX
PN 12-AUG-2004.
PD
XX
XX 29-JAN-2004; 2004WO-US0002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
KW

```

PI Van Ness J, Galas DJ, Van Ness LK;  
 DR WPI; 2004-581010/56.  
 XX  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX  
 XX Example 1; Page 75; 238pp; English.  
 PS  
 XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring quality assurance/control of  
 CC bacterial contamination, monitoring quality assurance/control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. This sequence  
 CC corresponds to nucleic acid used in the method of the invention.  
 XX  
 XX Sequence 6 BP; 1 A; 5 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 73.3%; Score 4.4; DB 13; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGGAGG 6  
 DB |||||  
 6 GGGTGG 1  
 RESULT 11  
 AAN93676/c  
 ID AAN93676 standard; DNA; 5 BP.  
 XX  
 XX AAN93676;  
 AC  
 XX 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 24-JUN-1990 (first entry)  
 XX  
 XX Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber  
 DE variant (HSV-c) and HSV grape variant (HSV-g).  
 DE  
 XX Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.  
 KW  
 XX Hop growth retardant viroid.  
 OS  
 XX JP01040000-A.  
 PN  
 XX 10-FEB-1989.  
 PD  
 XX 05-AUG-1987; 87JP-00194377.  
 PP  
 XX 05-AUG-1987; 87JP-00194377.  
 PR

(YUKI ) YUKI GOSHI YAKUHI KOGYO KK.  
 WPI; 1989-089715/12.  
 Fractionating and detecting of hop growth retarding viroids - using  
 synthetic DNA probe contg. specified base sequence.  
 Disclosure; Page 3; 5pp; Japanese.  
 The synthetic probes is complementary to the RNA of HSV-g bases 53-59.  
 HSV, HSV-c and HSV-g are fractionated and detected using the synthetic  
 probe. The probe is 15-25mer. The probe can be used to diagnose HSV  
 infections in plants. (Updated on 25-MAR-2003 to correct PR field.)  
 (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to  
 correct OS field.)  
 Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 66.7%; Score 4; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GAGG 6  
 DB |||||  
 5 GAGG 2  
 RESULT 12  
 AAH56407  
 ID AAH56407 standard; DNA; 5 BP.  
 XX  
 XX AAH56407;  
 AC  
 XX 06-SEP-2001 (first entry)  
 DT  
 XX Escherichia coli groE operon antisense oligonucleotide SEQ ID NO:55.  
 DE  
 XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;  
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;  
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;  
 KW antibacterial; antiviral; antiproliferative; antisense therapy;  
 KW microbial infection; ss.  
 XX  
 XX Escherichia coli.  
 OS  
 XX WO200136625-A2.  
 PN  
 XX 25-MAY-2001.  
 PD  
 XX 20-NOV-2000; 2000WO-CA001347.  
 PF  
 XX 18-NOV-1999; 99US-0166249P.  
 PR  
 XX (GENE-) GENESENSE TECHNOLOGIES INC.  
 PA  
 XX Wright JA, Young AH, Dugourd D;  
 PI  
 XX WPI; 2001-355633/37.  
 DR  
 XX Novel antisense compounds targeting nucleic acid encoding groEL or groES  
 PT gene of microorganism, which hybridize with and inhibit expression of the  
 PT genes, useful to inhibit growth of microorganism having the genes.  
 PT  
 XX Claim 3; Page 41; 110pp; English.  
 PS  
 XX The present invention specifically claims AAH56368 to AAH56832 which are  
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More  
 CC generally, antisense compounds (I) comprising antisense oligonucleotides  
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat  
 CC shock protein (HSP) 60) (GL) and groES (HSP10) (GS) gene from a  
 CC microorganism, where the antisense compound is complementary to GL or GS  
 CC of a microorganism and specifically hybridizes with and inhibits the

CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and  
 CC antiproliferative activities, and can be used in antisense therapy and  
 CC for inhibition of expression of GROES or groEL. (I) are useful for  
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are  
 CC also useful for inhibiting the growth of a microorganism, or inhibiting  
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a  
 CC virus) having a GL or GS gene which involves administering to the  
 CC microorganism or to a cell infected with the microorganism, (I). (I) are  
 CC also useful for treating a mammalian pathological condition mediated by  
 CC the microorganisms which involves identifying a eukaryotic organism  
 CC having a pathological condition mediated by microorganisms having a GL or  
 CC GS gene and administering (I) such that the growth of microorganism is  
 CC inhibited. The antisense compounds are utilised for diagnostics,  
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
 CC prevent or delay microbial infections in humans. They are also useful as  
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854  
 CC represent PCR primers for GROE sequences which are used in the  
 CC exemplification of the present invention. AAH56855 to AAH56870 represent  
 CC groE nucleotide sequence given in the present invention

XX  
 SQ Sequence 5 BP; 2 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5  
 DB ||||  
 2 GGAG 5

#### RESULT 13

ADP90315/c  
 ID ADF90315 standard; DNA; 5 BP.

XX AC ADF90315;  
 XX AC ADF90315;  
 DT 26-FEB-2004 (first entry)  
 XX DE NEO ribosomal binding site SEQ ID NO:24.  
 XX charged transfection-facilitating polypeptide;  
 KW growth hormone releasing hormone; GHRH; poly-L-glutamate; antidiabetic;  
 KW gene therapy; diabetes; gene; ds.

XX Synthetic.

OS WO2003099341-A1.

PN 04-DEC-2003.

XX PF 23-MAY-2003; 2003WO-US016541.

XX PR 28-MAY-2002; 2002US-00156670.

XX PR 24-MAR-2003; 2003US-00395709.

XX (ADVI-) ADVISYS INC.

XX PI Draghia-Akli R, Carpenter RH, Kern DR, Hill LA, Attra H, Hebel H;  
 XX WPI; 2004-062023/06.

XX Composition useful for delivering isolated nucleic acid constructs for

XX correcting genetic deficiencies, such as diabetes, comprises a nucleic  
 PT acid expression construct, and a charged transfection-facilitating  
 PT polypeptide.

XX Disclosure; SEQ ID NO 24; 80pp; English.

XX The present invention describes a composition (I) comprising a nucleic  
 CC acid expression construct, and a charged transfection-facilitating  
 CC polypeptide associated with it, where a ratio in moles of the charged  
 CC transfection-facilitating polypeptide to nucleic acid expression

CC construct comprises from 1 mole to 5000 moles of the charged transfection  
 CC -facilitating polypeptide per mole of nucleic acid expression construct.  
 CC Also described is a composition (II) comprising a nucleic acid expression  
 CC construct encoding a growth hormone releasing hormone (GHRH) or its  
 CC functional biological equivalent, and a charged transfection-facilitating  
 CC polypeptide or a poly-L-glutamate polypeptide associated with it. (I) and  
 CC (II) have antidiabetic activities, and can be used in gene therapy. The  
 CC methods and compositions of the present invention are useful for  
 CC delivering isolated nucleic acid constructs for correcting genetic  
 CC deficiencies, such as diabetes. The present sequence is used in an  
 CC example from the present invention.

SQ Sequence 5 BP; 0 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6  
 DB ||||  
 5 GAGG 2

#### RESULT 14

ADI61783/c  
 ID ADI61783 standard; DNA; 5 BP.

XX AC ADI61783;

XX AC ADI61783;

DT 22-APR-2004 (first entry)

XX DE NEO ribosomal binding site SEQ ID NO:13.

XX mammalian expression plasmid; eukaryotic promoter;  
 KW codon-optimised-eukaryotic therapeutic gene; poly adenylation signal;  
 KW selectable marker gene promoter; ribosomal binding site;  
 KW selectable marker gene; origin of replication;  
 KW plasmid mediated gene supplementation; growth hormone releasing hormone;  
 KW GHRH; gene; ds.

XX Synthetic.

XX WO2004007679-A2.

XX 22-JAN-2004.

XX PF 15-JUL-2003; 2003WO-US021917.

XX PR 16-JUL-2002; 2002US-0396247P.

XX (ADVI-) ADVISYS INC.

XX Draghia-Akli R, Abruzzese RV, Kern DR;

XX WPI; 2004-122918/12.

XX New codon optimized synthetic mammalian expression plasmids having  
 PT operatively linked therapeutic and replication elements, useful for  
 PT plasmid mediated gene supplementation.

XX Claim 6; SEQ ID NO 13; 76pp; English.

XX The present invention describes a synthetic mammalian expression plasmid  
 CC (I) comprising a synthetic or eukaryotic promoter, a codon-optimised-  
 CC eukaryotic therapeutic gene sequence, a poly adenylation signal, a  
 CC selectable marker gene promoter, a ribosomal binding site, a selectable  
 CC marker gene sequence and an origin of replication. Also described: (1) a  
 CC synthetic mammalian expression plasmid comprising a fully defined  
 CC sequence of 2722, 2725, 2716, 2716 or 2725 bp (ADI61787, ADI61788,  
 CC ADI61789, ADI61790 or ADI61791); and (2) a method for plasmid mediated  
 CC gene supplementation, comprising delivering into a subject a codon  
 CC optimised synthetic mammalian expression plasmid, wherein the codon  
 CC optimised synthetic mammalian expression plasmid encodes a growth hormone

CC releasing hormone (GHRH) or its functional biological equivalent in the  
 CC subject. The methods and compositions of the present invention are useful  
 CC for producing an optimised nucleic acid delivery vehicle or synthetic  
 CC expression plasmid containing many structural elements necessary for the  
 CC in vitro amplification of the plasmid in a bacterial host, and for  
 CC plasmid mediated gene supplementation. The present sequence represents a  
 CC NEO ribosomal binding site, which is used in the exemplification of the  
 CC present invention.

XX Sequence 5 BP; 0 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6  
 DB 5 GAGG 2

## RESULT 15

AAQ38797  
 ID AAQ38797 standard; DNA; 6 BP.

XX AC AAQ38797;

XX 25-MAR-2003 (revised)  
 DT 26-JUL-1993 (first entry)

XX PCR primer #11 for analysis of lower TCR Vbeta gene usage in RA SILs.

XX TCR; T cell receptor; autoimmune disease; rheumatoid arthritis; RA;  
 KW J beta domain; V beta domain; T-cell mediated autoimmune disease;  
 KW antagonists.

XX OS Homo sapiens.

XX PN W09306135-A1.

XX PD 01-APR-1993.

XX PF 23-SEP-1992; 92WO-US08094.

XX PR 23-SEP-1991; 91US-00765222.

XX PR 18-OCT-1991; 91US-00779445.

XX PR 18-MAR-1992; 92US-00853362.

XX (GETH ) GENENTECH INC.

XX Amento EP;

XX WPI; 1993-117475/14.

XX T-cell receptor antagonising polypeptide(s) - used in the diagnosis and  
 PT treatment of auto-immune disorders, partic. rheumatoid arthritis.

XX Example 1; Page 22; 51pp; English.

XX This 5' PCR primer was used with a 3' primer designated a constant region  
 CC sequence common to all TCR beta transcripts. It was used for the PCR  
 CC analysis of lower TCR usage in synovial Vbetas. This primer was used for  
 CC Vbeta family 2, subfamily 4.1, Jbeta 2.7. Cbeta 2 and corresponds to D &  
 CC J translation AAR34165. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4  
 DB 1 GGGA 4

## RESULT 16

AAV61657/c

ID AAV61657 standard; DNA; 6 BP.

XX AC AAV61657;

XX 03-DEC-1998 (first entry)

XX Fusarium sp. 18S rRNA DNA fragment #1.

XX 18S rRNA; detection; identification; fungus; ss.

XX Fusarium sp.

XX JP10234380-A.

XX 08-SEP-1998.

XX 28-FEB-1997; 97JP-00062104.

XX 28-FEB-1997; 97JP-00062104.

XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

XX WPI; 1998-535034/46.

XX Use of oligo:nucleotide for detecting and identification of fungus of

XX Fusarium genus - as primer or probe to detect of identify microbes

XX rapidly and exactly.

XX Claim 1; Page 6; 20pp; Japanese.

XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
 CC used in a method for the detection and identification of a fungus of  
 CC Fusarium genus. The process can be used to detect or identify microbes  
 CC rapidly and exactly  
 XX Sequence 6 BP; 1 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6

DB 4 GAGG 1

## RESULT 17

AAZ89322/c

ID AAZ89322 standard; DNA; 6 BP.

XX AC AAZ89322;

XX 13-JUN-2000 (first entry)

XX Human UCP3 promoter fragment #2.

XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
 KW fat metabolism; ss.  
 XX Homo sapiens.

XX DE19838837-A1.

XX 02-MAR-2000.

XX 27-AUG-1998; 98DE-01038837.

XX 27-AUG-1998; 98DE-01038837.

PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 XX (NOVO ) NOVO-NORDISK AS.  
 PI Baterbauer H, Oberkofler H, Patsch W;  
 XX WPI; 2000-272214/24.  
 DR  
 XX Recombinant fat and muscle tissue specific uncoupling protein 3 promoters  
 PT useful for identifying UCP3 modulators.  
 XX  
 PS Claim 2; Page 10; 38pp; German.  
 XX  
 CC This invention describes novel recombinant DNA molecules containing an  
 CC uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat cells  
 CC but not functional in muscle cells or vice versa. The recombinant DNA  
 CC molecules are useful for transcription of genes and, with host cells, to  
 CC test for substances that can influence transcription. They can also be  
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
 CC metabolism and control of the promoter is useful in combating diseases  
 CC with inappropriate fat tissue metabolism. This sequence represents a  
 CC fragment of the human UCP-3 promoter which is used to illustrate the  
 CC method of the invention  
 XX  
 SQ Sequence 6 BP; 1 A; 4 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GAGG 6  
 Db |||||  
 6 GAGG 3  
 RESULT 18  
 AAF24321  
 ID AAF24321 standard; DNA; 6 BP.  
 XX  
 AC AAF24321;  
 DT  
 XX 09-APR-2001 (first entry)  
 XX Human NFAR-1/NFAR-2 intron/exon junction sequence #21.  
 XX  
 KW Human; nuclear factor associated with dsRNA; NFAR-1; NFAR-2;  
 KW transcription regulator; chromosome 19p13.1-13.2; apoptosis;  
 KW tumorigenesis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200077205-A1.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 09-JUN-2000; 2000WO-US015767.  
 XX  
 PR 11-JUN-1999; 99US-0138612P.  
 XX  
 PA (BARB/) BARBER G N.  
 PA (SAUN/) SAUNDERS L.  
 PA (PERK/) PERKINS D J.  
 XX  
 PI Barber GN, Saunders L, Perkins DJ;  
 XX WPI; 2001-080688/09.  
 XX  
 CC Novel isolated human nuclear factor associated with dsRNA polypeptide  
 PT useful for determining structure-function relationships and as affinity  
 PT tag to identify and isolate interacting proteins that bind to the factor.  
 XX  
 PS Disclosure; Page 62; 73pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of two

CC human nuclear factors associated with dsRNA (NFAR-1 and NFAR-2). These  
 CC are transcriptional regulators and are thought to play a role in  
 CC apoptosis and tumorigenesis. The coding sequence (found on chromosome  
 CC 19p13.1-13.2) is useful as a probe to detect rearrangements in tumour  
 CC cells and the protein is useful for determining structure-function  
 CC relationships  
 XX  
 SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GAGG 6  
 Db |||||  
 1 GAGG 4  
 RESULT 19  
 ACA63330  
 ID ACA63330 standard; RNA; 6 BP.  
 XX  
 AC ACA63330;  
 DT 26-AUG-2003 (first entry)  
 XX  
 DE Self assembly ribozyme system 6 nucleotide component.  
 XX  
 KW Ribozyme; Pneumocystis carinii infection; chronic hepatitis D; ss;  
 KW delta hepatitis virus infection; group I intron RNA.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 1..6  
 FT /tag= b  
 FT /bound moiety= "28 nucleotide component"  
 FT /note= "Forms a Watson-Crick duplex with nucleotides 28-  
 FT 23 of sequence in ACA63331"  
 FT modified\_base 1  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 32P labelled"  
 XX  
 XX US2003040114-A1.  
 PN  
 XX 27-FEB-2003.  
 PD  
 XX 07-JUN-1999; 99US-00326956.  
 PF  
 XX 05-SEP-1996; 96US-0024685P.  
 PR  
 XX 04-SEP-1997; 97US-00923487.  
 PR  
 XX (WARN ) WARNER LAMBERT CO.  
 PA  
 XX Cui M, Czarnik AW, Mei H;  
 PI WPI; 2003-492174/46.  
 DR  
 XX  
 PT Selecting compounds that modulate ribozyme activity or that bind ribozyme  
 PT in vivo in an organism, for use in diagnosing or treating microbial  
 PT infections, by using a biological assay.  
 XX  
 PS Example 2; Fig 9; 20pp; English.  
 XX  
 CC The invention relates to a method of selecting a compound that modulates  
 CC the activity of ribozyme, or that detects the ribozyme in an organism,  
 CC comprising measuring in an assay the ability of the compound to modulate  
 CC the function of or to selectively bind to the ribozyme and selecting the  
 CC assayed compound for use in modulating the activity of the ribozyme or  
 CC detecting the ribozyme in the organism. The method is useful for  
 CC selecting a compound, preferably a small organic molecule having a  
 CC molecular weight of less than 1000 Daltons, that modulates the activity

CC of a ribozyme or that detects the presence of a ribozyme in an organism  
CC that is pathogenic for an animal or plant. The selected compound which  
CC modulates ribozyme activity is useful for treating an infection caused by  
CC a microorganism containing the ribozyme, especially for treating  
CC Pneumocystis carinii infections, delta hepatitis virus infections and  
CC chronic hepatitis D and selected compounds which binds to ribozyme are  
CC useful for diagnosing the conditions. The method allows rapid  
CC determination of small organic modulators that regulate the function of  
CC ribozymes. The present sequence represents the self assembly ribozyme  
CC system 6 nucleotide component  
XX  
SQ Sequence 6 BP; 1 A; 1 C; 3 G; 0 T; 1 U; 0 Other;  
Query Match 66.7%; Score 4; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GAGG 6  
Db ||||  
1 GAGG 4  
RESULT 20  
ADE38304  
ID ADE38304 standard; DNA; 6 BP.  
XX  
AC ADE38304;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:43.  
XX  
KW autoimmune disease; statin; antigen-specific immunomodulatory agent;  
KW non-antigen-specific immunomodulatory agent; immunomodulatory;  
KW antidiabetic; antiarthritic; vasotropic; gene therapy;  
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;  
KW rheumatoid arthritis; autoimmune uveitis; ss.  
XX  
OS Synthetic.  
XX  
FN WO2003082269-A1.  
XX  
PD 09-OCT-2003.  
XX  
PF 31-MAR-2003; 2003WO-US009807.  
XX  
PR 29-MAR-2002; 2002US-0368803P.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX (BAYH-) BAYHILL THERAPEUTICS INC.  
XX  
PI Garren H, Steinman L;  
XX  
DR WPI; 2003-803953/75.  
XX  
PT Treating an autoimmune disease by co-administering to a patient a statin  
PT and an antigen-specific non-antigen-specific immunomodulatory agent.  
XX  
PS Disclosure; SEQ ID NO 43; 90pp; English.  
XX  
CC The present invention describes a method for treating an autoimmune  
CC disease comprising co-administering to a patient a statin and an antigen-  
CC specific/non-antigen-specific immunomodulatory agent. The  
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic  
CC activities, and can be used in gene therapy. The method is useful for  
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent  
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;  
Query Match 66.7%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GAGG 6  
Db ||||  
1 GAGG 4  
RESULT 22  
ADE38300  
ID ADE38300 standard; DNA; 6 BP.  
XX  
AC ADE38300;  
XX  
DT 29-JAN-2004 (first entry)  
XX

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GAGG 6  
Db ||||  
1 GAGG 4  
RESULT 21  
ADE38308  
ID ADE38308 standard; DNA; 6 BP.  
XX  
AC ADE38308;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:47.  
XX  
KW autoimmune disease; statin; antigen-specific immunomodulatory agent;  
KW non-antigen-specific immunomodulatory agent; immunomodulatory;  
KW antidiabetic; antiarthritic; vasotropic; gene therapy;  
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;  
KW rheumatoid arthritis; autoimmune uveitis; ss.  
XX  
OS Synthetic.  
XX  
FN WO2003082269-A1.  
XX  
PD 09-OCT-2003.  
XX  
PF 31-MAR-2003; 2003WO-US009807.  
XX  
PR 29-MAR-2002; 2002US-0368803P.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX (BAYH-) BAYHILL THERAPEUTICS INC.  
XX  
PI Garren H, Steinman L;  
XX  
DR WPI; 2003-803953/75.  
XX  
PT Treating an autoimmune disease by co-administering to a patient a statin  
PT and an antigen-specific non-antigen-specific immunomodulatory agent.  
XX  
PS Disclosure; SEQ ID NO 47; 90pp; English.  
XX  
CC The present invention describes a method for treating an autoimmune  
CC disease comprising co-administering to a patient a statin and an antigen-  
CC specific/non-antigen-specific immunomodulatory agent. The  
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic  
CC activities, and can be used in gene therapy. The method is useful for  
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent  
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;  
Query Match 66.7%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GAGG 6  
Db ||||  
1 GAGG 4  
RESULT 22  
ADE38300  
ID ADE38300 standard; DNA; 6 BP.  
XX  
AC ADE38300;  
XX  
DT 29-JAN-2004 (first entry)  
XX

DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:39.  
 XX autoimmune disease; statin; antigen-specific immunomodulatory agent;  
 KW non-antigen-specific immunomodulatory agent; immunomodulatory;  
 KW anti-diabetic; antiarthritic; vasotropic; gene therapy;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;  
 KW rheumatoid arthritis; autoimmune uveitis; ss.  
 XX Synthetic.  
 OS  
 XX WO2003082269-A1.  
 PN  
 XX 09-OCT-2003.  
 PD  
 XX 31-MAR-2003; 2003WO-US009807.  
 PF  
 XX 29-MAR-2002; 2002US-0368803P.  
 PR  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (BAYH-) BAYHILL THERAPEUTICS INC.  
 PA  
 XX Garren H, Steinman L;  
 PI  
 XX WPI; 2003-803953/75.  
 DR  
 XX Treating an autoimmune disease by co-administering to a patient a statin  
 PT and an antigen-specific non-antigen-specific immunomodulatory agent.  
 PT  
 XX Disclosure; SEQ ID NO 39; 90pp; English.  
 PS  
 XX The present invention describes a method for treating an autoimmune  
 CC disease comprising co-administering to a patient a statin and an antigen-  
 CC specific/non-antigen-specific immunomodulatory agent. The  
 CC immunomodulatory agent has anti-diabetic, antiarthritic and vasotropic  
 CC activities, and can be used in gene therapy. The method is useful for  
 CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent  
 CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The  
 CC present sequence is used in the exemplification of the present invention.  
 CC  
 XX  
 SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GAGG 6  
 Db |||||  
 1 GAGG 4  
 RESULT 23  
 ADJ35691/c  
 ID ADJ35691 standard; DNA; 6 BP.  
 XX  
 AC ADJ35691;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Stabilising anti-repression, STAR, element dyad sequence #357.  
 DE  
 XX STAR affiliated proteinaceous molecule; post translational modification;  
 KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX  
 XX Unidentified.  
 OS  
 XX WO2003106674-A2.  
 PN  
 XX 24-DEC-2003.  
 PD  
 XX 30-MAY-2003; 2003WO-NL000410.  
 PF  
 XX 14-JUN-2002; 2002EP-00077344.  
 PR  
 XX (CHRO-) CHROMAGENICS BV.  
 PA  
 XX Otte AP, Kruckeberg AL, Satijn DPE;  
 PI  
 XX WPI; 2004-082195/08.  
 DR  
 XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 PT  
 XX Disclosure; Page 103; 177pp; English.  
 PS  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 CC  
 XX  
 SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GAGG 6  
 Db |||||  
 6 GAGG 3  
 RESULT 24  
 ADJ35735  
 ID ADJ35735 standard; DNA; 6 BP.  
 XX  
 AC ADJ35735;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Stabilising anti-repression, STAR, element dyad sequence #401.  
 DE  
 XX STAR affiliated proteinaceous molecule; post translational modification;  
 KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX  
 XX Unidentified.  
 OS  
 XX WO2003106674-A2.  
 PN  
 XX 24-DEC-2003.  
 PD  
 XX 30-MAY-2003; 2003WO-NL000410.  
 PF  
 XX 14-JUN-2002; 2002EP-00077344.  
 PR  
 XX (CHRO-) CHROMAGENICS BV.  
 PA  
 XX Otte AP, Kruckeberg AL, Satijn DPE;  
 PI  
 XX WPI; 2004-082195/08.  
 DR  
 XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 PT  
 XX Disclosure; Page 103; 177pp; English.  
 PS  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid

PA (CHRO-) CHROMAGENICS BV.  
 XX  
 PI Otte AP, Kruckeberg AL, Satijn DPE;  
 XX WPI; 2004-082195/08.  
 DR  
 XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 PT  
 XX Disclosure; Page 102; 177pp; English.  
 PS  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 CC  
 XX  
 SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GAGG 6  
 Db |||||  
 6 GAGG 3  
 RESULT 24  
 ADJ35735  
 ID ADJ35735 standard; DNA; 6 BP.  
 XX  
 AC ADJ35735;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Stabilising anti-repression, STAR, element dyad sequence #401.  
 DE  
 XX STAR affiliated proteinaceous molecule; post translational modification;  
 KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX  
 XX Unidentified.  
 OS  
 XX WO2003106674-A2.  
 PN  
 XX 24-DEC-2003.  
 PD  
 XX 30-MAY-2003; 2003WO-NL000410.  
 PF  
 XX 14-JUN-2002; 2002EP-00077344.  
 PR  
 XX (CHRO-) CHROMAGENICS BV.  
 PA  
 XX Otte AP, Kruckeberg AL, Satijn DPE;  
 PI  
 XX WPI; 2004-082195/08.  
 DR  
 XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 PT  
 XX Disclosure; Page 103; 177pp; English.  
 PS  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 XX  
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGA 4  
 DB 3 GGGA 6

RESULT 25  
 ADJ35654  
 ID ADJ35654 standard; DNA; 6 BP.  
 AC ADJ35654;  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Stabilising anti-repression, STAR, element dyad sequence #320.

XX STAR affiliated proteinaceous molecule; post translational modification;  
 KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX Unidentified.

OS  
 XX WO2003106674-A2.  
 PN 24-DEC-2003.

XX 30-MAY-2003; 2003WO-NL000410.  
 PF 14-JUN-2002; 2002BP-00077344.  
 PR (CHRO-) CHROMAGENICS BV.  
 XX Otte AP, Kruckeberg AL, Satiijn DPE;  
 PI WPI; 2004-082195/08.

XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.

XX Disclosure; Page 101; 177pp; English.  
 PS The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.

XX Sequence 6 BP; 1 A; 2 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGAG 5  
 DB 1 GGAG 4

RESULT 26  
 ADL09191  
 ID ADL09191 standard; DNA; 6 BP.  
 AC ADL09191;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE T7 promoter DNA fragment #3.  
 XX  
 KW amplification; primer; promoter; RNA polymerase; ds.  
 XX Enterobacteria phage T7.  
 OS WO2004016757-A2.  
 PN 26-FEB-2004.  
 PD 15-AUG-2003; 2003WO-US025564.  
 XX 16-AUG-2002; 2002US-0404075P.  
 PR (REGC ) UNIV CALIFORNIA.  
 PA Karin M, Park JM;  
 PI WPI; 2004-203788/19.  
 DR  
 XX Producing a nucleic acid sequence comprises amplifying double stranded  
 PT DNA sequence in the presence of first and second primers to produce a  
 PT first nucleic acid molecule having the double stranded DNA sequence in a  
 PT head to head orientation.  
 XX Disclosure; SEQ ID NO 7; 55pp; English.  
 PS This invention describes a novel method for producing a nucleic acid  
 CC sequence comprising amplifying the double stranded DNA sequence of  
 CC interest in the presence of the first primer and the second primer to  
 CC produce a first nucleic acid molecule comprising the double stranded DNA  
 CC sequence of interest flanked by at least a portion of the first promoter  
 CC in a head to head orientation. The method involves providing RNA  
 CC polymerase that specifically binds to the first promoter and contacting  
 CC the first nucleic acid molecule with the RNA polymerase to produce double  
 CC stranded RNA that is complementary to the double stranded DNA sequence of  
 CC interest. This method further comprises providing a third primer  
 CC complementary to at least a portion of the first promoter and amplifying  
 CC the first nucleic acid molecule produced in the presence of the third  
 CC primer to produce a second nucleic acid molecule comprising the double  
 CC stranded DNA sequence of interest flanked by the first promoter in a head  
 CC to head orientation. The method further comprises providing RNA  
 CC polymerase that specifically binds to the first promoter and contacting  
 CC the second nucleic acid molecule with the RNA polymerase to produce  
 CC double stranded RNA that is complementary to the double stranded DNA  
 CC sequence of interest. The second strand of the double-stranded DNA  
 CC sequence of interest comprises at least a portion of a second promoter.  
 CC The second promoter is different from the first promoter. The first  
 CC promoter comprises T7, T3 or SP6 promoter. The first strand of the double  
 CC stranded DNA comprises a nucleotide sequence linked to the 3' end of the  
 CC first promoter, and the first primer further comprises a second sequence  
 CC complementary to the nucleotide sequence, where the second sequence is  
 CC linked to the 3' end of the first sequence of the first primer. The first  
 CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The  
 CC first sequence comprises a second primer complementary to at least a  
 CC portion of a promoter. The methods and kits are useful for producing  
 CC nucleic acid sequences as powerful alternative tools for functional  
 CC genomics.  
 XX Sequence 6 BP; 2 A; 0 C; 3 G; 1 T; 0 U; 0 Other;



Query Match 66.7%; Score 4; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4  
| | | |  
| | | |  
Db 1 GGGA 4

RESULT 27  
ADL09189/c  
ID ADL09189 standard; DNA; 6 BP.  
XX  
AC ADL09189;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE T7 promoter DNA fragment #2.  
XX  
KW amplification; primer; promoter; RNA polymerase; ds.  
XX  
OS Enterobacteria phage T7.  
XX  
PN WO2004016757-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 15-AUG-2003; 2003WO-US025564.  
XX  
PR 16-AUG-2002; 2002US-0404075P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Karin M, Park JM;  
XX  
DR WPI; 2004-203788/19.  
XX  
PT Producing a nucleic acid sequence comprises amplifying double stranded  
PT DNA sequence in the presence of first and second primers to produce a  
PT first nucleic acid molecule having the double stranded DNA sequence in a  
PT head to head orientation.  
XX  
PS Disclosure; SEQ ID NO 5; 55pp; English.  
XX  
CC This invention describes a novel method for producing a nucleic acid  
CC sequence comprising amplifying the double stranded DNA sequence of  
CC interest in the presence of the first primer and the second primer to  
CC produce a first nucleic acid molecule comprising the double stranded DNA  
CC sequence of interest flanked by at least a portion of the first promoter  
CC in a head to head orientation. The method involves providing RNA  
CC polymerase that specifically binds to the first promoter and contacting  
CC the first nucleic acid molecule with the RNA polymerase to produce double  
CC stranded RNA that is complementary to the double stranded DNA sequence of  
CC interest. This method further comprises providing a third primer  
CC complementary to at least a portion of the first promoter and amplifying  
CC the first nucleic acid molecule produced in the presence of the third  
CC primer to produce a second nucleic acid molecule comprising the double  
CC stranded DNA sequence of interest flanked by the first promoter in a head  
CC to head orientation. The method further comprises providing RNA  
CC polymerase that specifically binds to the first promoter and contacting  
CC the second nucleic acid molecule with the RNA polymerase to produce  
CC double stranded RNA that is complementary to the double stranded DNA  
CC sequence of interest. The second strand of the double-stranded DNA  
CC sequence of interest comprises at least a portion of a second promoter.  
CC The second promoter is different from the first promoter. The first  
CC promoter comprises a nucleotide sequence linked to the 3' end of the  
CC first promoter, and the first primer further comprises a second sequence  
CC complementary to the nucleotide sequence, where the second sequence is  
CC linked to the 3' end of the first sequence of the first primer. The first  
CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The  
CC first sequence comprises a second primer complementary to at least a

CC portion of a promoter. The methods and kits are useful for producing  
CC nucleic acid sequences as powerful alternative tools for functional  
CC genomics.  
XX  
SQ Sequence 6 BP; 1 A; 3 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 4; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4  
| | | |  
| | | |  
Db 6 GGGA 3

RESULT 28  
ADL09220  
ID ADL09220 standard; DNA; 6 BP.  
XX  
AC ADL09220;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE T3 promoter DNA fragment #15.  
XX  
KW amplification; primer; promoter; RNA polymerase; ds.  
XX  
OS Bacteriophage T3.  
XX  
PN WO2004016757-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 15-AUG-2003; 2003WO-US025564.  
XX  
PR 16-AUG-2002; 2002US-0404075P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Karin M, Park JM;  
XX  
DR WPI; 2004-203788/19.  
XX  
PT Producing a nucleic acid sequence comprises amplifying double stranded  
PT DNA sequence in the presence of first and second primers to produce a  
PT first nucleic acid molecule having the double stranded DNA sequence in a  
PT head to head orientation.  
XX  
PS Disclosure; SEQ ID NO 36; 55pp; English.  
XX  
CC This invention describes a novel method for producing a nucleic acid  
CC sequence comprising amplifying the double stranded DNA sequence of  
CC interest in the presence of the first primer and the second primer to  
CC produce a first nucleic acid molecule comprising the double stranded DNA  
CC sequence of interest flanked by at least a portion of the first promoter  
CC in a head to head orientation. The method involves providing RNA  
CC polymerase that specifically binds to the first promoter and contacting  
CC the first nucleic acid molecule with the RNA polymerase to produce double  
CC stranded RNA that is complementary to the double stranded DNA sequence of  
CC interest. This method further comprises providing a third primer  
CC complementary to at least a portion of the first promoter and amplifying  
CC the first nucleic acid molecule produced in the presence of the third  
CC primer to produce a second nucleic acid molecule comprising the double  
CC stranded DNA sequence of interest flanked by the first promoter in a head  
CC to head orientation. The method further comprises providing RNA  
CC polymerase that specifically binds to the first promoter and contacting  
CC the second nucleic acid molecule with the RNA polymerase to produce  
CC double stranded RNA that is complementary to the double stranded DNA  
CC sequence of interest. The second strand of the double-stranded DNA  
CC sequence of interest comprises at least a portion of a second promoter.  
CC The second promoter is different from the first promoter. The first  
CC promoter comprises a nucleotide sequence linked to the 3' end of the  
CC first promoter, and the first primer further comprises a second sequence  
CC complementary to the nucleotide sequence, where the second sequence is  
CC linked to the 3' end of the first sequence of the first primer. The first  
CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The  
CC first sequence comprises a second primer complementary to at least a

CC first promoter, and the first primer further comprises a second sequence  
 CC complementary to the nucleotide sequence, where the second sequence is  
 CC linked to the 3' end of the first sequence of the first primer. The first  
 CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The  
 CC first sequence comprises a second primer complementary to at least a  
 CC portion of a promoter. The methods and kits are useful for producing  
 CC nucleic acid sequences as powerful alternative tools for functional  
 CC genomics.

XX Sequence 6 BP; 3 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4  
 DB ||||  
 3 GGGA 6

RESULT 29  
 ADQ89354  
 ID ADQ89354 standard; DNA; 6 BP.

AC ADQ89354;  
 DT 07-OCT-2004 (first entry)

XX Acute phase response factor consensus binding site.  
 XX ds; diarrhoea; infectious disease; necrotising enterocolitis;  
 KW urinary tract infection; acute phase response factor.

XX Synthetic.

XX US2004142415-A1.  
 XX 22-JUL-2004.

PF 21-JAN-2003; 2003US-00348304.  
 PR 21-JAN-2003; 2003US-00348304.

PA (UYNE-) UNIV NEBRASKA.

PI Mcdonald TL, Larson MA, Weber A;  
 XX WPI; 2004-579907/56.

XX New isolated nucleic acid molecule encoding a polypeptide having serum  
 PT amyloid A3 (SAA3) activity, useful for preventing or treating diarrhea,  
 PT infectious diseases, necrotizing enterocolitis, or urinary tract  
 PT infections.

PS Example; SEQ ID NO 12; 25pp; English.

XX The invention relates to an isolated nucleic acid molecule that encodes a  
 CC polypeptide having serum amyloid A3 (SAA3) activity. The nucleic acid  
 CC encoding the proteins having SAA3 activity is useful as probes to detect  
 CC the presence of and/or expression of the genes. They are also useful for  
 CC producing transgenic cells, tissues, or organs. They are also useful for  
 CC preventing or treating diarrhoea, infectious diseases, necrotising  
 CC enterocolitis or urinary tract infections. The present sequence  
 CC represents the acute phase response factor consensus binding site. Note:  
 CC SEQ ID Nos 1 and 2 are not disclosed in the specification.

XX Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4

DB ||||  
 3 GGGA 6

RESULT 30  
 ADR32741  
 ID ADR32741 standard; DNA; 6 BP.

AC ADR32741;

DT 04-NOV-2004 (first entry)

DE Human nicking agent target DNA #282.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.

OS Homo sapiens.

XX WO2004067765-A2.

XX 12-AUG-2004.

PF 29-JAN-2004; 2004WO-US002720.

PR 29-JAN-2003; 2003US-0443811P.

XX (KECK-) KECK GRADUATE INST.

PI Van Ness J, Galas DJ, Van Ness LK;

XX WPI; 2004-581010/56.

XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.

PS Example 1; Page 76; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. This sequence  
 CC corresponds to nucleic acid used in the method of the invention.

XX Sequence 6 BP; 2 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGA 4  
|  
|  
|  
|  
Db 3 GGA 6

Search completed: July 20, 2005, 22:59:09  
Job time : 189.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds  
(without alignments)  
393.838 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 999agg 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description        |
|------------|-------|---------------|--------|----|--------------------|
| 1          | 6     | 100.0         | 6      | 6  | AX175281 Sequence  |
| 2          | 6     | 100.0         | 6      | 6  | AX743310 Sequence  |
| 3          | 6     | 100.0         | 6      | 6  | AX743314 Sequence  |
| C 4        | 6     | 100.0         | 6      | 6  | AX805866 Sequence  |
| 5          | 6     | 100.0         | 6      | 6  | AX816715 Sequence  |
| C 6        | 5     | 83.3          | 5      | 6  | A70976 Sequence 30 |
| C 7        | 5     | 83.3          | 5      | 6  | BD244758 Isolation |
| C 8        | 5     | 83.3          | 5      | 6  | AX805860 Sequence  |
| C 9        | 5     | 83.3          | 5      | 6  | A93563 Sequence 1  |
| C 10       | 5     | 83.3          | 6      | 6  | CQ755704 Sequence  |
| C 11       | 5     | 83.3          | 6      | 6  | CQ755766 Sequence  |
| C 12       | 5     | 83.3          | 6      | 6  | CQ755813 Sequence  |
| C 13       | 5     | 83.3          | 6      | 6  | CQ755818 Sequence  |
| C 14       | 5     | 83.3          | 6      | 6  | CQ756128 Sequence  |
| C 15       | 5     | 83.3          | 6      | 6  | CQ757942 Sequence  |
| C 16       | 5     | 83.3          | 6      | 6  | CQ758004 Sequence  |
| C 17       | 5     | 83.3          | 6      | 6  | CQ758051 Sequence  |
| C 18       | 5     | 83.3          | 6      | 6  | CQ758056 Sequence  |
| C 19       | 5     | 83.3          | 6      | 6  | CQ758366 Sequence  |

|      |     |      |   |   |          |                    |
|------|-----|------|---|---|----------|--------------------|
| 20   | 5   | 83.3 | 6 | 6 | E08990   | E08990 Oligo DNA m |
| 21   | 5   | 83.3 | 6 | 6 | E09173   | E09173 Synthetic o |
| 22   | 5   | 83.3 | 6 | 6 | E09489   | E09489 Phosphoroth |
| 23   | 5   | 83.3 | 6 | 6 | AX093419 | AX093419 Sequence  |
| 24   | 5   | 83.3 | 6 | 6 | AX175283 | AX175283 Sequence  |
| 25   | 5   | 83.3 | 6 | 6 | AX361080 | AX361080 Sequence  |
| 26   | 5   | 83.3 | 6 | 6 | AX391507 | AX391507 Sequence  |
| 27   | 5   | 83.3 | 6 | 6 | AX574433 | AX574433 Sequence  |
| C 28 | 5   | 83.3 | 6 | 6 | AX764742 | AX764742 Sequence  |
| C 29 | 5   | 83.3 | 6 | 6 | AX764804 | AX764804 Sequence  |
| C 30 | 5   | 83.3 | 6 | 6 | AX764851 | AX764851 Sequence  |
| C 31 | 5   | 83.3 | 6 | 6 | AX764856 | AX764856 Sequence  |
| C 32 | 5   | 83.3 | 6 | 6 | AX765166 | AX765166 Sequence  |
| C 33 | 4.4 | 73.3 | 6 | 6 | CQ755693 | CQ755693 Sequence  |
| C 34 | 4.4 | 73.3 | 6 | 6 | CQ755744 | CQ755744 Sequence  |
| C 35 | 4.4 | 73.3 | 6 | 6 | CQ755745 | CQ755745 Sequence  |
| C 36 | 4.4 | 73.3 | 6 | 6 | CQ756172 | CQ756172 Sequence  |
| C 37 | 4.4 | 73.3 | 6 | 6 | CQ756501 | CQ756501 Sequence  |
| C 38 | 4.4 | 73.3 | 6 | 6 | CQ757931 | CQ757931 Sequence  |
| C 39 | 4.4 | 73.3 | 6 | 6 | CQ757982 | CQ757982 Sequence  |
| C 40 | 4.4 | 73.3 | 6 | 6 | CQ757983 | CQ757983 Sequence  |
| C 41 | 4.4 | 73.3 | 6 | 6 | CQ758410 | CQ758410 Sequence  |
| C 42 | 4.4 | 73.3 | 6 | 6 | CQ758739 | CQ758739 Sequence  |
| C 43 | 4.4 | 73.3 | 6 | 6 | AX063645 | AX063645 Sequence  |
| C 44 | 4.4 | 73.3 | 6 | 6 | AX103839 | AX103839 Sequence  |
| 45   | 4.4 | 73.3 | 6 | 6 | AX175261 | AX175261 Sequence  |
| 46   | 4.4 | 73.3 | 6 | 6 | AX175278 | AX175278 Sequence  |
| 47   | 4.4 | 73.3 | 6 | 6 | AX175280 | AX175280 Sequence  |
| 48   | 4.4 | 73.3 | 6 | 6 | AX175282 | AX175282 Sequence  |
| 49   | 4.4 | 73.3 | 6 | 6 | AX175310 | AX175310 Sequence  |
| C 50 | 4.4 | 73.3 | 6 | 6 | AX175315 | AX175315 Sequence  |
| 51   | 4.4 | 73.3 | 6 | 6 | AX189456 | AX189456 Sequence  |
| 52   | 4.4 | 73.3 | 6 | 6 | AX207279 | AX207279 Sequence  |
| 53   | 4.4 | 73.3 | 6 | 6 | AX235310 | AX235310 Sequence  |
| 54   | 4.4 | 73.3 | 6 | 6 | AX285288 | AX285288 Sequence  |
| 55   | 4.4 | 73.3 | 6 | 6 | AX355137 | AX355137 Sequence  |
| 56   | 4.4 | 73.3 | 6 | 6 | AX428534 | AX428534 Sequence  |
| C 57 | 4.4 | 73.3 | 6 | 6 | AX546892 | AX546892 Sequence  |
| 58   | 4.4 | 73.3 | 6 | 6 | AX574435 | AX574435 Sequence  |
| 59   | 4.4 | 73.3 | 6 | 6 | AX743309 | AX743309 Sequence  |
| C 60 | 4.4 | 73.3 | 6 | 6 | AX743311 | AX743311 Sequence  |
| 61   | 4.4 | 73.3 | 6 | 6 | AX743313 | AX743313 Sequence  |
| C 62 | 4.4 | 73.3 | 6 | 6 | AX743315 | AX743315 Sequence  |
| C 63 | 4.4 | 73.3 | 6 | 6 | AX764731 | AX764731 Sequence  |
| C 64 | 4.4 | 73.3 | 6 | 6 | AX764782 | AX764782 Sequence  |
| C 65 | 4.4 | 73.3 | 6 | 6 | AX764783 | AX764783 Sequence  |
| C 66 | 4.4 | 73.3 | 6 | 6 | AX765210 | AX765210 Sequence  |
| C 67 | 4.4 | 73.3 | 6 | 6 | AX765539 | AX765539 Sequence  |
| 68   | 4.4 | 73.3 | 6 | 6 | AX816714 | AX816714 Sequence  |
| C 69 | 4.4 | 73.3 | 6 | 6 | AX827233 | AX827233 Sequence  |
| 70   | 4.4 | 73.3 | 6 | 6 | BD080743 | BD080743 Presenili |
| C 71 | 4.4 | 73.3 | 6 | 6 | BD080744 | BD080744 Presenili |
| 72   | 4.2 | 70.0 | 6 | 6 | AX557115 | AX557115 Sequence  |
| C 73 | 4.2 | 70.0 | 6 | 6 | AX711257 | AX711257 Sequence  |
| 74   | 4   | 66.7 | 4 | 6 | AX794771 | AX794771 Sequence  |
| C 75 | 4   | 66.7 | 4 | 6 | AX805855 | AX805855 Sequence  |
| 76   | 4   | 66.7 | 4 | 6 | AX805859 | AX805859 Sequence  |
| C 77 | 4   | 66.7 | 4 | 6 | CQ787899 | CQ787899 Sequence  |
| C 78 | 4   | 66.7 | 5 | 6 | CQ787900 | CQ787900 Sequence  |
| C 79 | 4   | 66.7 | 5 | 6 | CQ854736 | CQ854736 Sequence  |
| 80   | 4   | 66.7 | 5 | 6 | CQ868987 | CQ868987 Sequence  |
| 81   | 4   | 66.7 | 5 | 6 | CQ868999 | CQ868999 Sequence  |
| 82   | 4   | 66.7 | 5 | 6 | CQ869006 | CQ869006 Sequence  |
| C 83 | 4   | 66.7 | 5 | 6 | CQ869010 | CQ869010 Sequence  |
| 84   | 4   | 66.7 | 5 | 6 | CQ869136 | CQ869136 Sequence  |
| 85   | 4   | 66.7 | 5 | 6 | CQ869148 | CQ869148 Sequence  |
| C 86 | 4   | 66.7 | 5 | 6 | CQ869155 | CQ869155 Sequence  |
| C 87 | 4   | 66.7 | 5 | 6 | CQ869159 | CQ869159 Sequence  |
| C 88 | 4   | 66.7 | 5 | 6 | CQ877118 | CQ877118 Sequence  |
| 89   | 4   | 66.7 | 5 | 6 | E09174   | E09174 Synthetic o |
| 90   | 4   | 66.7 | 5 | 6 | E09490   | E09490 Phosphoroth |
| 91   | 4   | 66.7 | 5 | 6 | AX148853 | AX148853 Sequence  |
| 92   | 4   | 66.7 | 5 | 6 | BD084756 | BD084756 Human ner |

```

c 93 4 66.7 6 6 BD268075 Cell spec
94 4 66.7 6 6 BD274470 IKAROS is
95 4 66.7 6 6 CQ755709 Sequence
96 4 66.7 6 6 CQ755713 Sequence
97 4 66.7 6 6 CQ755716 Sequence
98 4 66.7 6 6 CQ755740 Sequence
99 4 66.7 6 6 CQ755742 Sequence
100 4 66.7 6 6 CQ755749 Sequence

ALIGNMENTS

RESULT 1
AX175281
LOCUS AX175281 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 45 from Patent WO0144465.
ACCESSION AX175281
VERSION AX175281.1 GI:14598649
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..6
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGAGG 6

RESULT 2
AX743310
LOCUS AX743310 6 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 2 from Patent WO03028764.
ACCESSION AX743310
VERSION AX743310.1 GI:30577236
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..6
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGAGG 6

RESULT 3
AX743314
LOCUS AX743314 6 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 6 from Patent WO03028764.
ACCESSION AX743314
VERSION AX743314.1 GI:30577240
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..6
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide-3'-Triethyleneglycol
(TEG) Cholesteryl Synthetic Oligonucleotide"

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGAGG 6

RESULT 4
AX805866/c
LOCUS AX805866 6 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 12 from Patent WO03060163.
ACCESSION AX805866
VERSION AX805866.1 GI:38522777
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..6
/organism="synthetic construct"
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide-3'-Triethyleneglycol
(TEG) Cholesteryl Synthetic Oligonucleotide"

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGAGG 6

RESULT 5
AX816715
LOCUS AX816715 6 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 5 from Patent WO03028764.
ACCESSION AX816715
VERSION AX816715.1 GI:30577236
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..6
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGAGG 6

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LOCUS AX816715 6 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 3 from Patent WO02085340.
ACCESSION AX816715
VERSION AX816715.1 GI:39647044
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Filion,M.C. and Phillips,N.C.
TITLE Oligonucleotide compositions and their use to induce
 differentiation of cells
JOURNAL Patent: WO 02085340-A 3 31-OCT-2002;
 Bioniche Life Sciences Inc. (CA)
FEATURES source
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 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide"
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db |||||
 1 GGGAGG 6

RESULT 6
LOCUS A70976 5 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 30 from Patent WO9813522.
ACCESSION A70976
VERSION A70976.1 GI:4774961
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 5)
AUTHORS Uhlen,M. and Lundberg,J.
TITLE THE USE OF MODULAR OLIGONUCLEOTIDES AS PROBES OR PRIMERS IN NUCLEIC
 ACID BASED ASSAY
JOURNAL Patent: WO 9813522-A 30 02-APR-1998;
 DZIEGLEWSKA HANNA EVA (GB)
FEATURES source
 1..5
 Location/Qualifiers
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
 5 GGAGG 1

RESULT 7
LOCUS BD244758/c 5 bp DNA linear PAT 17-JUL-2003
DEFINITION Isolation method of primer extension products by modular
 oligonucleotide.
ACCESSION BD244758
VERSION BD244758.1 GI:33054528
KEYWORDS JP 2002525076-A/37.
SOURCE synthetic construct
ORGANISM synthetic construct

LOCUS AX816715 6 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 3 from Patent WO02085340.
ACCESSION AX816715
VERSION AX816715.1 GI:39647044
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Filion,M.C. and Phillips,N.C.
TITLE Oligonucleotide compositions and their use to induce
 differentiation of cells
JOURNAL Patent: WO 02085340-A 3 31-OCT-2002;
 Bioniche Life Sciences Inc. (CA)
FEATURES source
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 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide"
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db |||||
 1 GGGAGG 6

RESULT 6
LOCUS A70976 5 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 30 from Patent WO9813522.
ACCESSION A70976
VERSION A70976.1 GI:4774961
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 5)
AUTHORS Uhlen,M. and Lundberg,J.
TITLE THE USE OF MODULAR OLIGONUCLEOTIDES AS PROBES OR PRIMERS IN NUCLEIC
 ACID BASED ASSAY
JOURNAL Patent: WO 9813522-A 30 02-APR-1998;
 DZIEGLEWSKA HANNA EVA (GB)
FEATURES source
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 Location/Qualifiers
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
 5 GGAGG 1

RESULT 7
LOCUS BD244758/c 5 bp DNA linear PAT 17-JUL-2003
DEFINITION Isolation method of primer extension products by modular
 oligonucleotide.
ACCESSION BD244758
VERSION BD244758.1 GI:33054528
KEYWORDS JP 2002525076-A/37.
SOURCE synthetic construct
ORGANISM synthetic construct

LOCUS AX816715 6 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 3 from Patent WO02085340.
ACCESSION AX816715
VERSION AX816715.1 GI:39647044
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 5)
AUTHORS Lundberg,J. and Uhlen,M.
TITLE Isolation method of primer extension products by modular
 Patent: JP 2002525076-A 37 13-AUG-2002;
 DYNAL AS
SOURCE OS Artificial Sequence
 PN JP 2002525076-A/37
 PD 13-AUG-2002
 PF 15-SEP-1999 JP 2000570369
 PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
 JOAKIM LUNDBERG MATHIAS UHLEN
 PC C12N15/09,C12Q1/68 C12N15/00
 CC Description of Artificial Sequence: Synthetic oligonucleotide
FEATURES source
 1..5
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
 5 GGAGG 1

RESULT 8
LOCUS AX805860/c 5 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 6 from Patent WO03060163.
ACCESSION AX805860
VERSION AX805860.1 GI:38522771
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Eijk,M.J. and van Schaik,C.
TITLE Discrimination and detection of target nucleotide sequences using
 mass spectrometry
JOURNAL Patent: WO 03060163-A 6 24-JUL-2003;
 Keygene N.V. (NL)
FEATURES source
 1..5
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="stuffer sequence"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db |||||
 5 GGGAG 1

RESULT 9
LOCUS A93563/c 6 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9737040.
ACCESSION A93563

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|                       |                                                                                                                                                                                              |
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| JOURNAL               | Patent: WO 2003106674-A 267 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="oligonucleotide patterns over-represented in STAR elements" |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 1 GGAGG 5<br>                                                                                                                                                                                |
| Db                    | 5 GGAGG 1                                                                                                                                                                                    |
| RESULT 12             |                                                                                                                                                                                              |
| CQ755813/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755813 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 314 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755813                                                                                                                                                                                     |
| VERSION               | CQ755813.1 GI:44846618                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.                                                                                                                                                   |
| TITLE                 | Means and methods for regulating gene expression                                                                                                                                             |
| JOURNAL               | Patent: WO 2003106674-A 314 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="oligonucleotide patterns over-represented in STAR elements" |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 2 GGAGG 6<br>                                                                                                                                                                                |
| Db                    | 5 GGAGG 1                                                                                                                                                                                    |
| RESULT 13             |                                                                                                                                                                                              |
| CQ755818/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755818 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 319 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755818                                                                                                                                                                                     |
| VERSION               | CQ755818.1 GI:44846623                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.                                                                                                                                                   |
| TITLE                 | Means and methods for regulating gene expression                                                                                                                                             |
| JOURNAL               | Patent: WO 2003106674-A 319 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"                                                                       |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 2 GGAGG 6<br>                                                                                                                                                                                |
| Db                    | 5 GGAGG 1                                                                                                                                                                                    |
| RESULT 11             |                                                                                                                                                                                              |
| CQ755766/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755766 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 267 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755766                                                                                                                                                                                     |
| VERSION               | CQ755766.1 GI:44846571                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.                                                                                                                                                   |
| TITLE                 | Means and methods for regulating gene expression                                                                                                                                             |
| JOURNAL               | Patent: WO 2003106674-A 267 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="oligonucleotide patterns over-represented in STAR elements" |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 2 GGAGG 6<br>                                                                                                                                                                                |
| Db                    | 6 GGAGG 2                                                                                                                                                                                    |
| RESULT 10             |                                                                                                                                                                                              |
| CQ755704/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755704 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 205 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755704                                                                                                                                                                                     |
| VERSION               | CQ755704.1 GI:44846509                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.                                                                                                                                                   |
| TITLE                 | Means and methods for regulating gene expression                                                                                                                                             |
| JOURNAL               | Patent: WO 2003106674-A 205 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="oligonucleotide patterns over-represented in STAR elements" |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 2 GGAGG 6<br>                                                                                                                                                                                |
| Db                    | 6 GGAGG 2                                                                                                                                                                                    |
| RESULT 11             |                                                                                                                                                                                              |
| CQ755766/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755766 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 267 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755766                                                                                                                                                                                     |
| VERSION               | CQ755766.1 GI:44846571                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.                                                                                                                                                   |
| TITLE                 | Means and methods for regulating gene expression                                                                                                                                             |
| JOURNAL               | Patent: WO 2003106674-A 267 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32644"                                                                       |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 2 GGAGG 6<br>                                                                                                                                                                                |
| Db                    | 6 GGAGG 2                                                                                                                                                                                    |
| RESULT 10             |                                                                                                                                                                                              |
| CQ755704/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755704 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 205 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755704                                                                                                                                                                                     |
| VERSION               | CQ755704.1 GI:44846509                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.                                                                                                                                                   |
| TITLE                 | Means and methods for regulating gene expression                                                                                                                                             |
| JOURNAL               | Patent: WO 2003106674-A 205 24-DEC-2003;<br>Chromagenics B.V. (NL)                                                                                                                           |
| FEATURES              | Location/Qualifiers<br>1..6<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="oligonucleotide patterns over-represented in STAR elements" |
| ORIGIN                |                                                                                                                                                                                              |
| Query Match           | 83.3%; Score 5; DB 6; Length 6;                                                                                                                                                              |
| Best Local Similarity | 100.0%; Pred.No. 8.1e+09;                                                                                                                                                                    |
| Matches               | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                           |
| QY                    | 2 GGAGG 6<br>                                                                                                                                                                                |
| Db                    | 6 GGAGG 2                                                                                                                                                                                    |
| RESULT 11             |                                                                                                                                                                                              |
| CQ755766/c            |                                                                                                                                                                                              |
| LOCUS                 | CQ755766 6 bp DNA linear PAT 01-MAR-2004                                                                                                                                                     |
| DEFINITION            | Sequence 267 from Patent WO2003106674.                                                                                                                                                       |
| ACCESSION             | CQ755766                                                                                                                                                                                     |
| VERSION               | CQ755766.1 GI:44846571                                                                                                                                                                       |
| KEYWORDS              | .                                                                                                                                                                                            |
| SOURCE                | synthetic construct                                                                                                                                                                          |
| ORGANISM              | other sequences; artificial sequences.                                                                                                                                                       |
| REFERENCE             | 1                                                                                                                                                                                            |
| AUTHORS               | Otte,A.P., Kruckeberg,A.L. and Satijn,D                                                                                                                                                      |



/note="oligonucleotide patterns over-represented in STAR elements"

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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
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Qy 1 GGGAG 5
Db 6 GGGAG 2

RESULT 14
CQ756128/c
LOCUS CQ756128 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 629 from Patent WO2003106674.
ACCESSION CQ756128
VERSION CQ756128.1 GI:44846933
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
 other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 629 24-DEC-2003;
 Chromagenics B.V. (NL)
FEATURES Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAG 6
Db 6 GGGAG 2

RESULT 15
CQ757942/c
LOCUS CQ757942 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 246 from Patent WO2003106684.
ACCESSION CQ757942
VERSION CQ757942.1 GI:44847963
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
 other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 246 24-DEC-2003;
 Chromagenics B.V. (NL)
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
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Qy 1 GGGAG 5
Db 5 GGGAG 1

RESULT 16
CQ758004/c
LOCUS CQ758004 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 308 from Patent WO2003106684.
ACCESSION CQ758004
VERSION CQ758004.1 GI:44848025
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
 other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 308 24-DEC-2003;
 Chromagenics B.V. (NL)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAG 6
Db 5 GGGAG 1

RESULT 17
CQ758051/c
LOCUS CQ758051 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 355 from Patent WO2003106684.
ACCESSION CQ758051
VERSION CQ758051.1 GI:44848072
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
 other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 355 24-DEC-2003;
 Chromagenics B.V. (NL)
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RESULT 18
LOCUS CQ758056/c
DEFINITION Sequence 360 from Patent WO2003106684.
ACCESSION CQ758056
VERSION CQ758056.1 GI:44848077
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
JOURNAL vectors and cells for use therein
 Patent: WO 2003106684-A 360 24-DEC-2003;
 Chromagenics B.V. (NL)
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DB 6 GGAG 2

RESULT 19
LOCUS CQ758366/c
DEFINITION Sequence 670 from Patent WO2003106684.
ACCESSION CQ758366
VERSION CQ758366.1 GI:44848387
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
JOURNAL vectors and cells for use therein
 Patent: WO 2003106684-A 670 24-DEC-2003;
 Chromagenics B.V. (NL)
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QY 2 GGAGG 6
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DB 6 GGAGG 2

RESULT 20
LOCUS E08990
DEFINITION Oligo DNA modified to inhibit HIV proliferation.
ACCESSION E08990

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VERSION E08990.1 GI:22024628
KEYWORDS JP 1995087982-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 6)
AUTHORS Furukawa,H., Momota,K., Hotoda,H., Koizumi,M. and Kaneko,M.
TITLE MODIFIED OLIGODEOXYRIBONUCLEOTIDE
JOURNAL Patent: JP 1995087982-A 1 04-APR-1995;
 SANKYO CO LTD
COMMENT OS None
 OC Artificial sequences.
 PN JP 1995087982-A/1
 PD 04-APR-1995
 PF 31-JAN-1994 JP 1994009772
 PR 23-JAN-1993 JP 93P 13509, 10-JUN-1993 JP 93P 138517 PI
 FURUKAWA HIDEHIKO, MOMOTA KENJI, HOTODA HITOSHI, PI KOIZUMI
 MAKOTO,
 PI KANEKO MASAKATSU
 PC C12N15/11,A61K31/70,C07H21/04;
 CC strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FH source 1..6
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 FT tg9gc, tg9gt'.
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
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DB 2 GGAG 6

RESULT 21
LOCUS E09173
DEFINITION Synthetic oligonucleotides for anti-HIV agent.
ACCESSION E09173
VERSION E09173.1 GI:22025799
KEYWORDS JP 1995118289-A/15.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 6)
AUTHORS Azuma,T., Momota,K. and Furukawa,H.
TITLE OLIGODEOXYNUCLEOTIDE BOUND WITH SHORT PHOSPHOROTHIOATE
JOURNAL Patent: JP 1995118289-A 15 09-MAY-1995;
 SANKYO CO LTD
COMMENT OS None

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OC Artificial sequences.  
 PN JP 1995118289-A/15  
 PD 09-MAY-1995  
 PF 19-OCT-1993 JP 1993260581  
 PI AZUMA TOSHINORI, MOMOTA KENJI, FURUKAWA HIDEHIKO PC  
 C07H21/04/A61K31/70;  
 CC strandedness: Single;  
 CC topology: Linear;  
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 QY 1 GGGAG 5  
 DB 1  
 2 GGGAG 6  
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 E09489  
 LOCUS  
 DEFINITION  
 Phosphorothioate-bound oligodeoxynucleotide which inhibits HIV-1 growth.  
 E09489.1 GI:22026116  
 JP 1995157498-A/15.  
 unclassified  
 ORGANISM  
 unclassified.  
 REFERENCE  
 1 (bases 1 to 6)  
 Azuma,T., Momota,K. and Furukawa,H.  
 SHORT-CHAIN OLIGODEOXYNUCLEOTIDE BONDED THROUGH PHOSPHOROTHIOATE LINKAGES  
 Patent: JP 1995157498-A 15 20-JUN-1995;  
 SANKYO CO LTD  
 OS None  
 OC Artificial sequences.  
 PN JP 1995157498-A/15  
 PD 20-JUN-1995  
 PF 07-DEC-1993 JP 1993306213  
 PI AZUMA TOSHINORI, MOMOTA KENJI, FURUKAWA HIDEHIKO PC  
 C07H21/04,A61K31/70,C12N15/09;  
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 DB 2 GGGAG 6  
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 AX093419  
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 Sequence 1 from Patent WO0118195.  
 AX093419  
 ACCESSION  
 VERSION  
 AX093419.1 GI:13509869  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE  
 1 (bases 1 to 6)  
 Francis,K.P., Contag,P.R. and Joh,D.J.  
 TITLE  
 Luciferase expression cassettes and methods of use  
 JOURNAL  
 Patent: WO 0118195-A 1 15-MAR-2001;  
 Xenogen Corporation (US)  
 FEATURES  
 Location/Qualifiers  
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 DB 2 GGGAG 6  
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 AX175283  
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 DEFINITION  
 Sequence 47 from Patent WO0144465.  
 AX175283  
 ACCESSION  
 VERSION  
 AX175283.1 GI:14598651  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE  
 1 (bases 1 to 6)  
 Phillips,N.C. and Fillion,M.C.  
 TITLE  
 Therapeutically useful synthetic oligonucleotides  
 JOURNAL  
 Patent: WO 0144465-A 47 21-JUN-2001;  
 Bioniche Life Sciences Inc. (CA)  
 FEATURES  
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 QY 2 GGGAG 6  
 DB 1 GGGAG 5  
 RESULT 25

AX361080  
LOCUS AX361080 6 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 1 from Patent WO0208431.  
ACCESSION AX361080  
VERSION AX361080.1 GI:18693739  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Francis, K.P. and Purchio, A.P.  
TITLE Compositions and methods for use thereof in modifying the genomes of microorganisms  
JOURNAL Patent: WO 0208431-A 1 31-JAN-2002;  
Xenogen Corporation (US)  
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source Location/Qualifiers  
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Db 2 GGAGG 6  
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AX391507  
LOCUS AX391507 6 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 1 from Patent EP1184462.  
ACCESSION AX391507  
VERSION AX391507.1 GI:19700115  
KEYWORDS  
SOURCE Staphylococcus aureus  
ORGANISM Staphylococcus aureus  
REFERENCE 1  
AUTHORS Fan, F.G., He, Y.G., Huang, J.G., Jiang, X.G., Mcdevitt, D.G.,  
Rosenberg, M.G. and St John, A.G.  
TITLE Identification of targets of antimicrobial compounds  
JOURNAL Patent: EP 1184462-A 1 06-MAR-2002;  
SmithKline Beecham Corporation (US); SMITHKLINE BEECHAM PLC (GB)  
FEATURES  
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RESULT 27  
AX574433  
LOCUS AX574433 6 bp mRNA linear PAT 07-JAN-2003  
DEFINITION Sequence 5 from Patent WO02068629.  
ACCESSION AX574433  
VERSION AX574433.1 GI:27551757  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

unclassified.  
REFERENCE 1  
AUTHORS Pachuk, C.J. and McCallus, D.E.  
TITLE Dna constructs for cytoplasmic and mitochondrial expression and methods of making and using same  
JOURNAL Patent: WO 02068629-A 5 06-SEP-2002;  
Wyeth (US)  
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AX764742/c  
LOCUS AX764742 6 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 212 from Patent WO03004704.  
ACCESSION AX764742  
VERSION AX764742.1 GI:32258950  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Otte, A.P. and Kruckeberg, A.L.  
TITLE Dna sequences comprising gene transcription regulatory qualities and methods for detecting and using such dna sequences  
JOURNAL Patent: WO 03004704-A 212 16-JAN-2003;  
Chromagenics B.V. (NL)  
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LOCUS AX764804 6 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 274 from Patent WO03004704.  
ACCESSION AX764804  
VERSION AX764804.1 GI:32259012  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Otte, A.P. and Kruckeberg, A.L.  
TITLE Dna sequences comprising gene transcription regulatory qualities and methods for detecting and using such dna sequences  
JOURNAL Patent: WO 03004704-A 274 16-JAN-2003;

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Chromagenics B.V. (NL)
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LOCUS
 DEFINITION
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 ACCESSION
 AX764851
 VERSION
 AX764851.1 GI:32259059
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 AUTHORS
 Otte,A.P. and Kruckeberg,A.L.
 TITLE
 Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 JOURNAL
 Patent: WO 03004704-A 321 16-JAN-2003;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 00:00:54 ; Search time 710.6 Seconds  
(without alignments)  
53.568 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 gscggg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

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Post-processing: Minimum Match 0%

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Listing first 100 summaries

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- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 1          | 6     | 100.0       | 6      | 9  | US-09-735-363A-43    |
| 2          | 6     | 100.0       | 6      | 9  | US-09-879-668-15     |
| 3          | 6     | 100.0       | 6      | 15 | US-10-280-274-15     |
| 4          | 6     | 100.0       | 6      | 18 | US-10-420-513A-4     |
| 5          | 6     | 100.0       | 6      | 19 | US-10-716-029-169    |
| 6          | 5     | 83.3        | 5      | 13 | US-10-027-632-175366 |
| 7          | 5     | 83.3        | 5      | 13 | US-10-027-632-175371 |

|   |    |                      |      |   |      |                   |
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| 5 | 17 | US-10-027-632-175366 | 83.3 | 5 | 83.3 | Sequence 175366,  |
| 5 | 17 | US-10-027-632-175371 | 83.3 | 5 | 83.3 | Sequence 175371,  |
| 6 | 15 | US-10-269-790-14     | 83.3 | 5 | 83.3 | Sequence 14, Appl |
| 6 | 15 | US-10-269-790-14     | 83.3 | 5 | 83.3 | Sequence 14, Appl |
| 6 | 16 | US-10-187-264A-109   | 83.3 | 5 | 83.3 | Sequence 109, App |
| 6 | 16 | US-10-306-522-109    | 83.3 | 5 | 83.3 | Sequence 109, App |
| 6 | 16 | US-10-190-312A-198   | 83.3 | 5 | 83.3 | Sequence 198, App |
| 6 | 16 | US-10-190-312A-204   | 83.3 | 5 | 83.3 | Sequence 204, App |
| 6 | 16 | US-10-190-312A-204   | 83.3 | 5 | 83.3 | Sequence 204, App |
| 6 | 16 | US-10-190-312A-219   | 83.3 | 5 | 83.3 | Sequence 219, App |
| 6 | 16 | US-10-190-312A-220   | 83.3 | 5 | 83.3 | Sequence 220, App |
| 6 | 16 | US-10-190-312A-230   | 83.3 | 5 | 83.3 | Sequence 230, App |
| 6 | 16 | US-10-190-312A-275   | 83.3 | 5 | 83.3 | Sequence 275, App |
| 6 | 16 | US-10-190-312A-282   | 83.3 | 5 | 83.3 | Sequence 282, App |
| 6 | 16 | US-10-190-312A-332   | 83.3 | 5 | 83.3 | Sequence 332, App |
| 6 | 16 | US-10-190-312A-385   | 83.3 | 5 | 83.3 | Sequence 385, App |
| 6 | 16 | US-10-190-312A-385   | 83.3 | 5 | 83.3 | Sequence 385, App |
| 6 | 16 | US-10-190-312A-412   | 83.3 | 5 | 83.3 | Sequence 412, App |
| 6 | 16 | US-10-190-312A-531   | 83.3 | 5 | 83.3 | Sequence 531, App |
| 6 | 18 | US-10-719-493-109    | 83.3 | 5 | 83.3 | Sequence 109, App |
| 6 | 19 | US-10-666-022-14     | 83.3 | 5 | 83.3 | Sequence 14, Appl |
| 6 | 19 | US-10-666-022-14     | 83.3 | 5 | 83.3 | Sequence 14, Appl |
| 6 | 19 | US-10-627-331-109    | 83.3 | 5 | 83.3 | Sequence 109, App |
| 6 | 19 | US-10-296-085A-78    | 83.3 | 5 | 83.3 | Sequence 78, Appl |
| 6 | 19 | US-10-296-085A-79    | 83.3 | 5 | 83.3 | Sequence 79, Appl |
| 6 | 21 | US-10-627-413-109    | 83.3 | 5 | 83.3 | Sequence 109, App |
| 6 | 21 | US-10-921-086-109    | 83.3 | 5 | 83.3 | Sequence 109, App |
| 6 | 9  | US-09-735-363A-28    | 73.3 | 6 | 4.4  | Sequence 28, Appl |
| 6 | 9  | US-09-735-363A-46    | 73.3 | 6 | 4.4  | Sequence 46, Appl |
| 6 | 9  | US-09-879-668-8      | 73.3 | 6 | 4.4  | Sequence 8, Appl  |
| 6 | 9  | US-09-879-668-18     | 73.3 | 6 | 4.4  | Sequence 18, Appl |
| 6 | 9  | US-09-824-346-6      | 73.3 | 6 | 4.4  | Sequence 6, Appl  |
| 6 | 9  | US-09-728-574-20     | 73.3 | 6 | 4.4  | Sequence 20, Appl |
| 6 | 9  | US-09-728-574-21     | 73.3 | 6 | 4.4  | Sequence 21, Appl |
| 6 | 15 | US-10-280-274-8      | 73.3 | 6 | 4.4  | Sequence 8, Appl  |
| 6 | 15 | US-10-280-274-18     | 73.3 | 6 | 4.4  | Sequence 18, Appl |
| 6 | 16 | US-10-076-047A-133   | 73.3 | 6 | 4.4  | Sequence 133, App |
| 6 | 16 | US-10-240-305-12     | 73.3 | 6 | 4.4  | Sequence 12, Appl |
| 6 | 16 | US-10-109-363-5      | 73.3 | 6 | 4.4  | Sequence 5, Appl  |
| 6 | 16 | US-10-190-312A-201   | 73.3 | 6 | 4.4  | Sequence 201, App |
| 6 | 16 | US-10-190-312A-238   | 73.3 | 6 | 4.4  | Sequence 238, App |
| 6 | 17 | US-10-190-312A-680   | 73.3 | 6 | 4.4  | Sequence 680, App |
| 6 | 17 | US-10-182-329-4      | 73.3 | 6 | 4.4  | Sequence 4, Appl  |
| 6 | 18 | US-10-420-513A-7     | 73.3 | 6 | 4.4  | Sequence 7, Appl  |
| 6 | 19 | US-10-071-411-61     | 73.3 | 6 | 4.4  | Sequence 61, Appl |
| 6 | 19 | US-10-716-029-165    | 73.3 | 6 | 4.4  | Sequence 165, App |
| 6 | 21 | US-10-914-799-61     | 73.3 | 6 | 4.4  | Sequence 61, Appl |
| 6 | 21 | US-10-686-317-34     | 66.7 | 4 | 66.7 | Sequence 34, Appl |
| 4 | 19 | US-10-686-317-34     | 66.7 | 4 | 66.7 | Sequence 34, Appl |
| 5 | 13 | US-10-027-632-175366 | 66.7 | 4 | 66.7 | Sequence 175366,  |
| 5 | 13 | US-10-027-632-175371 | 66.7 | 4 | 66.7 | Sequence 175371,  |
| 5 | 17 | US-10-027-632-175366 | 66.7 | 4 | 66.7 | Sequence 175366,  |
| 5 | 17 | US-10-027-632-175371 | 66.7 | 4 | 66.7 | Sequence 175371,  |
| 5 | 19 | US-10-681-818-218    | 66.7 | 4 | 66.7 | Sequence 218, App |
| 5 | 19 | US-10-681-818-218    | 66.7 | 4 | 66.7 | Sequence 218, App |
| 5 | 20 | US-10-483-538-22     | 66.7 | 4 | 66.7 | Sequence 22, Appl |
| 5 | 20 | US-10-483-538-22     | 66.7 | 4 | 66.7 | Sequence 22, Appl |
| 5 | 20 | US-10-483-538-23     | 66.7 | 4 | 66.7 | Sequence 23, Appl |
| 6 | 8  | US-08-887-505-109    | 66.7 | 4 | 66.7 | Sequence 109, App |
| 6 | 9  | US-09-735-363A-43    | 66.7 | 4 | 66.7 | Sequence 43, Appl |
| 6 | 9  | US-09-785-269-16     | 66.7 | 4 | 66.7 | Sequence 16, Appl |
| 6 | 9  | US-09-785-269-16     | 66.7 | 4 | 66.7 | Sequence 16, Appl |
| 6 | 9  | US-09-785-269-18     | 66.7 | 4 | 66.7 | Sequence 18, Appl |
| 6 | 9  | US-09-785-269-18     | 66.7 | 4 | 66.7 | Sequence 18, Appl |
| 6 | 10 | US-09-879-668-15     | 66.7 | 4 | 66.7 | Sequence 15, Appl |
| 6 | 10 | US-09-220-794-11     | 66.7 | 4 | 66.7 | Sequence 11, Appl |
| 6 | 10 | US-09-731-289B-4     | 66.7 | 4 | 66.7 | Sequence 4, Appl  |
| 6 | 10 | US-09-731-289B-4     | 66.7 | 4 | 66.7 | Sequence 4, Appl  |
| 6 | 10 | US-09-798-883B-36    | 66.7 | 4 | 66.7 | Sequence 36, Appl |
| 6 | 10 | US-09-798-883B-36    | 66.7 | 4 | 66.7 | Sequence 36, Appl |
| 6 | 10 | US-09-326-883-36     | 66.7 | 4 | 66.7 | Sequence 36, Appl |

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c 82 4 66.7 6 10 US-09-947-209A-11 Sequence 11, Appl
c 83 4 66.7 6 10 US-09-947-209A-11 Sequence 11, Appl
c 84 4 66.7 6 12 US-09-989-933-5 Sequence 5, Appl
c 85 4 66.7 6 12 US-09-989-933-5 Sequence 5, Appl
c 86 4 66.7 6 15 US-10-099-379-11 Sequence 11, Appl
c 87 4 66.7 6 15 US-10-099-379-11 Sequence 11, Appl
c 88 4 66.7 6 15 US-10-280-274-15 Sequence 15, Appl
c 89 4 66.7 6 16 US-10-076-047A-134 Sequence 134, App
c 90 4 66.7 6 16 US-10-187-284A-109 Sequence 109, App
c 91 4 66.7 6 16 US-10-402-100-11 Sequence 11, Appl
c 92 4 66.7 6 16 US-10-402-100-11 Sequence 11, Appl
c 93 4 66.7 6 16 US-10-306-522-109 Sequence 109, App
c 94 4 66.7 6 16 US-10-190-312A-186 Sequence 186, App
c 95 4 66.7 6 16 US-10-190-312A-186 Sequence 186, App
c 96 4 66.7 6 16 US-10-190-312A-186 Sequence 186, App
c 97 4 66.7 6 16 US-10-190-312A-198 Sequence 198, App
c 98 4 66.7 6 16 US-10-190-312A-199 Sequence 199, App
c 99 4 66.7 6 16 US-10-190-312A-203 Sequence 203, App
c 100 4 66.7 6 16 US-10-190-312A-209 Sequence 209, App

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## ALIGNMENTS

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RESULT 1
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; Sequence 43, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-43

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Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCCGG 6
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Db 1 GGCCGG 6

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RESULT 2
US-09-879-668-15
; Sequence 15, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925

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; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-15

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Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCCGG 6
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Db 1 GGCCGG 6

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RESULT 3
US-10-280-274-15
; Sequence 15, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-15

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Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCCGG 6
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Db 1 GGCCGG 6

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RESULT 4
US-10-420-513A-4
; Sequence 4, Application US/10420513A
; Publication No. US2004005883A1
; GENERAL INFORMATION:

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; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fallon, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US/10/420,513A
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-420-513A-4

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Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCGG 6
Db 1 GGCCGG 6

RESULT 5
US-10-716-029-169
; Sequence 169, Application US/10716029
; Publication No. US20040171038A1
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Duff, Gordon
; APPLICANT: Korman, Kenneth
; APPLICANT: Kolpin, Maryam R
; APPLICANT: Hsieh, Chung-Ming
; APPLICANT: Govindaraju, Raju
; APPLICANT: Aziz, Nazneen
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-716-029-169

Query Match 100.0%; Score 6; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCGG 6
Db 1 GGCCGG 6

RESULT 6
US-10-027-632-175366
; Sequence 175366, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175366
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175366

Query Match 83.3%; Score 5; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
Db 1 GGCCG 5

RESULT 7
US-10-027-632-175371
; Sequence 175371, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175371
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175371

Query Match 83.3%; Score 5; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
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Db 1 GGCCG 5
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; SEQ ID NO 175371
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175371

Query Match 83.3%; Score 5; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 175371
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175371

QY 1 GGCCG 5
|||||
Db 1 GGCCG 5

RESULT 10
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; Sequence 14, Application US/10269790
; Publication No. US20030148335A1
; GENERAL INFORMATION:
; APPLICANT: Super Array, Inc.
; APPLICANT: Shen, Li
; APPLICANT: Cen, Hui
; APPLICANT: Yu, Xiang
; TITLE OF INVENTION: DETECTING TARGETS BY UNIQUE IDENTIFIER
; FILE REFERENCE: 49444-20003.00
; CURRENT APPLICATION NUMBER: US/10/269,790
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/327,763
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence for Spacer C accessory region
US-10-269-790-14

Query Match 83.3%; Score 5; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence for Spacer C accessory region
US-10-269-790-14

QY 1 GGCCG 5
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Db 2 GGCCG 6

RESULT 11
US-10-269-790-14/c
; Sequence 14, Application US/10269790
; Publication No. US20030148335A1
; GENERAL INFORMATION:
; APPLICANT: Super Array, Inc.
; APPLICANT: Shen, Li
; APPLICANT: Cen, Hui
; APPLICANT: Yu, Xiang
; TITLE OF INVENTION: DETECTING TARGETS BY UNIQUE IDENTIFIER
; FILE REFERENCE: 49444-20003.00
; CURRENT APPLICATION NUMBER: US/10/269,790
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/327,763
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence for Spacer C accessory region
US-10-269-790-14/c

Db 2 GGCCG 6

RESULT 8
US-10-027-632-175366
; Sequence 175366, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175366
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175366

Query Match 83.3%; Score 5; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 175366
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175366

QY 1 GGCCG 5
|||||
Db 1 GGCCG 5

RESULT 9
US-10-027-632-175371
; Sequence 175371, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175371
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175371
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; OTHER INFORMATION: Sequence for Spacer C accessory region  
US-10-269-790-14

Query Match 83.3%; Score 5; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGG 5  
| | | | |  
Db 5 GCCGG 1

## RESULT 12

US-10-187-264A-109

; Sequence 109, Application US/10187264A

; Publication No. US20030162734A1

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Klinman, Dennis

; APPLICANT: Steinberg, Alfred D.

; TITLE OF INVENTION: Methods for Treating and Preventing

; TITLE OF INVENTION: Infectious Disease

; FILE REFERENCE: C01039.70062.US

; CURRENT APPLICATION NUMBER: US/10/187,264A

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US 09/630,319

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 08/960,774

; PRIOR FILING DATE: 1997-10-30

; PRIOR APPLICATION NUMBER: US 08/738,652

; PRIOR FILING DATE: 1996-10-30

; PRIOR APPLICATION NUMBER: US 08/386,063

; PRIOR FILING DATE: 1995-02-07

; PRIOR APPLICATION NUMBER: US 08/276,358

; PRIOR FILING DATE: 1994-07-15

; NUMBER OF SEQ ID NOS: 124

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 109

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-187-264A-109

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
| | | | |  
Db 1 GCCGG 5

## RESULT 13

US-10-306-522-109

; Sequence 109, Application US/10306522

; Publication No. US20030191079A1

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Klinman, Dennis

; APPLICANT: Steinberg, Alfred D.

; TITLE OF INVENTION: Methods for Treating and Preventing

; TITLE OF INVENTION: Infectious Disease

; FILE REFERENCE: C01039.70062.US

; CURRENT APPLICATION NUMBER: US/10/306,522

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: US 09/630,319

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 08/960,774

; PRIOR FILING DATE: 1997-10-30

; PRIOR APPLICATION NUMBER: US 08/738,652

; PRIOR FILING DATE: 1996-10-30

; NUMBER OF SEQ ID NOS: 1079

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-187-264A-109

; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 109  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-306-522-109

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
| | | | |  
Db 1 GCCGG 5

## RESULT 14

US-10-190-312A-198/c

; Sequence 198, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; TITLE OF INVENTION: Methods for detecting and using such DNA sequences

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 198

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-198

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
| | | | |  
Db 5 GCCGG 1

## RESULT 15

US-10-190-312A-204

; Sequence 204, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; TITLE OF INVENTION: Methods for detecting and using such DNA sequences

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-204

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-204

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 16
US-10-190-312A-204/c
; Sequence 204, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-204

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 17
US-10-190-312A-219/c
; Sequence 219, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 219
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-219

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 5 GCCGG 1

RESULT 18
US-10-190-312A-220
; Sequence 220, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-220

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 2 GCCGG 6

RESULT 19
US-10-190-312A-230/c
; Sequence 230, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-230

Query Match 83.3%; Score 5; DB 16; Length 6;
```

Best Local Similarity 100.0%; Pred. No. 1.1e+09; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGG 5  
|||||

Db 5 GCCGG 1

RESULT 20  
US-10-190-312A-275/c  
; Sequence 275, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 275  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-275

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGG 5  
|||||

Db 6 GCCGG 2

RESULT 21  
US-10-190-312A-282/c  
; Sequence 282, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 282  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-282

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
|||||

Db 6 GCCGG 2

RESULT 22  
US-10-190-312A-332/c  
; Sequence 332, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 332  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-332

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
|||||

Db 6 GCCGG 2

RESULT 23  
US-10-190-312A-385  
; Sequence 385, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 385  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements  
US-10-190-312A-385

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
|||||

Db 1 GCCGG 5

RESULT 24  
US-10-190-312A-385/c

```
; Sequence 385, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 385
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-385

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 25
US-10-190-312A-412/c
; Sequence 412, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-412

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 5 GCCGG 1

RESULT 26
US-10-190-312A-531/c
; Sequence 531, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
```

```
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 531
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-531

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 5 GCCGG 1

RESULT 27
US-10-719-493-109
; Sequence 109, Application US/10719493
; Publication No. US20040087538A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT FILING DATE: 2003-11-21
; PRIOR FILING DATE: 1997-10-30
; PRIOR FILING DATE: 1996-10-30
; PRIOR FILING DATE: 1995-02-07
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-719-493-109

Query Match 83.3%; Score 5; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 28
US-10-666-022-14
; Sequence 14, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
```

```
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-14

Query Match 83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 29
US-10-666-022-14/c
; Sequence 14, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-14

Query Match 83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 30
US-10-627-331-109
; Sequence 109, Application US/10627331
; Publication No. US20040106586A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klimman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; TITLE OF INVENTION: Infectious Disease
; FILE REFERENCE: C01039.70062.US
```

```
; CURRENT APPLICATION NUMBER: US/10/627,331
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-627-331-109
```

```
Query Match 83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 GCCGG 6
Db 1 GCCGG 5
```

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Search completed: July 21, 2005, 07:13:21
Job time : 712.6 secs
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds  
(without alignments)  
172.240 Million cells

**Title:** US-09-735-363A-43

Perfect score: 6

Sequence: 1 ggccgg 6

Scoring table: IDENTITY NUC

scoring metric: identity\_nuc  
Gapop 10.0 ; Gapext 1.0

Searched: 1202784 seqs. 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

|         |    |     |         |   |
|---------|----|-----|---------|---|
| Minimum | DB | seq | length: | 0 |
| Maximum | DB | seq | length: | 6 |

Post-processing: Minimum March 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA:\*

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1: /cqn2 6/ptodata/1/ina/5A COMB.seq:*
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/pctus\_comb.seq:\*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query |       |        | DB | ID                | Description        |
|------------|-------|-------|--------|----|-------------------|--------------------|
|            | Score | Match | Length |    |                   |                    |
| 1          | 5     | 83.3  | 6      | 1  | US-07-627-538-1   | Sequence 1, Appli  |
| C 2        | 5     | 83.3  | 6      | 1  | US-07-627-538-1   | Sequence 1, Appli  |
| 3          | 5     | 83.3  | 6      | 1  | US-08-128-369-1   | Sequence 1, Appli  |
| C 4        | 5     | 83.3  | 6      | 1  | US-08-128-369-1   | Sequence 1, Appli  |
| 5          | 5     | 83.3  | 6      | 2  | US-08-692-825-24  | Sequence 24, Appl  |
| C 6        | 5     | 83.3  | 6      | 2  | US-08-692-825-24  | Sequence 24, Appl  |
| 7          | 5     | 83.3  | 6      | 3  | US-08-895-495-24  | Sequence 24, Appl  |
| C 8        | 5     | 83.3  | 6      | 3  | US-08-895-495-24  | Sequence 24, Appl  |
| 9          | 5     | 83.3  | 6      | 3  | US-09-337-619-109 | Sequence 109, Appl |
| 10         | 4.4   | 73.3  | 6      | 3  | US-08-920-422-15  | Sequence 15, Appl  |
| C 11       | 4.4   | 73.3  | 6      | 3  | US-08-920-422-15  | Sequence 15, Appl  |
| 12         | 4.4   | 73.3  | 6      | 3  | US-09-593-323-29  | Sequence 29, Appl  |
| C 13       | 4.4   | 73.3  | 6      | 3  | US-09-593-323-29  | Sequence 29, Appl  |
| 14         | 4.4   | 73.3  | 6      | 3  | US-09-344-300-29  | Sequence 29, Appl  |
| C 15       | 4.4   | 73.3  | 6      | 4  | US-09-324-346-6   | Sequence 6, Appli  |
| 16         | 4.4   | 73.3  | 6      | 4  | US-10-071-411A-61 | Sequence 61, Appl  |
| C 17       | 4.4   | 73.3  | 6      | 4  | US-09-483-184A-6  | Sequence 6, Appli  |
| 18         | 4     | 66.7  | 4      | 1  | US-08-169-950-6   | Sequence 6, Appli  |
| C 19       | 4     | 66.7  | 4      | 1  | US-08-169-950-6   | Sequence 6, Appli  |
| 20         | 4     | 66.7  | 4      | 1  | US-07-630-288A-14 | Sequence 14, Appl  |
| C 21       | 4     | 66.7  | 4      | 1  | US-07-630-288A-14 | Sequence 14, Appl  |
| 22         | 4     | 66.7  | 4      | 1  | US-08-468-049-14  | Sequence 14, Appl  |
| C 23       | 4     | 66.7  | 4      | 1  | US-08-468-049-14  | Sequence 14, Appl  |
| 24         | 4     | 66.7  | 4      | 3  | US-09-193-792-19  | Sequence 19, Appl  |
| C 25       | 4     | 66.7  | 4      | 3  | US-09-193-792-19  | Sequence 19, Appl  |
| 26         | 4     | 66.7  | 5      | 1  | US-08-357-399-2   | Sequence 2, Appli  |
| C 27       | 4     | 66.7  | 5      | 1  | US-08-357-399-2   | Sequence 2, Appli  |

## ALIGNMENTS

RESULT 1  
US-07-627-538-1  
; Sequence 1, Application US/07627538  
; Patent No. 5248600  
; GENERAL INFORMATION:  
; APPLICANT: Topal, Michael D.  
; APPLICANT: Conrad, Michael  
; TITLE OF INVENTION: Method of Cleaving DNA  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5248600th Carolina  
; COUNTRY: U.S.A.  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,538  
; FILING DATE: 19901214  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5052-24  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
US-07-627-538-1  
Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCCGG 6  
Db 1 GCCGG 5

RESULT 2  
US-07-627-538-1/c  
; Sequence 1, Application US/07627538  
; Patent No. 5248600  
; GENERAL INFORMATION:  
; APPLICANT: Topal, Michael D.  
; APPLICANT: Conrad, Michael  
; TITLE OF INVENTION: Method of Cleaving DNA  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5248600th Carolina  
; COUNTRY: U.S.A.

; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,538  
; FILING DATE: 19901214  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5052-24  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
US-07-627-538-1  
Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCCGG 6  
Db 6 GCCGG 2

RESULT 3  
US-08-128-369-1  
; Sequence 1, Application US/08128369  
; Patent No. 5418150  
; GENERAL INFORMATION:  
; APPLICANT: Topal, Michael D.  
; APPLICANT: Conrad, Michael J.  
; TITLE OF INVENTION: METHOD OF CLEAVING DNA  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Kenneth D. Sibley; Bell, Seltzer, Park and  
; ADDRESSEE: Gibson  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5418150th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/128,369  
; FILING DATE: 21-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5470-5A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-420-2200  
; TELEFAX: 919-881-3175  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-128-369-1
Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 4
US-08-128-369-1/c
; Sequence 1, Application US/08128369
; Patent No. 5418150
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael J.
; TITLE OF INVENTION: METHOD OF CLEAVING DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
; ADDRESSEE: Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5418150th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,369
; FILING DATE: 21-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-128-369-1
Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 5
US-08-692-825-24
; Sequence 24, Application US/08692825
; Patent No. 5858665
; GENERAL INFORMATION:
; APPLICANT: Hepp, Jozsef
; APPLICANT: Lengyel, Zsolt
; TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY
; TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; APPLICANT: Hepp, Jozsef
; APPLICANT: Lengyel, Zsolt
; TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY
; TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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/ SOFTWARE: FastSEQ for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/692,825  
/ FILING DATE: 25-JUL-1996  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Axford, Laurie A.  
/ REGISTRATION NUMBER: 35,053  
/ REFERENCE/DOCKET NUMBER: 32260-20002.00  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-813-5600  
/ TELEFAX: 415-494-0792  
/ TELEX: 706141  
/ INFORMATION FOR SEQ ID NO: 24:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-692-825-24

Query Match 83.3%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
Db 6 GCCGG 2

## RESULT 7

US-08-895-495-24  
/ Sequence 24, Application US/08895495  
/ Patent No. 6114117  
/ GENERAL INFORMATION:  
/ APPLICANT: Hepp, Jozsef  
/ APPLICANT: Lengyel, Zsolt  
/ TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY  
/ TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL  
/ NUMBER OF SEQUENCES: 40  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: MORRISON & FOERSTER  
/ STREET: 755 PAGE MILL ROAD  
/ CITY: Palo Alto  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 94304-1018  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSEQ for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/895,495  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Axford, Laurie A.  
/ REGISTRATION NUMBER: 35,053  
/ REFERENCE/DOCKET NUMBER: 32260-20002.20  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-813-5600  
/ TELEFAX: 415-494-0792  
/ TELEX: 706141  
/ INFORMATION FOR SEQ ID NO: 24:

/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-895-495-24

Query Match 83.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
Db 1 GCCGG 5

## RESULT 8

US-08-895-495-24/c  
/ Sequence 24, Application US/08895495  
/ Patent No. 6114117  
/ GENERAL INFORMATION:  
/ APPLICANT: Hepp, Jozsef  
/ APPLICANT: Lengyel, Zsolt  
/ APPLICANT: Pande, Rajiv  
/ TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY  
/ TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL  
/ NUMBER OF SEQUENCES: 40  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: MORRISON & FOERSTER  
/ STREET: 755 PAGE MILL ROAD  
/ CITY: Palo Alto  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 94304-1018  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSEQ for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/895,495  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Axford, Laurie A.  
/ REGISTRATION NUMBER: 35,053  
/ REFERENCE/DOCKET NUMBER: 32260-20002.20  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-813-5600  
/ TELEFAX: 415-494-0792  
/ TELEX: 706141  
/ INFORMATION FOR SEQ ID NO: 24:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-895-495-24

Query Match 83.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
Db 6 GCCGG 2

## RESULT 9

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US-09-337-619-109
; Sequence 109, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; TITLE OF INVENTION: Immunostimulatory Oligonucleotides
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-109

Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCCG 6
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Db 1 GCCCG 5

RESULT 10
US-08-920-422-15
; Sequence 15, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-920-422-15

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
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Db 1 GGCCGG 6

RESULT 11
US-08-920-422-16/c
; Sequence 16, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-920-422-16

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
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Db 1 GGCCGG 6

RESULT 12
US-09-593-323-29
; Sequence 29, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/593,323
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
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Db 1 GGCCGG 6

RESULT 13
US-09-594-108-29
; Sequence 29, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
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Db 1 GGCCGG 6

RESULT 14
US-09-594-108-29
; Sequence 29, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
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Db 1 GGCCGG 6
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; PRIOR APPLICATION NUMBER: 09/344,300  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6  
|||  
Db 1 GGCCGG 6

RESULT 14  
US-09-344-300-29  
; Sequence 29, Application US/09344300B  
; Patent No. 6297013  
; GENERAL INFORMATION:  
; APPLICANT: Morgan, Antony R.  
; APPLICANT: Severini, Alberto  
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity  
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of  
; TITLE OF INVENTION: Transcription  
; FILE REFERENCE: DNAB-02921  
; CURRENT APPLICATION NUMBER: US/09/344,300B  
; CURRENT FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-344-300-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6  
|||  
Db 1 GGCCGG 6

RESULT 15  
US-09-924-346-6  
; Sequence 6, Application US/09924346  
; Patent No. 6555674  
; GENERAL INFORMATION:  
; APPLICANT: Jens Tornoe  
; TITLE OF INVENTION: The Jet Promoter  
; FILE REFERENCE: 19313-005  
; CURRENT APPLICATION NUMBER: US/09/924,346  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/224,087  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chemically

; OTHER INFORMATION: Synthesized  
US-09-924-346-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6  
|||  
Db 1 GGCCGG 6

RESULT 16  
US-10-071-411A-61  
; Sequence 61, Application US/10071411A  
; Patent No. 6797475  
; GENERAL INFORMATION:  
; APPLICANT: Glenn Barnes  
; APPLICANT: Joanne Meyer  
; TITLE OF INVENTION: Detection of Polymorphisms in the Human  
; TITLE OF INVENTION: 5-Lipoxygenase Gene  
; FILE REFERENCE: MRI-021  
; CURRENT APPLICATION NUMBER: US/10/071,411A  
; CURRENT FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 60/267,515  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/314,248  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-071-411A-61

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6  
|||  
Db 1 GGCCGG 6

RESULT 17  
US-09-483-184A-6/c  
; Sequence 6, Application US/09483184A  
; Patent No. 6800750  
; GENERAL INFORMATION:  
; APPLICANT: DARTMOUTH COLLEGE  
; APPLICANT: CRAIG, Ruth W.  
; APPLICANT: BINGLE, Colin D.  
; APPLICANT: WHYTE, Moira  
; TITLE OF INVENTION: Mcl-1 GENE REGULATORY ELEMENTS AND A PRO-APOPTOTIC Mcl-1 VARIANT  
; FILE REFERENCE: DART1110-1  
; CURRENT APPLICATION NUMBER: US/09/483,184A  
; CURRENT FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: US 60/166,113  
; PRIOR FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide for PCR  
US-09-483-184A-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6  
|||  
Db 6 GGCCGG 1

## RESULT 18

US-08-169-950-6  
; Sequence 6, Application US/08169950  
; Patent No. 5366882  
; GENERAL INFORMATION:  
; APPLICANT: LUNNEN, KEITH D.  
; APPLICANT: WILSON, GEOFFREY G.  
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BGLI  
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/169,950  
; FILING DATE: 17-DEC-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 43959  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match 66.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
|||  
Db 1 GGCC 4

## RESULT 19

US-08-169-950-6/c  
; Sequence 6, Application US/08169950  
; Patent No. 5366882  
; GENERAL INFORMATION:  
; APPLICANT: LUNNEN, KEITH D.  
; APPLICANT: WILSON, GEOFFREY G.  
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BGLI  
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 WATER STREET

; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/169,950  
; FILING DATE: 17-DEC-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 43959  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match 66.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
|||  
Db 4 GGCC 1

## RESULT 20

US-07-630-288A-14  
; Sequence 14, Application US/07630288A  
; Patent No. 5472840  
; GENERAL INFORMATION:  
; APPLICANT: Stefano, James E.  
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
; TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Joanne M. Gieser  
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
; CITY: Naperville  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60563  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/630,288A  
; FILING DATE: 17-DEC-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/370,218  
; FILING DATE: 06-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/252,243  
; FILING DATE: 30-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gieser, Joanne M.  
; REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-14

Query Match 66.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
Db 1 GGCC 4

## RESULT 21

US-07-630-288A-14/c  
Sequence 14, Application US/07630288A  
Patent No. 5472840

## GENERAL INFORMATION:

APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/630,288A

FILING DATE: 17-DEC-1990

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218

FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/252,243

FILING DATE: 30-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Gieser, Joanne M.

REGISTRATION NUMBER: 32,938

REFERENCE/DOCKET NUMBER: 58190 2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-07-630-288A-14

Query Match 66.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
Db 4 GGCC 1

## RESULT 22

US-08-468-049-14

Sequence 14, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,049

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/630,288

FILING DATE: 17-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218

FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/252,243

FILING DATE: 30-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: No. 5763171val B. Galloway

REGISTRATION NUMBER: 33,595

REFERENCE/DOCKET NUMBER: CN 581903

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-468-049-14

Query Match 66.7%; Score 4; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
Db 1 GGCC 4

## RESULT 23

US-08-468-049-14/c

Sequence 14, Application US/08468049



Patent No. 5763171  
; GENERAL INFORMATION:  
; APPLICANT: Stefano, James E.  
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
; TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5763171val B. Galloway  
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
; CITY: Naperville  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60563  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,049  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/630,288  
; FILING DATE: 17-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/370,218  
; FILING DATE: 06-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/252,243  
; FILING DATE: 30-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5763171val B. Galloway  
; REGISTRATION NUMBER: 33,595  
; REFERENCE/DOCKET NUMBER: CN 581903  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 717-2443  
; TELEFAX: (708) 717-2430  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-468-049-14

Query Match 66.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
DB 4 GGCC 1

RESULT 24  
US-09-193-792-19  
; Sequence 19, Application US/09193792B  
; Patent No. 6180344  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Bin  
; TITLE OF INVENTION: 5( Upstream Region Sequences of the MYOD1 Gene  
; TITLE OF INVENTION: and Uses Thereof  
; FILE REFERENCE: D6015  
; CURRENT APPLICATION NUMBER: US/09/193,792B  
; CURRENT FILING DATE: 1998-11-17  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 20  
; SEQ ID NO 19

Query Match 66.7%; Score 4; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6  
DB 1 CCGG 4

RESULT 25  
US-09-193-792-19/c  
; Sequence 19, Application US/09193792B  
; Patent No. 6180344  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Bin  
; TITLE OF INVENTION: 5( Upstream Region Sequences of the MYOD1 Gene  
; TITLE OF INVENTION: and Uses Thereof  
; FILE REFERENCE: D6015  
; CURRENT APPLICATION NUMBER: US/09/193,792B  
; CURRENT FILING DATE: 1998-11-17  
; PRIOR APPLICATION NUMBER: US 60/065,113  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 20  
; SEQ ID NO 19

Query Match 66.7%; Score 4; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6  
DB 4 CCGG 1

RESULT 26  
US-08-357-399-2/c  
; Sequence 2, Application US/08357399  
; Patent No. 5536821  
; GENERAL INFORMATION:  
; APPLICANT: Agrawal, Sudhir  
; APPLICANT: Tang, Jin-Yan  
; TITLE OF INVENTION: Site-Specific Functionalization of  
; TITLE OF INVENTION: Oligodeoxynucleotides for  
; TITLE OF INVENTION: No. 5536821-Radioactive Labelling  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lappin & Kusmer  
; STREET: 200 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/357,399  
; FILING DATE: 16-DEC-1994

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206175  
FILING DATE: 03-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-014CPDV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-357-399-2

Query Match 66.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 GCCG 5  
Db 4 GCCG 1

RESULT 27  
US-08-357-666-2/c  
Sequence 2, Application US/08357666  
Patent No. 5541306  
GENERAL INFORMATION:  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: Site-Specific Functionalization of  
TITLE OF INVENTION: Oligodeoxynucleotides for  
TITLE OF INVENTION: Oligodeoxynucleotides for  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/357,666  
FILING DATE: 16-DEC-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206175  
FILING DATE: 03-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-014CPDV1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-357-666-2

Query Match 66.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 GCCG 5  
Db 4 GCCG 1

RESULT 28  
US-08-206-175-2/c  
Sequence 2, Application US/08206175  
Patent No. 5563253  
GENERAL INFORMATION:  
APPLICANT: Agrawal, Sudhir and  
APPLICANT: Jin-Yan Tang  
TITLE OF INVENTION: Site-Specific Functionalization of  
TITLE OF INVENTION: Oligodeoxynucleotides for  
TITLE OF INVENTION: No. 5563253-Radioactive Labelling  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206,175  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-014 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-206-175-2

Query Match 66.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 GCCG 5  
Db 4 GCCG 1

RESULT 29  
US-08-795-876-19  
Sequence 19, Application US/08795876  
Patent No. 6403305

GENERAL INFORMATION:  
APPLICANT: Gershengorn, Marvin C.  
ATTORNEY/AGENT INFORMATION:  
NAME: Geras-Raaka, Elizabeth  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/1280  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-795-876-19

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/795,876  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/1280  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-795-876-19

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCG 5  
DB 2 GCQG 5

RESULT 30  
US-08-169-950-4  
Sequence 4, Application US/08169950  
Patent No. 5366882  
GENERAL INFORMATION:  
APPLICANT: LUNNEN, KEITH D.  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, GEOFFREY G.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/1280  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-795-876-19

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/169,950

FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43959  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-169-950-4

Query Match 66.7%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4  
DB 2 GGCC 5

Search completed: July 21, 2005, 04:29:25  
Job time : 59 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds  
(without alignments)  
169.325 Million cell updates/sec

Title: US-09-735-363A-43  
Perfect score: 6  
Sequence: 1 gscgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

- EST:\*
- 1: gb\_est1:\*
  - 2: gb\_est2:\*
  - 3: gb\_hic:\*
  - 4: gb\_est3:\*
  - 5: gb\_est4:\*
  - 6: gb\_est5:\*
  - 7: gb\_est6:\*
  - 8: gb\_gss1:\*
  - 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| C 1        | 5     | 83.3        | 5      | 7  | CN612621 CsgEST00  |
| C 2        | 5     | 83.3        | 5      | 7  | CN612715 CsgEST00  |
| C 3        | 5     | 83.3        | 6      | 6  | CA851141 D10E10 J1 |
| C 4        | 5     | 83.3        | 6      | 7  | CR787556 DXFZp469C |
| C 5        | 4     | 66.7        | 5      | 7  | CF307095 HDAL--05- |
| C 6        | 4     | 66.7        | 5      | 7  | CN612621 CsgEST00  |
| C 7        | 4     | 66.7        | 5      | 7  | CN612715 CsgEST00  |
| C 8        | 4     | 66.7        | 6      | 6  | CA850792 D06E12 E1 |
| C 9        | 4     | 66.7        | 6      | 6  | CA850792 D06E12 E1 |
| C 10       | 4     | 66.7        | 6      | 6  | CA851141 D10E10 J1 |
| C 11       | 4     | 66.7        | 6      | 7  | CR787556 DXFZp469C |
| C 12       | 3.4   | 56.7        | 5      | 7  | CF327761 NACL--02- |
| C 13       | 3.4   | 56.7        | 5      | 7  | CF339974 RCL1--07- |
| C 14       | 3.4   | 56.7        | 5      | 7  | CF340386 RCL1--07- |
| C 15       | 3.4   | 56.7        | 5      | 7  | CF340514 RCL1--08- |
| C 16       | 3.4   | 56.7        | 6      | 7  | CF339116 RCL1--03- |
| C 17       | 3.4   | 56.7        | 6      | 7  | CF340012 RCL1--06- |
| C 18       | 3.4   | 56.7        | 6      | 7  | CF340239 RCL1--07- |
| C 19       | 3.4   | 56.7        | 6      | 7  | CF921483 gmhrRw3-  |
| C 20       | 3     | 50.0        | 3      | 5  | BX266151 BX266151  |
| C 21       | 3     | 50.0        | 3      | 5  | BX266151 BX266151  |
| C 22       | 3     | 50.0        | 3      | 5  | BX267257 BX267257  |
| C 23       | 3     | 50.0        | 3      | 5  | BX267257 BX267257  |
| C 24       | 3     | 50.0        | 3      | 7  | CF292073 14ROOT--0 |

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| C 25 | 3 | 50.0 | 3 | 7 | CF292073 14ROOT--0 |
| C 26 | 3 | 50.0 | 3 | 7 | CF306332 HDAL--03- |
| C 27 | 3 | 50.0 | 3 | 7 | CF306332 HDAL--03- |
| C 28 | 3 | 50.0 | 3 | 7 | CF306493 HDAL--04- |
| C 29 | 3 | 50.0 | 3 | 7 | CF306493 HDAL--04- |
| C 30 | 3 | 50.0 | 3 | 7 | CF306655 HDAL--04- |
| C 31 | 3 | 50.0 | 3 | 7 | CF306655 HDAL--04- |
| C 32 | 3 | 50.0 | 3 | 7 | CF306732 HDAL--04- |
| C 33 | 3 | 50.0 | 3 | 7 | CF306732 HDAL--04- |
| C 34 | 3 | 50.0 | 3 | 7 | CF306759 HDAL--04- |
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| C 36 | 3 | 50.0 | 3 | 7 | CF306836 HDAL--04- |
| C 37 | 3 | 50.0 | 3 | 7 | CF306836 HDAL--04- |
| C 38 | 3 | 50.0 | 3 | 7 | CF306855 HDAL--05- |
| C 39 | 3 | 50.0 | 3 | 7 | CF306855 HDAL--05- |
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| C 43 | 3 | 50.0 | 3 | 7 | CF306921 HDAL--05- |
| C 44 | 3 | 50.0 | 3 | 7 | CF306992 HDAL--05- |
| C 45 | 3 | 50.0 | 3 | 7 | CF306992 HDAL--05- |
| C 46 | 3 | 50.0 | 3 | 7 | CF307052 HDAL--05- |
| C 47 | 3 | 50.0 | 3 | 7 | CF307052 HDAL--05- |
| C 48 | 3 | 50.0 | 3 | 7 | CF307058 HDAL--05- |
| C 49 | 3 | 50.0 | 3 | 7 | CF307058 HDAL--05- |
| C 50 | 3 | 50.0 | 3 | 7 | CF307069 HDAL--05- |
| C 51 | 3 | 50.0 | 3 | 7 | CF307069 HDAL--05- |
| C 52 | 3 | 50.0 | 3 | 7 | CF307073 HDAL--05- |
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| C 56 | 3 | 50.0 | 3 | 7 | CF307117 HDAL--05- |
| C 57 | 3 | 50.0 | 3 | 7 | CF307117 HDAL--05- |
| C 58 | 3 | 50.0 | 3 | 7 | CF307203 HDAL--06- |
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| C 60 | 3 | 50.0 | 3 | 7 | CF307223 HDAL--06- |
| C 61 | 3 | 50.0 | 3 | 7 | CF307223 HDAL--06- |
| C 62 | 3 | 50.0 | 3 | 7 | CF307246 HDAL--06- |
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| C 64 | 3 | 50.0 | 3 | 7 | CF307290 HDAL--06- |
| C 65 | 3 | 50.0 | 3 | 7 | CF307290 HDAL--06- |
| C 66 | 3 | 50.0 | 3 | 7 | CF307313 HDAL--06- |
| C 67 | 3 | 50.0 | 3 | 7 | CF307313 HDAL--06- |
| C 68 | 3 | 50.0 | 3 | 7 | CF307367 HDAL--06- |
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| C 70 | 3 | 50.0 | 3 | 7 | CF307404 HDAL--06- |
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| C 72 | 3 | 50.0 | 3 | 7 | CF307480 HDAL--06- |
| C 73 | 3 | 50.0 | 3 | 7 | CF307480 HDAL--06- |
| C 74 | 3 | 50.0 | 3 | 7 | CF307489 HDAL--06- |
| C 75 | 3 | 50.0 | 3 | 7 | CF307489 HDAL--06- |
| C 76 | 3 | 50.0 | 3 | 7 | CF307511 HDAL--06- |
| C 77 | 3 | 50.0 | 3 | 7 | CF307511 HDAL--06- |
| C 78 | 3 | 50.0 | 3 | 7 | CF307516 HDAL--06- |
| C 79 | 3 | 50.0 | 3 | 7 | CF307516 HDAL--06- |
| C 80 | 3 | 50.0 | 3 | 7 | CF307535 HDAL--06- |
| C 81 | 3 | 50.0 | 3 | 7 | CF307535 HDAL--06- |
| C 82 | 3 | 50.0 | 3 | 7 | CF920868 gmhrRw3-  |
| C 83 | 3 | 50.0 | 3 | 7 | CF920868 gmhrRw3-  |
| C 84 | 3 | 50.0 | 3 | 7 | CF921385 gmhrRw3-  |
| C 85 | 3 | 50.0 | 3 | 7 | CF921385 gmhrRw3-  |
| C 86 | 3 | 50.0 | 3 | 9 | CL423550 01S0557-0 |
| C 87 | 3 | 50.0 | 3 | 9 | CL423550 01S0557-0 |
| C 88 | 3 | 50.0 | 4 | 6 | CA853244 B06A04.se |
| C 89 | 3 | 50.0 | 4 | 6 | CA853244 B06A04.se |
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| C 91 | 3 | 50.0 | 4 | 7 | CF298748 7LEAF--02 |
| C 92 | 3 | 50.0 | 4 | 7 | CF306914 HDAL--05- |
| C 93 | 3 | 50.0 | 4 | 7 | CF306914 HDAL--05- |
| C 94 | 3 | 50.0 | 5 | 7 | CF282401 14ETL--09 |
| C 95 | 3 | 50.0 | 5 | 7 | CF282401 14ETL--09 |
| C 96 | 3 | 50.0 | 5 | 7 | CF307095 HDAL--05- |
| C 97 | 3 | 50.0 | 5 | 7 | CF307095 HDAL--05- |

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 99 3 50.0 5 7 CF323326 HDN--03-I  
 c 100 3 50.0 5 7 CF323326 HDN--03-I

ALIGNMENTS

RESULT 1  
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 DEFINITION CsgEST00264 Culicoides sonorensis female salivary gland cDNA  
 library Culicoides sonorensis cDNA, mRNA sequence.  
 ACCESSION CN612621  
 VERSION CN612621.1 GI:47120661  
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 SOURCE Culicoides sonorensis  
 ORGANISM Culicoides sonorensis  
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 Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;  
 Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.  
 1 (bases 1 to 5)  
 REFERENCE Campbell,C.L., Vandyke,K., Letchworth,G.J. and Wilson,W.C.  
 Expressed sequence tags from Culicoides sonorensis adult female  
 salivary glands  
 Unpublished (2004)  
 JOURNAL Arthropod-borne Animal Diseases Research Lab  
 COMMENT College of Agriculture, Dept. 3354, 1000 E. University Ave.,  
 Laramie, WY 82071, USA  
 Tel: 307 766 3626  
 Fax: 307 766 3500  
 Email: camcorey@uwo.edu.  
 Location/Qualifiers  
 1..5  
 /organism="Culicoides sonorensis"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:179676"  
 /sex="female"  
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 cDNA Library"

Query Match 83.3%; Score 5; DB 7; Length 5;  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5  
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 Db 5 GGCCG 1

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 /tissue\_type="salivary gland"  
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 /clone\_lib="Culicoides sonorensis female salivary gland  
 cDNA Library"

ORIGIN  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5  
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 Db 5 GGCCG 1

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 DEFINITION CA851141  
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 cDNA clone D10E10 5', mRNA sequence.  
 ACCESSION CA851141  
 VERSION CA851141.1 GI:33387934  
 KEYWORDS EST:  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 6)  
 REFERENCE Alkharouf,N.W., Khan,R. and Matthews,B.F.  
 AUTHORS Analysis of expressed sequence tags from roots of resistant soybean  
 TITLE infected by the soybean cyst nematode  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Alkharouf, N.W.  
 Soybean Genomics and Improvement Laboratory (SGLI)  
 US Department of Agriculture (USDA), ARS, PSI  
 Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
 USA  
 Tel: 301 504 5750  
 Fax: 301 504 5728  
 Email: alkharouf@ba.ars.usda.gov.  
 Location/Qualifiers  
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 /organism="Glycine max"  
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 /cultivar="Peking"  
 /db\_xref="taxon:3847"  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 5 GGCCG 1

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 DEFINITION CsgEST00395 Culicoides sonorensis female salivary gland cDNA  
 library Culicoides sonorensis cDNA, mRNA sequence.  
 ACCESSION CN612715  
 VERSION CN612715.1 GI:47120755  
 KEYWORDS EST:  
 SOURCE Culicoides sonorensis  
 ORGANISM Culicoides sonorensis  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;  
 Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.  
 1 (bases 1 to 5)  
 REFERENCE Campbell,C.L., Vandyke,K., Letchworth,G.J. and Wilson,W.C.  
 AUTHORS Expressed sequence tags from Culicoides sonorensis adult female  
 TITLE salivary glands

ORIGIN

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Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
Db 6 GGCCG 2

RESULT 4
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LOCUS 6 bp mRNA linear EST 01-OCT-2004
DEFINITION DKFZp469C0243_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
VERSION CR787556
KEYWORDS CR787556.1 GI:53706553
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
REFERENCE 1 (bases 1 to 6)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 1 (bases 1 to 6)
 Ansorge, W.; Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
 Mewes, H.W.; Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansorge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; riin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C0243
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES source
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 Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 GGCCG 1

RESULT 5
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LOCUS 5 bp mRNA linear EST 15-AUG-2003
DEFINITION HDAl-05-L19, g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA
 clone HDAl-05-L19, mRNA sequence.
 CF307095
 CF307095.1 GI:33678856
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 GGCCG 1

RESULT 6
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DEFINITION CsesEST00264 Culicoides sonorensis female salivary gland cDNA
 Library Culicoides sonorensis cDNA, mRNA sequence.
 CN612621
 CN612621.1 GI:47120661
 EST.
 Culicoides sonorensis
 Culicoides sonorensis
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
 1 (bases 1 to 5)
 Campbell, C.B., VanDyke, K., Letchworth, G.J. and Wilson, W.C.
 Expressed sequence tags from Culicoides sonorensis adult female
 salivary glands
 Unpublished (2004)
 Contact: Campbell, C.B. Diseases Research Lab
 Arthropod-borne Animal Diseases Research Lab
 Agricultural Research Service
 College of Agriculture, Dept. 3354, 1000 E. University Ave.,
 Laramie, WY 82071, USA
 Tel: 307 766 3626
 Fax: 307 766 3500
 Email: camcore@uwyo.edu.

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REFERENCE
AUTHORS Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 5)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm, B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 phage cDNA library I (HDAl)"
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 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
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 rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 66.7%; Score 4; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
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QY 2 GGCG 5
Db 5 GGCG 2

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCC 4
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Db 2 GGCC 5

RESULT 7
CN612715
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DEFINITION CsgEST00395 Culicoides sonorensis female salivary gland cDNA
ACCESSION CN612715.1 GI:47120755
VERSION
KEYWORDS
SOURCE
ORGANISM
Culicoides sonorensis
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
1 (bases 1 to 5)
Campbell,C.L., VanDyke,K., Letchworth,G.J. and Wilson,W.C.
Expressed sequence tags from Culicoides sonorensis adult female
salivary glands
Unpublished (2004)
Contact: Campbell, C.L.
Arthropod-borne Animal Diseases Research Lab
Agricultural Research Service
College of Agriculture, Dept. 3354, 1000 E. University Ave.,
Laramie, WY 82071, USA
Tel: 307 766 3626
Fax: 307 766 3500
Email: camcore@uwyo.edu.

FEATURES
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cDNA Library"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCC 4
 ||||
Db 2 GGCC 5

RESULT 8
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DEFINITION D06E12_E12_10.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION CA850792
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
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1..6
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/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06E12"
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/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCGG 6
 ||||
Db 1 CCGG 4

RESULT 9
CA850792/c
LOCUS
DEFINITION D06E12_E12_10.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION CA850792
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
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/organism="Glycine max"

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/db xref="taxon:3847"
/clone="D06E12"
/tissue_type="Roots"
/dev stage="Seedlings"
/clone lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match
Best Local Similarity 66.7%; Score 4; DB 6; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCC 6
Db 4 CGCC 1

RESULT 10
CA851141
LOCUS
DEFINITION
CA851141 6 bp mRNA linear EST 01-AUG-2003
CDNA clone D10E10 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
/clone lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
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1. .6
/organism="Glycine max"
/mol type="mRNA"
/cultivar="Peking"
/db xref="taxon:3847"
/clone="D10E10"
/tissue_type="Roots"
/dev stage="Seedlings"
/clone lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match
Best Local Similarity 66.7%; Score 4; DB 6; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
Db 3 GGCC 6

RESULT 11
CR787556
LOCUS

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DEFINITION
DKFZp469C0243_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469C0243 5', mRNA sequence.
CR787556
VERSION
KEYWORDS
SOURCE
ORGANISM
Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
1 (bases 1 to 6)
/clone lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@kfz-heidelberg.de; rlin, Germany. Please contact
RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C0243
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
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1. .6
/organism="Pongo pygmaeus"
/mol type="mRNA"
/db xref="taxon:9600"
/clone="DKFZp469C0243"
/tissue_type="kidney"
/dev stage="adult"
/lab host="DH10B"
/clone lib="469 (synonym: pkid1)"
/notes="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Query Match
Best Local Similarity 66.7%; Score 4; DB 7; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
Db 2 GGCC 5

RESULT 12
CF327761/c
LOCUS
DEFINITION
CF327761 5 bp mRNA linear EST 18-AUG-2003
NACL--02-G02.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--02-G02, mRNA
sequence.
CF327761
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 5)
/clone lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Nahn B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

```

```

FEATURES
source
 Location/Qualifiers
 1..5
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--02-G02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCG 5
 ||||
Db 5 GCGCG 1

RESULT 13
LOCUS CF339974
DEFINITION RCL1--06-118-g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-118,
mRNA sequence.
ACCESSION CF339974
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
 1..5
 /organism="Oryza sativa (japonica cultivar-group)"
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 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCG 6
 ||||
Db 1 GCTGG 5

RESULT 14
LOCUS CF340386
DEFINITION RCL1--07-N21-g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-N21,
mRNA sequence.
ACCESSION CF340386
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCG 6
 ||||
Db 1 GCTGG 5

RESULT 15
LOCUS CF340514
DEFINITION RCL1--08-E10-g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--08-E10,
mRNA sequence.
ACCESSION CF340514
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="RCL1--08-E10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCGG 6
 |||
DB 1 GCTGG 5

RESULT 16
LOCUS CF339116
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-N11,
mRNA sequence.
ACCESSION CF339116.1 GI:33826619
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="RCL1--03-N11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCGG 6
 |||
DB 1 GCTGG 5

RESULT 16
LOCUS CF339116
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-N11,
mRNA sequence.
ACCESSION CF339116.1 GI:33826619
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1..6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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/clone="RCL1--03-N11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCGG 6
 |||
DB 2 GCTGG 6

RESULT 17
LOCUS CF340012
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-K19,
mRNA sequence.
ACCESSION CF340012
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="RCL1--06-K19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCGG 6
 |||

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Db 2 GCTGG 6

RESULT 18
CF340239
LOCUS
DEFINITION
RCL1--07-G09.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-G09,
mRNA sequence.
ACCESSION
CF340239
VERSION
CF340239.1 GI:33828836
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1..6
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--07-G09"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCGG 6
 |||
 2 GCTGG 6

Db 2 GCTGG 6

RESULT 19
CF921483
LOCUS
DEFINITION
gmrRw3-09 H07.1.049 Soybean root hair subtracted cDNA library
gmrRw3 Glycine max cDNA, mRNA sequence.
ACCESSION
CF921483
VERSION
CF921483.1 GI:38192277
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
REFERENCE
AUTHORS
Scheffier,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

Expressed sequence tags from soybean root hair subtractive cDNA
library
Unpublished (2003)
Contact: Gary Stacey
University Of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: 17.

FEATURES
 Location/Qualifiers
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 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /tissue_type="root hairs"
 /clone_lib="Soybean root hair subtracted cDNA library
 gmrRw3"
 /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
 generated from soybean root hair tissue treated with
 Bradyrhizobium japonicum for 3 hours."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCGG 6
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 1 GCGGG 5

Db 1 GCGGG 5

RESULT 20
BX266151
LOCUS
DEFINITION
BX266151 AGENAE Gallus gallus multi-tissues normalized and
once-subtracted cDNA library (gcal) Gallus gallus cDNA clone
gcal0011c.i.02 3prim, mRNA sequence.
ACCESSION
BX266151
VERSION
BX266151.2 GI:47714113
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Chordata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3)
REFERENCE
AUTHORS
Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Piumi,F.,
Klopp,C. and Douaire,M.
TITLE
Construction and primary characterization of chicken normalized
multi-tissue cDNA libraries
JOURNAL
Unpublished (2003)
COMMENT
On Feb 27, 2003 this sequence version replaced gi:28588749.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0011 row: 1 column: 2
Seq primer: M13F.

FEATURES
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 /mol_type="mRNA"
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCG 5
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Db 1 CCG 3

RESULT 23
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LOCUS BX267257 3 bp mRNA linear EST 26-MAY-2004
DEFINITION BX267257 AGENAE Gallus gallus multi-tissues normalized and
once-subtracted cDNA library (gcail) Gallus gallus cDNA clone
gcail0011c.a.24 3prim, mRNA sequence.
ACCESSION BX267257
VERSION 2.2 GI:47714995
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 3)
AUTHORS Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Piumi,F.,
Klopp,C. and Douaire,M.
TITLE Construction and primary characterization of chicken normalized
multi-tissue cDNA libraries
JOURNAL Unpublished (2003)
COMMENT On Feb 27, 2003 this sequence version replaced gi:28589855.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@razhon.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0011 row: a column: 24
Seq primer: M13F.
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/organism="Gallus gallus"
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/lab_host="DH10B"
/clone_lib="AGENAE Gallus gallus multi-tissues normalized
and once-subtracted cDNA library (gcail)"
/note="Vector: pT7T3D-pac; tissues: adipose tissue, brain,
kidney, liver, multi-tissues, muscle, ovary, testis, bone
marrow, caecum, duodenum, embryos, fabricius gland,
granulosa, hypothalamus, ileon, jejunum, oviduct,
pancreas, skin, spleen, thymus, utero-vaginal gland,
pituitary gland, hematopoietic progenitor cells, small
follicle. Clone distribution : AGENAE Resource centre.
Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA
Radiobiologie et Brude du genome (LREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN
Query Match 50.0%; Score 3; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCG 6
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Db 3 CCG 1

RESULT 24
CF292073
LOCUS CF292073 3 bp mRNA linear EST 14-AUG-2003
DEFINITION CF292073 14ROOT--02-M03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA
sequence.
ACCESSION CF292073
VERSION 1.3 GI:33661106
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
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/tissue_type="root"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCC 4
 |||
Db 1 GCC 3

RESULT 25
CF292073/c
LOCUS CF292073 3 bp mRNA linear EST 14-AUG-2003
DEFINITION CF292073 14ROOT--02-M03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA
sequence.
ACCESSION CF292073
VERSION 1.3 GI:33661106
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 3)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

#### FEATURES

source

1..3  
Location/Qualifiers  
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/lab\_host="E.coli SOLR"  
/clone\_lib="OshDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

#### ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGC 3

|||

Db 1 GGC 3

#### RESULT 29

CF306493/C

LOCUS

DEFINITION HDAL--04-A07.g1 OshDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA clone HDAL--04-A07, mRNA sequence.

ACCESSION CF306493

VERSION CF306493.1 GI:33678254

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 3)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

#### FEATURES

source

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Location/Qualifiers  
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/mol\_type="mRNA"

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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OshDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

#### ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGC 4

|||

Db 3 GGC 1

#### RESULT 30

CF306655

LOCUS

DEFINITION HDAL--04-H21.g1 OshDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA clone HDAL--04-H21, mRNA sequence.

ACCESSION CF306655

VERSION CF306655.1 GI:33678416

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 3)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

#### FEATURES

source

1..3  
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDAL--04-H21"  
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/lab\_host="E.coli SOLR"  
/clone\_lib="OshDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

#### ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 GGC 3  
|||  
Db 1 GGC 3

Search completed: July 21, 2005, 01:54:37  
Job time : 1349.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds  
(without alignments)  
189.533 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 gcccgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
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| 1          | 5     | 83.3        | 6      | 12 | ADJ35370 Stabilisi  |
| 2          | 5     | 83.3        | 6      | 12 | ADJ35370 Stabilisi  |
| 3          | 5     | 83.3        | 6      | 12 | ADJ35397 Stabilisi  |
| 4          | 5     | 83.3        | 6      | 12 | ADJ35516 Stabilisi  |
| 5          | 5     | 83.3        | 6      | 12 | ADJ35516 Stabilisi  |
| 6          | 5     | 83.3        | 6      | 12 | ADN96880 Immunosti  |
| 7          | 5     | 83.3        | 6      | 12 | ADN96880 Immunosti  |
| 8          | 4.6   | 76.7        | 6      | 13 | ADN96880 Cpg oligo  |
| 9          | 4.6   | 76.7        | 6      | 13 | ADN96880 Human nic  |
| 10         | 4.6   | 76.7        | 6      | 13 | ADN96880 Human nic  |
| 11         | 4.6   | 76.7        | 6      | 13 | ADN96880 Human nic  |
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| 13         | 4.4   | 73.3        | 6      | 6  | ABK87321 Mammalian  |
| 14         | 4.4   | 73.3        | 6      | 6  | ABK87320 Mammalian  |
| 15         | 4.4   | 73.3        | 6      | 12 | ADJ35665 Stabilisi  |
| 16         | 4     | 66.7        | 6      | 1  | AAAN60771 Restricti |
| 17         | 4     | 66.7        | 6      | 1  | AAAN60771 Restricti |
| 18         | 4     | 66.7        | 6      | 2  | AAQ27868 Cfr91 rec  |
| 19         | 4     | 66.7        | 6      | 2  | AAQ27868 Cfr91 rec  |
| 20         | 4     | 66.7        | 6      | 2  | AAT80319 Oligo HCV  |

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| C | 25 | 4   | 66.7 | 6 | 2  | AAAX21981 | Hexamer O |
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| C | 27 | 4   | 66.7 | 6 | 6  | ABSF5903  | Inhibitor |
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| C | 30 | 4   | 66.7 | 6 | 8  | ACC69109  | Cucumber  |
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| C | 32 | 4   | 66.7 | 6 | 10 | ADN38330  | Immune mo |
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| C | 34 | 4   | 66.7 | 6 | 10 | ADN38329  | Immune mo |
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| C | 70 | 3.6 | 60.0 | 6 | 13 | ADR35722  | Human nic |
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| C | 76 | 3.6 | 60.0 | 6 | 13 | ADR35721  | Human nic |
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| C | 78 | 3.6 | 60.0 | 6 | 13 | ADR34423  | Human nic |
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| C | 81 | 3.6 | 60.0 | 6 | 13 | ADR34421  | Human nic |
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| C | 83 | 3.4 | 56.7 | 5 | 6  | ABT12403  | Orestes s |
| C | 84 | 3.4 | 56.7 | 5 | 8  | ABZ75669  | Helicase- |
| C | 85 | 3.4 | 56.7 | 5 | 8  | ABZ75665  | Helicase- |
| C | 86 | 3.4 | 56.7 | 5 | 8  | ABZ75667  | Helicase- |
| C | 87 | 3.4 | 56.7 | 5 | 8  | ABZ75663  | Helicase- |
| C | 88 | 3.4 | 56.7 | 5 | 10 | ACD91697  | Human col |
| C | 89 | 3.4 | 56.7 | 6 | 2  | AAQ35911  | Portion O |
| C | 90 | 3.4 | 56.7 | 6 | 2  | AAT80318  | Oligo HCV |
| C | 91 | 3.4 | 56.7 | 6 | 4  | AAQ06240  | PCR prime |
| C | 92 | 3.4 | 56.7 | 6 | 6  | ABSF5902  | Inhibitor |
| C | 93 | 3.4 | 56.7 | 6 | 6  | ABK88579  | Hepatitis |

94 3.4 56.7 6 8 ABZ75668 Helicase-  
 c 95 3.4 56.7 6 10 ADE38284 Immune mo  
 c 96 3.4 56.7 6 10 ADE38283 Immune mo  
 c 97 3.4 56.7 6 12 ADJ35778 Stabilisi  
 c 98 3.4 56.7 6 12 ADJ35694 Stabilisi  
 c 99 3.4 56.7 6 12 ADJ35808 Stabilisi  
 c 100 3.4 56.7 6 12 ADJ35483 Stabilisi

## ALIGNMENTS

RESULT 1  
 ID ADJ35370 standard; DNA; 6 BP.  
 XX AC ADJ35370;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Stabilising anti-repression, STAR, element dyad sequence #36.  
 XX KW STAR affiliated proteinaceous molecule; post translational modification;  
 XX KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX OS Unidentified.  
 XX PN WO2003106674-A2.  
 XX PD 24-DEC-2003.  
 XX PF 30-MAY-2003; 2003WO-NL000410.  
 XX PR 14-JUN-2002; 2002EP-00077344.  
 XX PA (CHRO-) CHROMAGENICS BV.  
 XX PI Otte AP, Kruckeberg AL, Satijn DPE;  
 XX DR WPI; 2004-082195/08.  
 XX PT Producing proteinaceous molecules in cells by selecting a cell, providing  
 a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti  
 -Repression sequence and expressing proteinaceous molecule.  
 XX PS Disclosure; Page 95; 177pp; English.

CC The invention relates to a method of producing a proteinaceous molecule  
 (I) in a cell comprising selecting a cell for its suitability for  
 producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 comprising a stabilising Anti-Repression (STAR) sequence, expressing the  
 resulting nucleic acid in the cell and collecting (I). The method is  
 useful for producing (I). A cell line (II) provided with a nucleic acid  
 comprising a STAR sequence is useful for producing (I). (II) Enables  
 production of affiliated proteinaceous molecule, as cell carries out  
 proper post-translational modifications of produced proteins. The present  
 sequence represents a stabilising anti-repression, STAR, element primer  
 dyad sequence.  
 XX SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 PS Disclosure; Page 95; 177pp; English.

CC The invention relates to a method of producing a proteinaceous molecule  
 (I) in a cell comprising selecting a cell for its suitability for  
 producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 comprising a stabilising Anti-Repression (STAR) sequence, expressing the  
 resulting nucleic acid in the cell and collecting (I). The method is  
 useful for producing (I). A cell line (II) provided with a nucleic acid  
 comprising a STAR sequence is useful for producing (I). (II) Enables  
 production of affiliated proteinaceous molecule, as cell carries out  
 proper post-translational modifications of produced proteins. The present  
 sequence represents a stabilising anti-repression, STAR, element primer  
 dyad sequence.

XX SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 5; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
 Db |||||  
 1 GCCGG 5

RESULT 2  
 ID ADJ35370/c  
 ADJ35370 standard; DNA; 6 BP.

XX AC ADJ35370;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Stabilising anti-repression, STAR, element dyad sequence #36.  
 XX KW STAR affiliated proteinaceous molecule; post translational modification;  
 XX KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX OS Unidentified.  
 XX PN WO2003106674-A2.  
 XX PD 24-DEC-2003.  
 XX PF 30-MAY-2003; 2003WO-NL000410.  
 XX PR 14-JUN-2002; 2002EP-00077344.  
 XX PA (CHRO-) CHROMAGENICS BV.  
 XX PI Otte AP, Kruckeberg AL, Satijn DPE;  
 XX DR WPI; 2004-082195/08.  
 XX PT Producing proteinaceous molecules in cells by selecting a cell, providing  
 a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti  
 -Repression sequence and expressing proteinaceous molecule.  
 XX PS Disclosure; Page 95; 177pp; English.

CC The invention relates to a method of producing a proteinaceous molecule  
 (I) in a cell comprising selecting a cell for its suitability for  
 producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 comprising a stabilising Anti-Repression (STAR) sequence, expressing the  
 resulting nucleic acid in the cell and collecting (I). The method is  
 useful for producing (I). A cell line (II) provided with a nucleic acid  
 comprising a STAR sequence is useful for producing (I). (II) Enables  
 production of affiliated proteinaceous molecule, as cell carries out  
 proper post-translational modifications of produced proteins. The present  
 sequence represents a stabilising anti-repression, STAR, element primer  
 dyad sequence.  
 XX SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 5; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6  
 Db |||||  
 6 GCCGG 2

RESULT 3  
 ID ADJ35397/c  
 ADJ35397 standard; DNA; 6 BP.

XX AC ADJ35397;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Stabilising anti-repression, STAR, element dyad sequence #63.  
 XX KW STAR affiliated proteinaceous molecule; post translational modification;  
 XX KW stabilising anti-repression; STAR; STAR element; ds; dyad.

XX OS Unidentified.  
 XX PN WO2003106674-A2.  
 XX PD 24-DEC-2003.

XX 30-MAY-2003; 2003WO-NL000410.  
 XX 14-JUN-2002; 2002EP-00077344.  
 XX (CHRO-) CHROMAGENICS BV.  
 XX Otte AP, Kruckeberg AL, Satijn DPE;  
 XX WPI; 2004-082195/08.  
 DR Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 XX  
 PS Disclosure; Page 96; 177pp; English.  
 CC The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 XX  
 SQ Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 5; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 2 GCCGG 6  
 DB |||||  
 5 GCCGG 1  
 RESULT 4  
 ID ADJ35516/c  
 AC ADJ35516;  
 XX 22-APR-2004 (first entry)  
 XX Stabilising anti-repression, STAR, element dyad sequence #182.  
 DE STAR affiliated proteinaceous molecule; post translational modification;  
 KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
 XX Unidentified.  
 OS  
 XX WO2003106674-A2.  
 PN 24-DEC-2003.  
 XX 30-MAY-2003; 2003WO-NL000410.  
 PF 14-JUN-2002; 2002EP-00077344.  
 XX (CHRO-) CHROMAGENICS BV.  
 XX Otte AP, Kruckeberg AL, Satijn DPE;  
 XX WPI; 2004-082195/08.  
 DR Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilising Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 XX

PS Disclosure; Page 98; 177pp; English.  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 XX  
 SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 5; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GCCGG 6  
 DB |||||  
 5 GCCGG 1  
 RESULT 5  
 ID ADN96880 standard; DNA; 6 BP.  
 AC ADN96880;  
 XX 26-AUG-2004 (first entry)  
 DE Immunostimulatory CpG oligonucleotide seqid 14.  
 XX  
 KW virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;  
 KW tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;  
 KW dermatological; bacterial growth inhibitor; immunostimulator;  
 KW immune response; immunostimulatory; opportunistic infection;  
 KW Leishmania infection; human immunodeficiency virus infection; AIDS;  
 KW viral infection; bacterial infection; fungal infection;  
 KW salmonellosis; syphilis; neurosyphilis; tuberculosis;  
 KW bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;  
 KW cryptococcal meningitis; hepatitis B; histoplasmosis; cryptosporidiosis;  
 KW isosporiasis; microsporidiosis; pneumocystis carinii pneumonia;  
 KW toxoplasmosis; cytomegalovirus; hepatitis; herpes simplex; herpes zoster;  
 KW human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;  
 KW progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;  
 KW systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;  
 KW HSV; genital herpes; HZV; shingles; genital wart; cervical cancer;  
 KW immunostimulatory CpG oligonucleotide; ss.  
 XX  
 OS Synthetic.  
 XX US2004105872-A1.  
 PN 03-JUN-2004.  
 XX 17-SEP-2003; 2003US-00666022.  
 PF 18-SEP-2002; 2002US-0411944P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Klimman DM, Verthelyi D;  
 XX WPI; 2004-419442/39.  
 XX Increasing an immune response to an opportunistic infection e.g.  
 PT bacterial infections in an immunocompromised subject involves  
 PT administering immunostimulatory D oligodeoxynucleotide or an  
 PT immunostimulatory K oligodeoxynucleotide.



KW systemic lupus erythematosus; sepsis; inflammatory bowel disease;  
 KW psoriasis; gingivitis; arthritis; Crohn's disease; Grave's disease;  
 KW cancer; viral; fungal; bacterial; parasitic; antineoplastic; antineoplastic;  
 KW dermatological; immunosuppressive; antibacterial; antiparasitic;  
 KW antiparasitic; antithyroid; cytostatic; virucide; fungicide;  
 KW antiparasitic; ss.  
 XX Synthetic.  
 OS  
 XX US2004106568-A1.  
 PN  
 XX 03-JUN-2004.  
 PD  
 XX  
 XX 25-JUL-2003; 2003US-00627331.  
 PF  
 XX 15-JUL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 30-OCT-1996; 96US-00738652.  
 PR 30-OCT-1997; 97US-00960774.  
 PR 31-JUL-2000; 2000US-00630319.  
 PR 02-JUL-2002; 2002US-00187489.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA  
 PI Krieg AM, Klinman D, Steinberg AD;  
 XX WPI; 2004-419485/39.  
 DR  
 XX New nucleic acid sequence containing unmethylated cytosine-guanine (CpG)  
 PT dinucleotide, useful for modulating immune response, e.g. stimulating Th1  
 PT pattern of immune activation, cytokine production, or B cell  
 PT proliferation.  
 PT  
 XX Disclosure; SEQ ID NO 109; 72pp; English.  
 PS  
 XX The present invention relates to oligonucleotide sequences containing at  
 CC least one unmethylated CpG dinucleotide that are able of modulating an  
 CC immune response such as stimulating T helper cell (Th) pattern of immune  
 CC activation, cytokine production, natural killer cell (NK) lytic activity,  
 CC and B cell proliferation in a subject, preferably human. The  
 CC immunostimulatory oligonucleotides of the invention are useful for  
 CC treating autoimmune disorders, autoimmune or other CpG associated  
 CC disorders (e.g. systemic lupus erythematosus, sepsis, inflammatory bowel  
 CC disease, psoriasis, gingivitis, arthritis, Crohn's disease, Grave's  
 CC disease), cancer, and viral, fungal, bacterial, and parasitic diseases.  
 CC The present sequence represents an unmethylated CpG dinucleotide  
 CC oligonucleotide that is tested for its ability to modulate an immune  
 CC response.  
 XX  
 SQ Sequence 6 BP; 0 A; 2 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 5; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GCCGG 6  
 Db 1 GCCGG 5  
 RESULT 8  
 ADR34424  
 ID ADR34424 standard; DNA; 6 BP.  
 XX ADR34424;  
 AC ADR34424;  
 XX 04-NOV-2004 (first entry)  
 DT Human nicking agent DNA containing BstNBI restriction site #844.  
 DE ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW

KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 XX Homo sapiens.  
 OS  
 XX WO2004067765-A2.  
 PN  
 XX 12-AUG-2004.  
 PD  
 XX 29-JAN-2004; 2004WO-US002720.  
 PF  
 XX 29-JAN-2003; 2003US-0443811P.  
 PR  
 XX (KECK-) KECK GRADUATE INST.  
 PA  
 XX Van Ness J, Galas DJ, Van Ness LK;  
 PI WPI; 2004-581010/56.  
 DR  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 PT  
 XX Example 3; Page 105-219; 238pp; English.  
 PS  
 XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring quality assurance/quality control of  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.

XX Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;  
 SQ  
 Query Match 76.7%; Score 4.6; DB 13; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 9.8e+08;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GCCGG 6  
 Db 2 GCCGG 6

RESULT 9  
 ADR34422  
 ID ADR34422 standard; DNA; 6 BP.  
 XX ADR34422;  
 AC ADR34422;  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX

DE Human nicking agent DNA containing BstNBI restriction site #842.  
XX  
XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
XX  
XX Homo sapiens.  
PN WO2004067765-A2.  
XX  
XX 12-AUG-2004.  
PD  
XX 29-JAN-2004; 2004WO-US002720.  
PF  
XX 29-JAN-2003; 2003US-0443811P.  
PR  
XX (KECK-) KECK GRADUATE INST.  
PA  
XX Van Ness J, Galas DJ, Van Ness LK;  
PI WPI; 2004-581010/56.  
XX  
XX Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
XX Example 3; Page 105-219; 238pp; English.  
PS  
XX The invention relates to a method of treating a nucleic acid sample with  
CC components under nicking conditions, where the components comprise a  
CC nicking agent, and the conditions cause the nicking agent to nick the  
CC nucleic acid sample to thus produce a family of initiating  
CC oligonucleotide fragments, and subjecting one or more members of the  
CC family of initiating oligonucleotide fragments to a characterization  
CC process to thus provide results. The method is useful for creating an  
CC assay panel of diagnostic oligonucleotides that can identify any organism  
CC or individual. The method is useful for characterizing other DNA  
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
CC The method, kit or composition is useful for identifying the source  
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
CC non-human animal or human. The method is particularly useful for rapidly  
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.  
CC It is especially useful for identifying different bacterial strains involved  
CC in e.g., nosocomial infections. Furthermore, the method is useful for  
CC diagnosing bacterial disease in plants and humans, monitoring for  
CC bacterial content and/or contamination in the environment, monitoring  
CC food for bacterial contamination, monitoring quality assurance/quality control of  
CC laboratory tests involving microbiological assays, tracing bacterial  
CC contamination and/or outbreaks of bacterial infections, genome mapping,  
CC monitoring bioremediation sites, and for monitoring agricultural sites  
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
CC restriction site and used in the method of the invention.  
XX  
XX Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;  
SQ  
Query Match 76.7%; Score 4.6; DB 13; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.8e+08;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCCGG 6  
DB 2 GCCSG 6  
|||:|  
|||:|  
RESULT 10  
ADR34423  
ID ADR34423 standard; DNA; 6 BP.  
XX  
XX AC ADR34423;

XX 04-NOV-2004 (first entry)  
DT Human nicking agent DNA containing BstNBI restriction site #843.  
XX  
XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
XX  
XX Homo sapiens.  
OS  
XX WO2004067765-A2.  
PN  
XX 12-AUG-2004.  
PD  
XX 29-JAN-2004; 2004WO-US002720.  
PF  
XX 29-JAN-2003; 2003US-0443811P.  
PR  
XX (KECK-) KECK GRADUATE INST.  
PA  
XX Van Ness J, Galas DJ, Van Ness LK;  
PI WPI; 2004-581010/56.  
XX  
XX Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
XX Example 3; Page 105-219; 238pp; English.  
PS  
XX The invention relates to a method of treating a nucleic acid sample with  
CC components under nicking conditions, where the components comprise a  
CC nicking agent, and the conditions cause the nicking agent to nick the  
CC nucleic acid sample to thus produce a family of initiating  
CC oligonucleotide fragments, and subjecting one or more members of the  
CC family of initiating oligonucleotide fragments to a characterization  
CC process to thus provide results. The method is useful for creating an  
CC assay panel of diagnostic oligonucleotides that can identify any organism  
CC or individual. The method is useful for characterizing other DNA  
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
CC The method, kit or composition is useful for identifying the source  
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
CC non-human animal or human. The method is particularly useful for rapidly  
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.  
CC It is especially useful for identifying different bacterial strains involved  
CC in e.g., nosocomial infections. Furthermore, the method is useful for  
CC diagnosing bacterial disease in plants and humans, monitoring for  
CC bacterial content and/or contamination in the environment, monitoring  
CC food for bacterial contamination, monitoring quality assurance/quality control of  
CC laboratory tests involving microbiological assays, tracing bacterial  
CC contamination and/or outbreaks of bacterial infections, genome mapping,  
CC monitoring bioremediation sites, and for monitoring agricultural sites  
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
CC restriction site and used in the method of the invention.  
XX  
XX Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;  
SQ  
Query Match 76.7%; Score 4.6; DB 13; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.8e+08;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCCGG 6  
DB 2 GCCSG 6  
|||:|  
|||:|  
RESULT 11  
ADR34421



ADR34421 standard; DNA; 6 BP.  
ADR34421;  
04-NOV-2004 (first entry)  
Human nicking agent DNA containing BstNBI restriction site #841.  
ss; nicking agent; assay panel; diagnosis; expression pattern;  
DNA fingerprinting; nosocomial infection; microbiological assay;  
bacterial contamination; genome mapping; bioremediation.  
Homo sapiens.  
WO2004067765-A2.  
12-AUG-2004.  
29-JAN-2004; 2004WO-US002720.  
29-JAN-2003; 2003US-0443811P.  
(KECK-) KECK GRADUATE INST.  
Van Ness J, Galas DJ, Van Ness LK;  
WPI; 2004-591010/56.  
Identifying nucleic acid sample source, useful for identifying bacterial strains involved in nosocomial infections, comprises treating the nucleic acid sample with components comprising a nicking agent under nicking conditions.  
Example 3; Page 105-219; 238pp; English.  
The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a nicking agent, and the conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating oligonucleotide fragments, and subjecting one or more members of the family of initiating oligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA molecules e.g., cDNA, and for characterizing cDNA expression patterns. The method, kit or composition is useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, non-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species, subspecies, and especially strains or individuals of the subspecies. It is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for bacterial content and/or contamination in the environment, monitoring food for bacterial contamination, monitoring quality assurance/control of bacterial contamination, monitoring quality assurance/control of laboratory tests involving microbiological assays, tracing bacterial contamination and/or outbreaks of bacterial infections, genome mapping, monitoring bioremediation sites, and for monitoring agricultural sites for test crops, bacteria and recombinant molecules. Sequences ADR33581-ADR37496 correspond to target nucleic acids containing an NBstNBI restriction site and used in the method of the invention.  
Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;  
Query Match 76.7%; Score 4.6; DB 13; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.8e+08;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCGCG 6  
Db 2 GCGSG 6

ADR34421 standard; DNA; 6 BP.  
AAF91686/c  
AAF91686;  
10-MAY-2001 (first entry)  
Breast-cancer associated protein isoform BPI-42 preferred probe #10.  
Human; breast cancer; breast cancer associated protein isoform; BPI;  
breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.  
Homo sapiens.  
WO200113117-A2.  
22-FEB-2001.  
14-AUG-2000; 2000WO-GB003143.  
13-AUG-1999; 99GB-00019258.  
30-MAR-2000; 2000GB-00007754.  
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Herath HMAG;  
WPI; 2001-211252/21.  
Screening, diagnosis or prognosis of breast cancer, by analyzing a sample of serum or plasma by two dimensional electrophoresis to detect the presence or level of a breast cancer-associated feature.  
Claim 152; Page 42; 146pp; English.  
The present invention describes a method for the screening, diagnosis or prognosis of breast cancer (BC), determining the stage or severity of BC, and monitoring the effect of therapy administered to a subject having BC, comprising analysing a sample of body fluid by two dimensional electrophoresis to generate a two-dimensional array of features, comprising a chosen feature whose relative abundance correlates with BC or predicts the onset of BC; and (b) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in the body fluid from one or more persons free from BC, or with a previously determined reference range for that feature in subjects free from BC, or with the abundance of an expression reference feature (ERF) in the test sample. The method is useful for screening, diagnosis or prognosis of breast cancer, determining the stage or severity of BC, monitoring the effect of therapy administered to a subject having BC, and for identifying a subject at risk of developing BC. AAB87186 to AAB87340 represents breast cancer associated protein isoform (BPI) peptide sequences, and AAF91643 to AAF91848 represent BPI probes used in the exemplification of the present invention  
Sequence 6 BP; 0 A; 5 C; 1 G; 0 T; 0 U; 0 Other;  
Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 9.8e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCGCG 6  
Db 6 GCGCG 1

RESULT 13  
ABR87321/c



XX Otte AP, Kruckeberg AL, Satijn DPE;  
 XX WPI; 2004-082195/08.  
 XX Producing proteinaceous molecules in cells by selecting a cell, providing  
 PT a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti  
 PT -Repression sequence and expressing proteinaceous molecule.  
 XX Disclosure; Page 101; 177pp; English.  
 XX The invention relates to a method of producing a proteinaceous molecule  
 CC (I) in a cell comprising selecting a cell for its suitability for  
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
 CC resulting nucleic acid in the cell and collecting (I). The method is  
 CC useful for producing (I). A cell line (II) provided with a nucleic acid  
 CC comprising a STAR sequence is useful for producing (I). (II) Enables  
 CC production of affiliated proteinaceous molecule, as cell carries out  
 CC proper post-translational modifications of produced proteins. The present  
 CC sequence represents a stabilising anti-repression, STAR, element primer  
 CC dyad sequence.  
 XX Sequence 6 BP; 0 A; 5 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 12; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.8e+08;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6  
 |||||  
 Db 6 GGCCGG 1

RESULT 16  
 AAN60771  
 ID AAN60771 standard; DNA; 6 BP.  
 XX AC AAN60771;  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 02-AUG-1991 (first entry)  
 XX Restriction endonuclease recognition site.  
 DE Restriction enzyme; recognition site; XcyI; ss DNA.  
 KW Xanthomonas campestris pv. cyanopsidis.  
 XX US4588689-A.  
 PN 13-MAY-1986.  
 XX 02-MAR-1984; 84US-00585752.  
 XX 02-MAR-1984; 84US-00585752.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Kado CI, Rodriguez RL, Froman BE, Tait RC;  
 PI WPI; 1986-143870/22.  
 XX New restriction endonuclease designated XcyI - isolated from Xanthomonas  
 PT cyanopsidis.  
 XX Claim 1; Page 4; 4pp; English.

XX The DNA sequence is the recognition site of a new restriction enzyme  
 CC XcyI. The enzyme cuts between the first and second C residues. The enzyme  
 CC is derived from X.cyanopsidis 13D5, ATCC 39587 using the rapid purificn.  
 CC method of Greene et al, Nucl. Acids Res. 1978; 5: 2373-80. The enzyme is

CC used for the manipulation and modification of DNA in vitro. The enzyme  
 CC can be obt'd. at a high degree of purity, free of contaminating exo- and  
 CC endonuclease activities. The enzyme is stable and can be stored for long  
 CC periods prior to use. XcyI is an isoschizomer of both XmaI and SmaI, and  
 CC shares a common cleavage pattern with XmaI. Optimal enzyme activity is at  
 CC 37 deg C. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-  
 CC OCT-2003 to standardise OS field)  
 XX Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6  
 |||||  
 Db 2 CCGG 5

RESULT 17  
 AAN60771/c  
 ID AAN60771 standard; DNA; 6 BP.  
 XX AC AAN60771;  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 02-AUG-1991 (first entry)  
 XX Restriction endonuclease recognition site.  
 DE Restriction enzyme; recognition site; XcyI; ss DNA.  
 KW Xanthomonas campestris pv. cyanopsidis.  
 XX US4588689-A.  
 PN 13-MAY-1986.  
 XX 02-MAR-1984; 84US-00585752.  
 XX 02-MAR-1984; 84US-00585752.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Kado CI, Rodriguez RL, Froman BE, Tait RC;  
 PI WPI; 1986-143870/22.  
 XX New restriction endonuclease designated XcyI - isolated from Xanthomonas  
 PT cyanopsidis.

XX Claim 1; Page 4; 4pp; English.

XX The DNA sequence is the recognition site of a new restriction enzyme  
 CC XcyI. The enzyme cuts between the first and second C residues. The enzyme  
 CC is derived from X.cyanopsidis 13D5, ATCC 39587 using the rapid purificn.  
 CC method of Greene et al, Nucl. Acids Res. 1978; 5: 2373-80. The enzyme is  
 CC used for the manipulation and modification of DNA in vitro. The enzyme  
 CC can be obt'd. at a high degree of purity, free of contaminating exo- and  
 CC endonuclease activities. The enzyme is stable and can be stored for long  
 CC periods prior to use. XcyI is an isoschizomer of both XmaI and SmaI, and  
 CC shares a common cleavage pattern with XmaI. Optimal enzyme activity is at  
 CC 37 deg C. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-  
 CC OCT-2003 to standardise OS field)  
 XX Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6

```

Db |||||
 5 CCGG 2

RESULT 18
AAQ27868
ID AAQ27868 standard; DNA; 6 BP.
XX
AC AAQ27868;
XX
DT 25-MAR-2003 (revised)
DT 12-FEB-1993 (first entry)
XX
DE Cfr91 recognition site.
XX
KW Restriction endonuclease; Cfr91; ds.
XX
OS Synthetic.
XX
PN DD299440-A5.
XX
PD 16-APR-1992.
XX
PF 29-JUN-1989; 89DD-00330100.
PR 29-JUN-1989; 89DD-00330100.
XX
PA (UYBE) UNIV BERLIN HUMBOLDT.
XX
PI Krueger D, Butkus V, Reuter M, Janulaitis A, Petrusyte M, Pein CD;
PI Hansen S, Cech D;
XX
DR WPI; 1992-301182/37.
XX
PT Rapid and complete degradation of DNA with restriction endonuclease - by
PT adding second DNA sequence contg. the appropriate recognition site, for
PT cleavage of phage, vector etc.
XX
PF Example 1; Page 2; 3pp; German.
XX
CC Example 1 illustrates that incompletely cleaved DNA mols. by particular
CC restriction endonucleases (RE) when using known methods, are completely
CC and rapidly degraded into specific fragments by adding a second DNA
CC species; Cfr91 recognises the sequence below which is present 3 times in
CC lambda phage, although even under optimum conditions only incomplete
CC restriction is achieved. A reaction mixt. was prepd. from 0.5 micromole
CC of the duplex given in AAQ27869, 2 microg lambda DNA and 5 units Cfr91 in
CC 20 microl buffer. After 1 hr at 37 degrees C, reaction was stopped and
CC the fragments sepd. by agarose gel electrophoresis. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6
Db |||||
5 CCGG 2

RESULT 20
AAT80319
ID AAT80319 standard; DNA; 6 BP.
XX
AC AAT80319;
XX
DT 16-OCT-1997 (first entry)
XX
DE Oligo HCV-215, targetted to HCV mRNA position +235 to +240.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..6
FT /*tag= a
FT /note= "Comprises phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002427.

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XX 06-JUN-1995; 95US-00471968.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PA carcinoma.
XX Claim 1; Page 18; 100pp; English.
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma
XX Claim 1; Page 18; 100pp; English.
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma
XX Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
Db ||||
3 CCGG 6
RESULT 21
AAT80319/C
ID AAT80319 standard; DNA; 6 BP.
XX AC AAT77251;
XX AC AAT77251;
XX 18-MAR-1998 (first entry)
XX Immunostimulatory polynucleotide 10.
XX Immunostimulatory polynucleotide; ISP; palindromic; vaccine;
KW immune response; antigen; naked gene expression vector; Ig; antibody;
KW immunotherapy; ss.
XX Synthetic.
XX WO9728259-A1.
XX 07-AUG-1997.
XX 28-JAN-1997; 97WO-US001277.
XX 30-JAN-1996; 96US-00593554.
XX (REGC) UNIV CALIFORNIA.
XX Carson DA, Raz E;
XX WPI; 1997-402613/37.
XX Recombinant vector containing immunostimulatory palindromic
PT polynucleotide - useful for selectively enhancing the TH1 immune response
PT in a host, whilst reducing the risk of anaphylaxis.
XX Claim 16; Page 15; 102pp; English.
XX This sequence represents a non-coding immunostimulatory polynucleotide
CC (ISP) comprised of at least one strand of a palindromic, which includes at
CC least one dinucleotide consisting of adjacent, unmethylated cytosine and
CC guanine residues. ISP's could be used in vaccination methods for
CC enhancing the immune response of a host to an antigen. Administration of
CC naked gene expression vectors which encode antigens or their
CC immunostimulatory fragments suppresses IgE antibody production reducing
CC the risk of anaphylaxis posed by conventional immunotherapy
```

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XX 06-JUN-1995; 95US-00471968.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PA carcinoma.
XX Claim 1; Page 18; 100pp; English.
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma
XX Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
Db ||||
3 CCGG 6
RESULT 21
AAT80319/C
ID AAT80319 standard; DNA; 6 BP.
XX AC AAT80319;
XX 16-OCT-1997 (first entry)
XX Oligo HCV-215, targetted to HCV mRNA position +235 to +240.
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..6
FT /*tag= a
FT /note= "Comprises phosphorothioate linkages"
XX WO9639500-A2.
XX 12-DEC-1996.
XX 04-JUN-1996; 96WO-EP002427.
XX 06-JUN-1995; 95US-00471968.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
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XX SQ Sequence 6 BP; 1 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
DB 2 CCGG 5

RESULT 23
AAT77251/c
ID AAT77251 standard; DNA; 6 BP.
XX AC AAT77251;
XX DT 18-MAR-1998 (first entry)
XX DE Immunostimulatory polynucleotide 10.
XX KW Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
XX KW immune response; antigen; naked gene expression vector; Igs; antibody;
XX KW immunotherapy; ss.
XX OS Synthetic.
XX PN WO9728259-A1.
XX PD 07-AUG-1997.
XX PF 28-JAN-1997; 97WO-US001277.
XX PR 30-JAN-1996; 96US-00593554.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Carson DA, Raz E;
XX WPI; 1997-402613/37.
XX SQ Recombinant vector containing immunostimulatory palindromic
PT polynucleotide - useful for selectively enhancing the TH1 immune response
PT in a host, whilst reducing the risk of anaphylaxis.
XX PS Claim 16; Page 15; 102pp; English.
XX CC This sequence represents a non-coding immunostimulatory polynucleotide
CC (ISP) comprised of at least one strand of a palindrome, which includes at
CC least one dinucleotide consisting of adjacent, unmethylated cytosine and
CC guanine residues. ISP's could be used in vaccination methods for
CC enhancing the immune response of a host to an antigen. Administration of
CC naked gene expression vectors which encode antigens or their
CC immunostimulatory fragments suppresses IGE antibody production reducing
CC the risk of anaphylaxis posed by conventional immunotherapy
XX SQ Sequence 6 BP; 1 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
DB 5 CCGG 2

RESULT 24
AAX21981
ID AAX21981 standard; DNA; 6 BP.
XX AC AAX21981;
XX DT 18-MAY-1999 (first entry)
XX DE Hexamer oligonucleotide vaccine adjuvant #3.
XX KW Vaccine adjuvant; cell mediated response; antibody response;
XX KW cytotoxic T lymphocyte; CTL response; ss.
XX OS Synthetic.
XX PN WO9852962-A1.
XX PD 26-NOV-1998.
XX PF 19-MAY-1998; 98WO-US010459.
XX PR 19-MAY-1997; 97US-0047121P.
XX PA (MERI) MERCK & CO INC.
XX PI Caulfield MJ;
XX WPI; 1999-131687/11.
XX SQ New oligonucleotide vaccine adjuvants that generate cell
PT mediated/antibody responses in animals - useful in the vaccination of
PT animals.
XX PS Claim 1; Page 37; 42pp; English.
XX CC The invention relates to an oligonucleotide vaccine adjuvant for
CC generating a cell mediated/antibody response in an animal, comprising one
CC of the sequences shown in AAX21979-X21981. The oligonucleotide adjuvant
CC forms a method of vaccinating animals. The antigen can be any derivative
CC of hepatitis B, hepatitis C virus, hepatocellular carcinoma antigens
CC induced by hepatitis B virus, rotavirus, HIV proteins, varicella, and
CC antigens derived from bacteria or humans/animals. The oligonucleotide
CC adjuvants provide a method of eliciting a cytotoxic T lymphocyte (CTL)
CC response to an antigen presented in a vaccine. CTLs are known to kill
CC viral or bacterial infected cells
XX SQ Sequence 6 BP; 1 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
DB 2 CCGG 5

RESULT 25
AAX21981/c
ID AAX21981 standard; DNA; 6 BP.
XX AC AAX21981;
XX DT 18-MAY-1999 (first entry)
XX DE Hexamer oligonucleotide vaccine adjuvant #3.
XX KW Vaccine adjuvant; cell mediated response; antibody response;
XX KW cytotoxic T lymphocyte; CTL response; ss.
XX OS Synthetic.
XX PN WO9852962-A1.
XX PD 26-NOV-1998.
XX PF 19-MAY-1998; 98WO-US010459.
XX PS 19-MAY-1998; 98WO-US010459.
XX
```

PR 19-MAY-1997; 97US-0047121P.  
XX (MERI ) MERCK & CO INC.  
XX Caulfield MJ;  
XX WPI; 1999-131687/11.  
XX New oligonucleotide vaccine adjuvants that generate cell  
PT mediated/antibody responses in animals - useful in the vaccination of  
PT animals.  
XX  
XX Claim 1; Page 37; 42pp; English.  
XX The invention relates to an oligonucleotide vaccine adjuvant for  
CC generating a cell mediated/antibody response in an animal, comprising one  
CC of the sequences shown in AAX21979-X21981. The oligonucleotide adjuvant  
CC forms a method of vaccinating animals. The antigen can be any derivative  
CC of hepatitis B, hepatitis C virus, hepatocellular carcinoma antigens  
CC induced by hepatitis B virus, rotavirus, HIV proteins, varicella, and  
CC antigens derived from bacteria or humans/animals. The oligonucleotide  
CC adjuvants provide a method of eliciting a cytotoxic T lymphocyte (CTL)  
CC response to an antigen presented in a vaccine. CTLs are known to kill  
CC viral or bacterial infected cells  
XX  
XX Sequence 6 BP; 1 A; 2 C; 2 G; 1 T; 0 U; 0 Other;  
SQ Query Match 66.7%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 CCGG 6  
DB 5 CCGG 2  
  
RESULT 26  
ID AAF91710/c  
XX AAF91710 standard; DNA; 6 BP.  
XX  
XX AAF91710;  
XX  
XX 10-MAY-2001 (first entry)  
XX  
XX Breast-cancer associated protein isoform BPI-42 degenerate probe #10.  
XX  
XX Human; breast cancer; breast cancer associated protein isoform; BPI;  
XX breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200113117-A2.  
XX  
XX 22-FEB-2001.  
XX  
XX 14-AUG-2000; 2000WO-GB003143.  
XX  
XX 13-AUG-1999; 99GB-00019258.  
XX  
XX 30-MAR-2000; 2000GB-00007754.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Herath HMAc;  
XX  
XX WPI; 2001-211252/21.  
XX  
XX Screening, diagnosis or prognosis of breast cancer, by analyzing a sample  
PT of serum or plasma by two dimensional electrophoresis to detect the  
PT presence or level of a breast cancer-associated feature.  
XX  
XX Claim 144; Page 42; 146pp; English.  
XX  
XX The present invention describes a method for the screening, diagnosis or

CC prognosis of breast cancer (BC), determining the stage or severity of BC,  
CC and monitoring the effect of therapy administered to a subject having BC,  
CC comprising analysing a sample of body fluid by two dimensional  
CC electrophoresis to generate a two-dimensional array of features,  
CC comprising a chosen feature whose abundance correlates with BC or  
CC predicts the onset or course of BC. The method (I) involves: (a)  
CC analysing a sample of body fluid from the subject by two-dimensional  
CC electrophoresis to generate a two-dimensional array of features,  
CC comprising a chosen feature whose relative abundance correlates with BC  
CC or predicts the onset of BC; and (b) comparing the abundance of each  
CC chosen feature in the sample with the abundance of that chosen feature in  
CC the body fluid from one or more persons free from BC, or with a  
CC previously determined reference range for that feature in subjects free  
CC from BC, or with the abundance of an expression reference feature (ERF)  
CC in the test sample. The method is useful for screening, diagnosis or  
CC prognosis of breast cancer, determining the stage or severity of BC,  
CC monitoring the effect of therapy administered to a subject having BC, and  
CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340  
CC represents breast cancer associated protein isoform (BPI) peptide  
CC sequences, and AAF91543 to AAF91848 represent BPI probes used in the  
CC exemplification of the present invention  
XX  
XX Sequence 6 BP; 0 A; 3 C; 1 G; 0 T; 0 U; 2 Other;  
SQ Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.8e+08; 1; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 1;  
  
QY 2 GCGG 6  
DB 5 GCNGG 1  
  
RESULT 27  
ID ABS65903  
XX ABS65903 standard; DNA; 6 BP.  
XX  
XX ABS65903;  
XX  
XX 15-NOV-2002 (first entry)  
XX  
XX Inhibitory oligonucleotide specific for hepatitis C virus #109.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
XX non-B hepatitis; acute hepatitis; chronic hepatitis;  
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
XX gene therapy; ss.  
XX  
XX Synthetic.  
XX  
XX US2002081577-A1.  
XX  
XX 27-JUN-2002.  
XX  
XX 02-JUL-1997; 97US-00887505.  
XX  
XX 06-JUN-1995; 95US-00471968.  
XX  
XX 02-JUL-1996; 96US-0021104P.  
XX  
XX (KILK/) KILKUSKIE R L.  
XX (FRAN/) FRANK B L.  
XX (GOOD/) GOODCHILD J.  
XX (WOLF/) WOLFE J L.  
XX (ROBE/) ROBERTS P C.  
XX (HAML/) HAMLIN H A.  
XX (ROBE/) ROBERTS N A.  
XX (WALT/) WALTHER D M.  
XX  
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
XX Hamlin HA, Roberts NA, Walther DM;  
XX WPI; 2002-537132/57.  
XX

```

PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
PS Claim 1; Page 6; 74pp; English.
XX
XX The invention describes synthetic oligonucleotides complementary to a
XX portion of the 5' untranslated region of hepatitis C virus. The
XX oligonucleotides may be used in methods for controlling, preventing, and
XX treating hepatitis C virus infection, in antisense technology and gene
XX therapy, and of detecting the presence of hepatitis C virus in a sample.
XX Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
XX RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
XX -B, acute and chronic hepatitis, and has been associated with
XX hepatocellular carcinoma. The invention describes methods and kits for
XX inhibiting replication of HCV, inhibiting the expression of HCV nucleic
XX acid and protein, and for treating HCV infections. This sequence
XX represents a synthetic oligonucleotide used for inhibiting HCV
XX replication and expression of HCV
XX
SQ Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
Db |||||
3 CCGG 6
RESULT 28
ABS65903/c
ID ABS65903 standard; DNA; 6 BP.
XX
XX
AC ABS65903;
XX
XX 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #109.
XX
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX non-B hepatitis; acute hepatitis; chronic hepatitis;
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
XX gene therapy; ss.
XX
XX Synthetic.
XX
XX US2002081577-A1.
XX
XX 27-JUN-2002.
XX
XX 02-JUL-1997; 97US-00887505.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
XX (FRAN/) FRANK B L.
XX (GOOD/) GOODCHILD J.
XX (WOLF/) WOLFE J L.
XX (ROBE/) ROBERTS P C.
XX (HAML/) HAMLIN H A.
XX (ROBE/) ROBERTS N A.
XX (WALT/) WALTHER D M.
XX
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
XX Hamlin HA, Roberts NA, Walther DM;
XX WPI; 2002-537132/57.
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
XX untranslated region of hepatitis C virus (HCV), useful for diagnosing and
XX
PT

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PT treating HCV infections and hepatocellular carcinoma.
XX Claim 1; Page 6; 74pp; English.
XX
XX The invention describes synthetic oligonucleotides complementary to a
XX portion of the 5' untranslated region of hepatitis C virus. The
XX oligonucleotides may be used in methods for controlling, preventing, and
XX treating hepatitis C virus infection, in antisense technology and gene
XX therapy, and of detecting the presence of hepatitis C virus in a sample.
XX Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
XX RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
XX -B, acute and chronic hepatitis, and has been associated with
XX hepatocellular carcinoma. The invention describes methods and kits for
XX inhibiting replication of HCV, inhibiting the expression of HCV nucleic
XX acid and protein, and for treating HCV infections. This sequence
XX represents a synthetic oligonucleotide used for inhibiting HCV
XX replication and expression of HCV
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Query Match 66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||
6 CCGG 3
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XX ACC69109;
XX
XX 10-JUL-2003 (first entry)
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XX
XX Cucurbit; expression profiling; DNA sequencing; plant; developmental;
XX physiological; horticultural; agricultural; target; ss.
XX
XX Cucumis sp.
XX Synthetic.
XX
XX EP1295950-A1.
XX
XX 26-MAR-2003.
XX
XX 25-SEP-2001; 2001EP-00203617.
XX
XX 25-SEP-2001; 2001EP-00203617.
XX (GTDI-) GT DIAGNOSTICS BV.
XX
XX Langeveld SA, Van Der Kop DAM, De Boer AD;
XX
XX WPI; 2003-383798/37.
XX
XX Determining developmental/physiological stage of organism (especially in
XX plants), comprises determining expression of first and second genes by
XX hybridizing nucleic acid templates derived from the genes with specific
XX primers.
XX
XX Example; Fig 1A; 27pp; English.
XX
XX The present invention describes a method (M) for determining a
XX developmental or physiological stage of an organism by determining
XX expression of a first and second gene (I)-(II), respectively, or gene
XX fragment. (M) comprises: (a) providing first and second nucleic acid
XX templates (T1)-(T2) derived from (I) and (II), respectively; (b)
XX hybridising first and second primers (P1)-(P2) to (T1) and (T2),
XX respectively; and (c) determining binding of the primers to the templates
XX

```



CC in one reaction vessel. (M) is useful for determining a developmental or  
 CC physiological stage of an organism (especially a plant). (M) is  
 CC particularly useful for expression profiling for use in testing plant  
 CC quality of horticultural and agricultural products. With quality loss,  
 CC e.g. stress-induced senescence, oxidative damage or desiccation, the  
 CC plant tissues will go through various physiological stages, in which  
 CC different genes are switched on or off. The level of expression of these  
 CC marker genes reflects the physiological stage and therefore the condition  
 CC and quality of the plant and/or product. Quality of fresh products is  
 CC generally judged on subjective criteria that usually involves visual  
 CC examination. The present invention provides a way of taking objective  
 CC quantitative measurements using biotechnology: there is a direct relation  
 CC between the pattern of gene expression at the RNA and protein level, and  
 CC the physiological status of a cell. The present sequence represents a  
 CC cucumber BGL target sequence, which is used in an example from the  
 CC present invention  
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Query Match 66.7%; Score 4; DB 8; Length 6;  
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RESULT 30  
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 AC ACC69109;  
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 DT 10-JUL-2003 (first entry)  
 XX  
 DE Cucumber BGL related target sequence SEQ ID NO:16.

XX Cucumber; expression profiling; DNA sequencing; plant; developmental;  
 KW physiological; horticultural; agricultural; target; ss.

XX Cucumis sp.  
 OS Synthetic.

XX EP1295950-A1.

XX 26-MAR-2003.

XX 25-SEP-2001; 2001EP-00203617.

XX 25-SEP-2001; 2001EP-00203617.

XX (GTDI-) GT DIAGNOSTICS BV.

XX Langeveld SA, Van Der Kop DAM, De Boer AD;

XX WPI; 2003-383798/37.

XX Determining developmental/physiological stage of organism (especially in  
 PT plants); comprises determining expression of first and second genes by  
 PT hybridizing nucleic acid templates derived from the genes with specific  
 PT primers.

XX Example; Fig 1A; 27pp; English.

XX The present invention describes a method (M) for determining a  
 CC developmental or physiological stage of an organism by determining  
 CC expression of a first and second gene (I)-(II), respectively, or gene  
 CC fragment. (M) comprises: (a) providing first and second nucleic acid  
 CC templates (T1)-(T2) derived from (I) and (II), respectively; (b)  
 CC hybridizing first and second primers (P1)-(P2) to (T1) and (T2),  
 CC respectively; and (c) determining binding of the primers to the templates  
 CC in one reaction vessel. (M) is useful for determining a developmental or

CC physiological stage of an organism (especially a plant). (M) is  
 CC particularly useful for expression profiling for use in testing plant  
 CC quality of horticultural and agricultural products. With quality loss,  
 CC e.g. stress-induced senescence, oxidative damage or desiccation, the  
 CC plant tissues will go through various physiological stages, in which  
 CC different genes are switched on or off. The level of expression of these  
 CC marker genes reflects the physiological stage and therefore the condition  
 CC and quality of the plant and/or product. Quality of fresh products is  
 CC generally judged on subjective criteria that usually involves visual  
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 CC between the pattern of gene expression at the RNA and protein level, and  
 CC the physiological status of a cell. The present sequence represents a  
 CC cucumber BGL target sequence, which is used in an example from the  
 CC present invention  
 XX  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
393.838 Million cell updates/sec

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Sequence: 1 ggcggg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 100 summaries

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- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sta.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 43 from Patent WO0144465.
ACCESSION AX175279
VERSION AX175279.1 GI:14598647
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 43 21-JUN-2001;
 Bioniche Life Sciences Inc. (CA)
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DEFINITION Sequence 14 from Patent WO0183737.
ACCESSION AX359007
VERSION AX359007.1 GI:18675406
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nagy,E., Tuboly,T. and Nagy,M.
TITLE Porcine adenovirus vaccine
JOURNAL Patent: WO 0183737-A 14 08-NOV-2001;
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us-09-735-363a-43.szlm6.rge

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LOCUS BD194759 6 bp DNA linear PAT 17-JUL-2003
DEFINITION Homogeneous diagnostic assay method utilizing simultaneous target
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ACCESSION BD194759
VERSION BD194759.1 GI:33004506
KEYWORDS JP 2002515749-A/24.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 6)
AUTHORS Hepp,J., Lengyel,Z., Pande,R., Botyanszki,J. and Toth,M.S.
TITLE Homogeneous diagnostic assay method utilizing simultaneous target
 and signal amplification
JOURNAL Patent: JP 2002515749-A 24 28-MAY-2002;
 NAVIX INC
COMMENT OS Unidentified
 PN JP 2002515749-A/24
 PD 28-MAY-2002
 PF 16-JUL-1997 JP 1998508863
 PR 25-JUL-1996 US 08/692825
 PI JOZSEF HEPP,ZSOLT LENGYEL,RAJIV PANDE,JANOS BOTYANSZKI,MIKLOS
 PI SAHIN TOTTH
 PC C12Q1/68
 CC Strandedness: Single;
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 CC Homogeneous diagnostic assay method utilizing simultaneous CC
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LOCUS BD194759/c 6 bp DNA linear PAT 17-JUL-2003
DEFINITION Homogeneous diagnostic assay method utilizing simultaneous target
 and signal amplification.
ACCESSION BD194759
VERSION BD194759.1 GI:33004506
KEYWORDS JP 2002515749-A/24.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 6)
AUTHORS Hepp,J., Lengyel,Z., Pande,R., Botyanszki,J. and Toth,M.S.
TITLE Homogeneous diagnostic assay method utilizing simultaneous target
 and signal amplification
JOURNAL Patent: JP 2002515749-A 24 28-MAY-2002;
 NAVIX INC
COMMENT OS Unidentified
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 PD 28-MAY-2002
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| PR | 25-JUL-1996 US                                                | 08/692825 |  |
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| PI | SAHIN TOTU                                                    |           |  |
| PC | C12Q1/68                                                      |           |  |
| CC | Strandedness: Single;                                         |           |  |
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| CC | Homogeneous diagnostic assay method utilizing simultaneous CC |           |  |
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RESULT 8
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DEFINITION Targeted gene modification by parvoviral vectors.
ACCESSION BD244964
VERSION BD244964.1 GI:33054734
KEYWORDS JP 2002528088-A/18.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1 (bases 1 to 6)
REFERENCE
AUTHORS Russell,D.W. and Hirata,R.K.
TITLE Targeted gene modification by parvoviral vectors
JOURNAL Patent: JP 2002528088-A 18 03-SEP-2002;
UNIVERSITY OF WASHINGTON
COMMENT OS Escherichia coli
PN JP 2002528088-A/18
PD 03-SEP-2002
PF 27-OCT-1999 JP 2000578469
PR 28-OCT-1998 US 60/106191
PI DAVID W RUSSELL,ROLI K HIRATA
PC C12N15/09,A01K67/027,A61K48/00,C12N5/10,C12Q1/68//A61K35/76,
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QY 1 GGCCG 5
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Db 5 GGCCG 1

RESULT 9
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LOCUS CQ755690 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 191 from Patent WO2003106674.
ACCESSION CQ755690
VERSION CQ755690.1 GI:44846495
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 191 24-DEC-2003;
Chromagenics B.V. (NL)
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QY 2 GCCGG 6
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Db 5 GCCGG 1

RESULT 10
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LOCUS CQ755696 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 197 from Patent WO2003106674.
ACCESSION CQ755696
VERSION CQ755696.1 GI:44846501
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 197 24-DEC-2003;
Chromagenics B.V. (NL)
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QY 2 GCCGG 6
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LOCUS CQ755696 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 197 from Patent WO2003106674.
ACCESSION CQ755696
VERSION CQ755696.1 GI:44846501
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 197 24-DEC-2003;
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QY 2 GCCGG 6
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RESULT 12
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LOCUS CQ755711 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 212 from Patent WO2003106674.
ACCESSION CQ755711
VERSION CQ755711.1 GI:44846516
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 212 24-DEC-2003;
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QY 2 GCCGG 6
Db 5 GCCGG 1

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LOCUS CQ755712 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 213 from Patent WO2003106674.
ACCESSION CQ755712
VERSION CQ755712.1 GI:44846517
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 213 24-DEC-2003;
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Db 6 GCCGG 2

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CQ755722/c
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ACCESSION CQ755722
VERSION CQ755722.1 GI:44846527
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 223 24-DEC-2003;
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Db 5 GCCGG 1

RESULT 15
CQ755767/c
LOCUS CQ755767 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 268 from Patent WO2003106674.
ACCESSION CQ755767
VERSION CQ755767.1 GI:44846572
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 268 24-DEC-2003;
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Db 6 GCCGG 2

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Best Local Similarity 100.0%; Pred. No. 8e+09;
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RESULT 14
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DEFINITION Sequence 223 from Patent WO2003106674.
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KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
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TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 223 24-DEC-2003;
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Db 5 GCCGG 1

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ACCESSION CQ755767
VERSION CQ755767.1 GI:44846572
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 268 24-DEC-2003;
Chromagenics B.V. (NL)
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Db 6 GCCGG 2

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DEFINITION Sequence 275 from Patent WO2003106674.  
ACCESSION CQ755774  
VERSION CQ755774.1 GI:44846579  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 275 24-DEC-2003;  
Chromagenics B.V. (NL)  
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LOCUS CQ755824 6 bp DNA linear PAT 01-MAR-2004  
DEFINITION Sequence 325 from Patent WO2003106674.  
ACCESSION CQ755824  
VERSION CQ755824.1 GI:44846629  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 325 24-DEC-2003;  
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DEFINITION Sequence 378 from Patent WO2003106674.  
ACCESSION CQ755877  
VERSION CQ755877.1 GI:44846682

KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 378 24-DEC-2003;  
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LOCUS CQ755877 6 bp DNA linear PAT 01-MAR-2004  
DEFINITION Sequence 378 from Patent WO2003106674.  
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VERSION CQ755877.1 GI:44846682  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 378 24-DEC-2003;  
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LOCUS CQ755904 6 bp DNA linear PAT 01-MAR-2004  
DEFINITION Sequence 405 from Patent WO2003106674.  
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VERSION CQ755904.1 GI:44846709  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
TITLE Means and methods for regulating gene expression  
JOURNAL Patent: WO 2003106674-A 405 24-DEC-2003;  
Chromagenics B.V. (NL)





QY 2 GCCGG 6  
 Db 6 GCCGG 2

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 VERSION CQ757949.1 GI:44847970  
 KEYWORDS .  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
 TITLE A method for the simultaneous production of multiple proteins;  
 vectors and cells for use therein  
 JOURNAL Patent: WO 2003106684-A 253 24-DEC-2003;  
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 VERSION CQ757950.1 GI:44847971  
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 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
 TITLE A method for the simultaneous production of multiple proteins;  
 vectors and cells for use therein  
 JOURNAL Patent: WO 2003106684-A 254 24-DEC-2003;  
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QY 2 GCCGG 6  
 Db 2 GCCGG 6

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 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
 TITLE A method for the simultaneous production of multiple proteins;  
 vectors and cells for use therein  
 JOURNAL Patent: WO 2003106684-A 264 24-DEC-2003;  
 Chromagenics B.V. (NL)  
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 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
 TITLE A method for the simultaneous production of multiple proteins;  
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VERSION CQ758012.1 GI:44848033  
KEYWORDS synthetic construct  
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AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
TITLE A method for the simultaneous production of multiple proteins;  
vectors and cells for use therein  
JOURNAL Patent: WO 2003106684-A 316 24-DEC-2003;  
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ACCESSION CQ758062  
VERSION CQ758062.1 GI:44848083  
KEYWORDS synthetic construct  
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ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
TITLE A method for the simultaneous production of multiple proteins;  
vectors and cells for use therein  
JOURNAL Patent: WO 2003106684-A 366 24-DEC-2003;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 00:00:54 ; Search time 710.6 Seconds

(without alignments)  
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Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

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| 5                 | 5     | 83.3        | 6      | 19 | US-10-433-258-10  |
| 6                 | 4.6   | 76.7        | 6      | 9  | US-09-816-763-95  |
| 7                 | 4.6   | 76.7        | 6      | 19 | US-10-821-568-95  |
| Sequence 42, Appl |       |             |        |    |                   |
| Sequence 14, Appl |       |             |        |    |                   |
| Sequence 14, Appl |       |             |        |    |                   |
| Sequence 86, Appl |       |             |        |    |                   |
| Sequence 10, Appl |       |             |        |    |                   |
| Sequence 95, Appl |       |             |        |    |                   |

|   |    |                      |      |     |   |    |                       |
|---|----|----------------------|------|-----|---|----|-----------------------|
| 6 | 9  | US-09-735-363A-28    | 73.3 | 4.4 | C | 8  | Sequence 28, Appl     |
| 6 | 9  | US-09-735-363A-45    | 73.3 | 4.4 | C | 9  | Sequence 45, Appl     |
| 6 | 9  | US-09-735-363A-47    | 73.3 | 4.4 | C | 10 | Sequence 47, Appl     |
| 6 | 9  | US-09-879-668-8      | 73.3 | 4.4 | C | 11 | Sequence 8, Appl      |
| 6 | 9  | US-09-879-668-17     | 73.3 | 4.4 | C | 12 | Sequence 17, Appl     |
| 6 | 10 | US-09-953-348-91     | 73.3 | 4.4 | C | 13 | Sequence 91, Appl     |
| 6 | 10 | US-09-953-348-93     | 73.3 | 4.4 | C | 14 | Sequence 93, Appl     |
| 6 | 14 | US-10-127-645-3      | 73.3 | 4.4 | C | 15 | Sequence 3, Appl      |
| 6 | 15 | US-10-280-274-8      | 73.3 | 4.4 | C | 16 | Sequence 8, Appl      |
| 6 | 15 | US-10-280-274-17     | 73.3 | 4.4 | C | 17 | Sequence 17, Appl     |
| 6 | 15 | US-10-267-255-91     | 73.3 | 4.4 | C | 18 | Sequence 91, Appl     |
| 6 | 15 | US-10-267-255-93     | 73.3 | 4.4 | C | 19 | Sequence 93, Appl     |
| 6 | 15 | US-10-264-280-2      | 73.3 | 4.4 | C | 20 | Sequence 2, Appl      |
| 6 | 15 | US-10-264-280-6      | 73.3 | 4.4 | C | 21 | Sequence 6, Appl      |
| 6 | 16 | US-10-041-860-191    | 73.3 | 4.4 | C | 22 | Sequence 191, Appl    |
| 6 | 16 | US-10-190-312A-212   | 73.3 | 4.4 | C | 23 | Sequence 212, Appl    |
| 6 | 16 | US-10-190-312A-259   | 73.3 | 4.4 | C | 24 | Sequence 259, Appl    |
| 6 | 16 | US-10-312A-636       | 73.3 | 4.4 | C | 25 | Sequence 636, Appl    |
| 6 | 18 | US-10-420-513A-6     | 73.3 | 4.4 | C | 26 | Sequence 6, Appl      |
| 6 | 19 | US-10-716-029-165    | 73.3 | 4.4 | C | 27 | Sequence 165, Appl    |
| 6 | 19 | US-10-716-029-168    | 73.3 | 4.4 | C | 28 | Sequence 168, Appl    |
| 4 | 13 | US-10-027-632-177937 | 66.7 | 4   | C | 29 | Sequence 177937, Appl |
| 4 | 14 | US-10-196-332-8      | 66.7 | 4   | C | 30 | Sequence 8, Appl      |
| 4 | 17 | US-10-027-632-177937 | 66.7 | 4   | C | 31 | Sequence 177937, Appl |
| 5 | 9  | US-09-792-875-4      | 66.7 | 4   | C | 32 | Sequence 4, Appl      |
| 5 | 9  | US-09-804-653-1      | 66.7 | 4   | C | 33 | Sequence 1, Appl      |
| 5 | 9  | US-09-804-653-14     | 66.7 | 4   | C | 34 | Sequence 14, Appl     |
| 5 | 13 | US-10-084-700-9      | 66.7 | 4   | C | 35 | Sequence 9, Appl      |
| 5 | 13 | US-10-027-632-178455 | 66.7 | 4   | C | 36 | Sequence 178455, Appl |
| 5 | 13 | US-10-027-632-178477 | 66.7 | 4   | C | 37 | Sequence 178477, Appl |
| 5 | 14 | US-10-085-395-6      | 66.7 | 4   | C | 38 | Sequence 6, Appl      |
| 5 | 16 | US-10-368-442-1      | 66.7 | 4   | C | 39 | Sequence 1, Appl      |
| 5 | 16 | US-10-368-442-14     | 66.7 | 4   | C | 40 | Sequence 14, Appl     |
| 5 | 17 | US-10-320-210A-118   | 66.7 | 4   | C | 41 | Sequence 118, Appl    |
| 5 | 17 | US-10-027-632-178455 | 66.7 | 4   | C | 42 | Sequence 178455, Appl |
| 5 | 17 | US-10-027-632-178477 | 66.7 | 4   | C | 43 | Sequence 178477, Appl |
| 5 | 18 | US-10-068-085A-4     | 66.7 | 4   | C | 44 | Sequence 4, Appl      |
| 5 | 19 | US-10-673-938-17     | 66.7 | 4   | C | 45 | Sequence 17, Appl     |
| 5 | 19 | US-10-673-938-23     | 66.7 | 4   | C | 46 | Sequence 23, Appl     |
| 5 | 19 | US-10-673-938-57     | 66.7 | 4   | C | 47 | Sequence 57, Appl     |
| 5 | 19 | US-10-681-818-222    | 66.7 | 4   | C | 48 | Sequence 222, Appl    |
| 5 | 20 | US-10-622-088-155    | 66.7 | 4   | C | 49 | Sequence 155, Appl    |
| 6 | 9  | US-09-320-337-2      | 66.7 | 4   | C | 50 | Sequence 2, Appl      |
| 6 | 9  | US-09-320-337-10     | 66.7 | 4   | C | 51 | Sequence 10, Appl     |
| 6 | 9  | US-09-851-271A-14    | 66.7 | 4   | C | 52 | Sequence 14, Appl     |
| 6 | 9  | US-09-804-653-13     | 66.7 | 4   | C | 53 | Sequence 13, Appl     |
| 6 | 10 | US-09-792-861A-25    | 66.7 | 4   | C | 54 | Sequence 25, Appl     |
| 6 | 10 | US-09-792-861A-26    | 66.7 | 4   | C | 55 | Sequence 26, Appl     |
| 6 | 10 | US-09-770-875-25     | 66.7 | 4   | C | 56 | Sequence 25, Appl     |
| 6 | 10 | US-09-770-875-26     | 66.7 | 4   | C | 57 | Sequence 26, Appl     |
| 6 | 10 | US-09-882-274-5      | 66.7 | 4   | C | 58 | Sequence 5, Appl      |
| 6 | 13 | US-10-014-973A-16    | 66.7 | 4   | C | 59 | Sequence 16, Appl     |
| 6 | 13 | US-10-003-035-7      | 66.7 | 4   | C | 60 | Sequence 7, Appl      |
| 6 | 13 | US-10-003-035-8      | 66.7 | 4   | C | 61 | Sequence 8, Appl      |
| 6 | 13 | US-10-057-050-1      | 66.7 | 4   | C | 62 | Sequence 1, Appl      |
| 6 | 13 | US-10-133-888-2      | 66.7 | 4   | C | 63 | Sequence 2, Appl      |
| 6 | 13 | US-10-133-888-20     | 66.7 | 4   | C | 64 | Sequence 20, Appl     |
| 6 | 13 | US-10-117-641-10     | 66.7 | 4   | C | 65 | Sequence 10, Appl     |
| 6 | 14 | US-10-085-395-1      | 66.7 | 4   | C | 66 | Sequence 1, Appl      |
| 6 | 14 | US-10-085-395-8      | 66.7 | 4   | C | 67 | Sequence 8, Appl      |
| 6 | 15 | US-10-235-113-10     | 66.7 | 4   | C | 68 | Sequence 10, Appl     |
| 6 | 15 | US-10-286-332A-7     | 66.7 | 4   | C | 69 | Sequence 7, Appl      |
| 6 | 15 | US-10-286-332A-8     | 66.7 | 4   | C | 70 | Sequence 8, Appl      |
| 6 | 16 | US-10-076-047A-340   | 66.7 | 4   | C | 71 | Sequence 340, Appl    |
| 6 | 16 | US-10-368-442-13     | 66.7 | 4   | C | 72 | Sequence 13, Appl     |
| 6 | 16 | US-10-265-031-10     | 66.7 | 4   | C | 73 | Sequence 10, Appl     |
| 6 | 16 | US-10-190-312A-257   | 66.7 | 4   | C | 74 | Sequence 257, Appl    |
| 6 | 16 | US-10-190-312A-329   | 66.7 | 4   | C | 75 | Sequence 329, Appl    |
| 6 | 16 | US-10-190-312A-335   | 66.7 | 4   | C | 76 | Sequence 335, Appl    |
| 6 | 17 | US-10-280-915-7      | 66.7 | 4   | C | 77 | Sequence 7, Appl      |
| 6 | 17 | US-10-280-915-8      | 66.7 | 4   | C | 78 | Sequence 8, Appl      |
| 6 | 17 | US-10-360-123A-50    | 66.7 | 4   | C | 79 | Sequence 50, Appl     |
| 6 | 17 | US-10-360-123A-51    | 66.7 | 4   | C | 80 | Sequence 51, Appl     |



APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
APPLICANT: MAURO, Vincent P.  
APPLICANT: EDELMAN, Gerald M.  
APPLICANT: CHAPPELL, Stephen A.  
APPLICANT: JONES, Frederick S.  
APPLICANT: OWENS, Geoffrey  
APPLICANT: MEECH, Robin  
TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATIONAL  
FILE REFERENCE: SCRIPI380-1  
CURRENT APPLICATION NUMBER: US/10/182,329  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: PCT/US 01/02733  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: US 60/261,312  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/230,956  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/230,852  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/207,804  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: US 60/186,496  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/178,816  
PRIOR FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 86  
LENGTH: 5  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: core motif  
US-10-182-329-86

Query Match 83.3%; Score 5; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAGG 6  
Db 1 GAAGG 5

RESULT 5  
US-10-433-258-10  
Sequence 10, Application US/10433258  
Publication No. US20040132033A1  
GENERAL INFORMATION:  
APPLICANT: Alan P. WOLFFE  
TITLE OF INVENTION: HUMAN HEPARANASE GENE REGULATORY SEQUENCES  
FILE REFERENCE: SABI-016/01US (\$22-US1)  
CURRENT APPLICATION NUMBER: US/10/433,258  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: PCT/US01/44798  
PRIOR FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: EST1 binding site  
US-10-433-258-10

Query Match 83.3%; Score 5; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5

Db 2 GGAAG 6

RESULT 6  
US-09-816-763-95  
Sequence 95, Application US/09816763  
Patent No. US20020110814A1  
GENERAL INFORMATION:  
APPLICANT: Remacle, Jose  
APPLICANT: Renard, Patricia  
APPLICANT: Art, Muriel  
TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
TITLE OF INVENTION: FACTORS  
FILE REFERENCE: VANM212.001AUS  
CURRENT APPLICATION NUMBER: US/09/816,763  
CURRENT FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: EP 00870057.7  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 95  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Consensus sequence for transcriptional factor PEA3  
US-09-816-763-95

Query Match 76.7%; Score 4.6; DB 9; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1e+09;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5  
Db 2 GGAAR 6

RESULT 7  
US-10-821-568-95  
Sequence 95, Application US/10821568  
Publication No. US20040185497A1  
GENERAL INFORMATION:  
APPLICANT: Remacle, Jose  
APPLICANT: Renard, Patricia  
APPLICANT: Art, Muriel  
TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
TITLE OF INVENTION: FACTORS  
FILE REFERENCE: VANM212.001DV1  
CURRENT APPLICATION NUMBER: US/10/821,568  
CURRENT FILING DATE: 2004-04-08  
PRIOR APPLICATION NUMBER: US 09/816,763  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: EP 00870057.7  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 95  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Consensus sequence for transcriptional factor PEA3  
US-10-821-568-95

Query Match 76.7%; Score 4.6; DB 19; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1e+09;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5

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Db 2 GGAAR 6

RESULT 8
US-09-735-363A-28/c
; Sequence 28, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-28

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
 |||||
Db 6 GGACGG 1

RESULT 9
US-09-735-363A-45
; Sequence 45, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-45

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
 |||||
Db 1 GGAAGG 6

RESULT 10
US-09-735-363A-47
; Sequence 47, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-47

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
 |||||
Db 6 GGACGG 1

RESULT 11
US-09-879-668-8/c
; Sequence 8, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Phillip, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-8

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
 |||||
Db 6 GGACGG 1

RESULT 12
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US-09-879-668-17  
; Sequence 17, Application US/09879668  
; Patent No. US20020091095A1  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0241 42368-256931  
; CURRENT APPLICATION NUMBER: US/09/879,668  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-09-879-668-17

Query Match 73.3%; Score 4.4; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
|||  
Db 1 GGGAGG 6

RESULT 13  
US-09-953-348-91  
; Sequence 91, Application US/09953348  
; Publication No. US20030134398A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, David. H  
; APPLICANT: Mao, Yingqing  
; APPLICANT: Varoglu, Mustafa  
; APPLICANT: He, Min  
; APPLICANT: Sheldon, Paul  
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER  
; FILE REFERENCE: 600.530US1  
; CURRENT APPLICATION NUMBER: US/09/953,348  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: PCT/US00/06394  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 09/266965  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Streptomyces lavendulae  
US-09-953-348-91

Query Match 73.3%; Score 4.4; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
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Db 1 GAAAGG 6

RESULT 14  
US-09-953-348-93  
; Sequence 93, Application US/09953348  
; Publication No. US20030134398A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, David. H  
; APPLICANT: Mao, Yingqing  
; APPLICANT: Varoglu, Mustafa  
; APPLICANT: He, Min  
; APPLICANT: Sheldon, Paul  
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER  
; FILE REFERENCE: 600.530US1  
; CURRENT APPLICATION NUMBER: US/09/953,348  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: PCT/US00/06394  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 09/266965  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 93  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Streptomyces lavendulae  
US-09-953-348-93

Query Match 73.3%; Score 4.4; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
|||  
Db 1 GGAACG 6

RESULT 15  
US-10-127-645-3  
; Sequence 3, Application US/10127645  
; Publication No. US20030045493A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; APPLICANT: Phillips, Nigel C.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiation  
; FILE REFERENCE: 02811-0261 (42368-273010)  
; CURRENT APPLICATION NUMBER: US/10/127,645  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US 60/286,158  
; PRIOR FILING DATE: 2001-04-24  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-10-127-645-3

Query Match 73.3%; Score 4.4; DB 14; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
|||  
Db 1 GGGAGG 6

RESULT 16  
US-10-280-274-8/c  
; Sequence 8, Application US/10280274  
; Publication No. US20030119776A1  
; GENERAL INFORMATION:

/ APPLICANT: Phillips, Nigel C.  
/ APPLICANT: Fillon, Mario C.  
/ TITLE OF INVENTION: Modulation of Fas and FasL Expression  
/ FILE REFERENCE: 02811-0242 42368-279803  
/ CURRENT APPLICATION NUMBER: US/10/280,274  
/ CURRENT FILING DATE: 2003-02-14  
/ PRIOR APPLICATION NUMBER: PCT/CA00/01467  
/ PRIOR FILING DATE: 2000-12-12  
/ PRIOR APPLICATION NUMBER: US 09/879,668  
/ PRIOR FILING DATE: 2001-06-12  
/ PRIOR APPLICATION NUMBER: US 60/228,925  
/ PRIOR FILING DATE: 2000-08-29  
/ PRIOR APPLICATION NUMBER: US 60/266,229  
/ PRIOR FILING DATE: 2001-02-02  
/ PRIOR APPLICATION NUMBER: US 09/735,363  
/ PRIOR FILING DATE: 2000-12-12  
/ PRIOR APPLICATION NUMBER: US 60/170,325  
/ PRIOR FILING DATE: 1999-12-13  
/ NUMBER OF SEQ ID NOS: 18  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 8  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-8

Query Match 73.3%; Score 4.4; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
DB 6 GGACGG 1

RESULT 17  
US-10-280-274-17  
/ Sequence 17, Application US/10280274  
/ Publication No. US20030119776A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Phillips, Nigel C.  
/ TITLE OF INVENTION: Modulation of Fas and FasL Expression  
/ FILE REFERENCE: 02811-0242 42368-279803  
/ CURRENT APPLICATION NUMBER: US/10/280,274  
/ CURRENT FILING DATE: 2003-02-14  
/ PRIOR APPLICATION NUMBER: PCT/CA00/01467  
/ PRIOR FILING DATE: 2000-12-12  
/ PRIOR APPLICATION NUMBER: US 09/879,668  
/ PRIOR FILING DATE: 2001-06-12  
/ PRIOR APPLICATION NUMBER: US 60/228,925  
/ PRIOR FILING DATE: 2000-08-29  
/ PRIOR APPLICATION NUMBER: US 60/266,229  
/ PRIOR FILING DATE: 2001-02-02  
/ PRIOR APPLICATION NUMBER: US 09/735,363  
/ PRIOR FILING DATE: 2000-12-12  
/ PRIOR APPLICATION NUMBER: US 60/170,325  
/ PRIOR FILING DATE: 1999-12-13  
/ NUMBER OF SEQ ID NOS: 18  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 17  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-17

Query Match 73.3%; Score 4.4; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
DB 1 GGAGG 6  
RESULT 18  
US-10-267-255-91  
/ Sequence 91, Application US/10267255  
/ Publication No. US20030124689A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sherman, D  
/ APPLICANT: Mao, Y  
/ APPLICANT: Varoglu, M  
/ APPLICANT: He, M  
/ APPLICANT: Sheldon, P  
/ TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
/ FILE REFERENCE: 600.456US1  
/ CURRENT APPLICATION NUMBER: US/10/267,255  
/ CURRENT FILING DATE: 2002-10-09  
/ PRIOR APPLICATION NUMBER: US 09/266,965  
/ PRIOR FILING DATE: 1999-03-12  
/ PRIOR APPLICATION NUMBER: US 08/624,447  
/ PRIOR FILING DATE: 1996-08-19  
/ PRIOR APPLICATION NUMBER: PCT/US94/11279  
/ PRIOR FILING DATE: 1994-10-06  
/ PRIOR APPLICATION NUMBER: US 08/133,963  
/ PRIOR FILING DATE: 1993-10-07  
/ NUMBER OF SEQ ID NOS: 145  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 91  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Streptomyces lavendulae  
US-10-267-255-91

Query Match 73.3%; Score 4.4; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
DB 1 GAAAGG 6

RESULT 19  
US-10-267-255-93  
/ Sequence 93, Application US/10267255  
/ Publication No. US20030124689A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sherman, D  
/ APPLICANT: Mao, Y  
/ APPLICANT: Varoglu, M  
/ APPLICANT: He, M  
/ APPLICANT: Sheldon, P  
/ TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
/ FILE REFERENCE: 600.456US1  
/ CURRENT APPLICATION NUMBER: US/10/267,255  
/ CURRENT FILING DATE: 2002-10-09  
/ PRIOR APPLICATION NUMBER: US 09/266,965  
/ PRIOR FILING DATE: 1999-03-12  
/ PRIOR APPLICATION NUMBER: US 08/624,447  
/ PRIOR FILING DATE: 1996-08-19  
/ PRIOR APPLICATION NUMBER: PCT/US94/11279  
/ PRIOR FILING DATE: 1994-10-06  
/ PRIOR APPLICATION NUMBER: US 08/133,963  
/ PRIOR FILING DATE: 1993-10-07  
/ NUMBER OF SEQ ID NOS: 145  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 93  
/ LENGTH: 6  
/ TYPE: DNA  
/ ORGANISM: Streptomyces lavendulae

## US-10-267-255-93

Query Match 73.3%; Score 4.4; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6  
|||  
Db 1 GGAACG 6

## RESULT 20

US-10-264-280-2  
; Sequence 2, Application US/10264280  
; Publication No. US20030125290A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillon, Mario C.  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Herrera-Gayol, Andrea C.  
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide  
; FILE REFERENCE: 02811-0271 42368-277492  
; CURRENT APPLICATION NUMBER: US/10/264,280  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 60/326,884  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-264-280-2

Query Match 73.3%; Score 4.4; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6  
|||  
Db 1 GGAAGG 6

## RESULT 21

US-10-264-280-6  
; Sequence 6, Application US/10264280  
; Publication No. US20030125290A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillon, Mario C.  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Herrera-Gayol, Andrea C.  
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide  
; FILE REFERENCE: 02811-0271 42368-277492  
; CURRENT APPLICATION NUMBER: US/10/264,280  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 60/326,884  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; NAME/KEY: misc feature  
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide  
US-10-264-280-6

Query Match 73.3%; Score 4.4; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6  
|||  
Db 1 GGAAGG 6

## RESULT 22

US-10-041-860-191/c  
; Sequence 191, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R. F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Peng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 191  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-041-860-191

Query Match 73.3%; Score 4.4; DB 16; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6  
|||  
Db 6 GGAAGG 1

## RESULT 23

US-10-190-312A-212/c  
; Sequence 212, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities;  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 212  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-212

Query Match 73.3%; Score 4.4; DB 16; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6  
|||

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Db 6 GGAGGG 1

RESULT 24
US-10-190-312A-259/c
; Sequence 259, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 259
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-259

Query Match 73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db |||||
 6 GGAAGG 1

RESULT 25
US-10-190-312A-636/c
; Sequence 636, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 636
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-636

Query Match 73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db |||||
 6 GGAGGG 1

RESULT 26
US-10-420-513A-6
; Sequence 168, Application US/10716029
; Publication No. US20040171038A1
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; Sequence 6, Application US/10420513A
; Publication No. US2004005883A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillon, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; TITLE OF INVENTION: Immune Response
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-420-513A-6

Query Match 73.3%; Score 4.4; DB 18; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db |||||
 1 GGGAGG 6

RESULT 27
US-10-716-029-165
; Sequence 165, Application US/10716029
; Publication No. US20040171038A1
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Duff, Gordon
; APPLICANT: Kornman, Kenneth
; APPLICANT: Kolpin, Maryam R
; APPLICANT: Hsieh, Chung-Ming
; APPLICANT: Govindaraju, Raju
; APPLICANT: Aziz, Nazneen
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; TITLE OF INVENTION: and Haplotypes
; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-716-029-165

Query Match 73.3%; Score 4.4; DB 19; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db |||||
 1 GGCAGG 6

RESULT 28
US-10-716-029-168
; Sequence 168, Application US/10716029
; Publication No. US20040171038A1
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Db 4 GGAA 1

RESULT 30  
US-10-196-332-8  
; Sequence 8, Application US/10196332  
; Publication No. US20030087865A1  
; GENERAL INFORMATION:  
; APPLICANT: Golub, Todd R.  
; APPLICANT: Sasaki, Koichi  
; APPLICANT: Martinez, Robert V.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: Leukemogenic Transcription Factors  
; FILE REFERENCE: 2825.2035-001  
; CURRENT APPLICATION NUMBER: US/10/196,332  
; CURRENT FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: US 60/305,554  
; PRIOR FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Repeat sequence  
US-10-196-332-8

Query Match 66.7%; Score 4; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
|||||

Db 1 GGAA 4

Search completed: July 21, 2005, 07:13:19  
Job time : 714.6 secs

GENERAL INFORMATION:  
; APPLICANT: Nicklin, Martin  
; APPLICANT: Duff, Gordon  
; APPLICANT: Kornman, Kenneth  
; APPLICANT: Kolpin, Maryam R  
; APPLICANT: Hsieh, Chung-Ming  
; APPLICANT: Govindaraju, Raju  
; APPLICANT: Aziz, Nazneen  
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms  
; FILE REFERENCE: 24299-524 CON  
; CURRENT APPLICATION NUMBER: US/10/716,029  
; CURRENT FILING DATE: 2003-11-17  
; PRIOR APPLICATION NUMBER: 10/351,702  
; PRIOR FILING DATE: 2003-01-25  
; PRIOR APPLICATION NUMBER: 60/351,951  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 277  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 168  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-716-029-168

Query Match 73.3%; Score 4.4; DB 19; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
|||||

Db 1 GGTAGG 6

RESULT 29  
US-10-027-632-177937/c  
; Sequence 177937, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 10827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 177937  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-177937

Query Match 66.7%; Score 4; DB 13; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
|||||

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds  
(without alignments)  
172.240 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents NA.\*

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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 5     | 83.3        | 6      | 1  | US-08-533-912-7   |
| 2          | 4.4   | 73.3        | 6      | 4  | US-09-266-965-91  |
| 3          | 4.4   | 73.3        | 6      | 4  | US-09-266-965-93  |
| 4          | 4.4   | 73.3        | 6      | 4  | US-09-798-542-23  |
| 5          | 4.4   | 73.3        | 6      | 4  | US-09-798-542-24  |
| 6          | 4     | 66.7        | 5      | 1  | US-08-717-526-76  |
| 7          | 4     | 66.7        | 5      | 3  | US-08-873-709-8   |
| 8          | 4     | 66.7        | 5      | 3  | US-08-537-765-3   |
| 9          | 4     | 66.7        | 5      | 3  | US-08-623-428B-62 |
| 10         | 4     | 66.7        | 5      | 4  | US-09-869-875-5   |
| 11         | 4     | 66.7        | 5      | 4  | US-09-869-875-11  |
| 12         | 4     | 66.7        | 5      | 5  | PCT-US93-03027-8  |
| 13         | 4     | 66.7        | 6      | 1  | US-08-211-682-7   |
| 14         | 4     | 66.7        | 6      | 1  | US-08-211-682-8   |
| 15         | 4     | 66.7        | 6      | 2  | US-08-553-185-5   |
| 16         | 4     | 66.7        | 6      | 2  | US-08-442-809A-2  |
| 17         | 4     | 66.7        | 6      | 2  | US-08-442-809A-10 |
| 18         | 4     | 66.7        | 6      | 3  | US-09-056-868B-14 |
| 19         | 4     | 66.7        | 6      | 3  | US-09-632-538C-10 |
| 20         | 4     | 66.7        | 6      | 4  | US-09-608-598-50  |
| 21         | 4     | 66.7        | 6      | 4  | US-09-608-598-51  |
| 22         | 4     | 66.7        | 6      | 4  | US-09-435-327A-1  |
| 23         | 4     | 66.7        | 6      | 4  | US-09-585-599A-7  |
| 24         | 4     | 66.7        | 6      | 4  | US-09-585-599A-8  |
| 25         | 4     | 66.7        | 6      | 4  | US-10-014-973A-16 |
| 26         | 4     | 66.7        | 6      | 4  | US-09-851-271A-14 |
| 27         | 4     | 66.7        | 6      | 4  | US-10-134-188-13  |
| 28         |       |             |        |    | Sequence 7, Appl  |
| 29         |       |             |        |    | Sequence 91, Appl |
| 30         |       |             |        |    | Sequence 93, Appl |
| 31         |       |             |        |    | Sequence 23, Appl |
| 32         |       |             |        |    | Sequence 24, Appl |
| 33         |       |             |        |    | Sequence 76, Appl |
| 34         |       |             |        |    | Sequence 8, Appl  |
| 35         |       |             |        |    | Sequence 3, Appl  |
| 36         |       |             |        |    | Sequence 62, Appl |
| 37         |       |             |        |    | Sequence 5, Appl  |
| 38         |       |             |        |    | Sequence 11, Appl |
| 39         |       |             |        |    | Sequence 8, Appl  |
| 40         |       |             |        |    | Sequence 7, Appl  |
| 41         |       |             |        |    | Sequence 8, Appl  |
| 42         |       |             |        |    | Sequence 5, Appl  |
| 43         |       |             |        |    | Sequence 2, Appl  |
| 44         |       |             |        |    | Sequence 10, Appl |
| 45         |       |             |        |    | Sequence 50, Appl |
| 46         |       |             |        |    | Sequence 51, Appl |
| 47         |       |             |        |    | Sequence 1, Appl  |
| 48         |       |             |        |    | Sequence 7, Appl  |
| 49         |       |             |        |    | Sequence 8, Appl  |
| 50         |       |             |        |    | Sequence 14, Appl |
| 51         |       |             |        |    | Sequence 10, Appl |
| 52         |       |             |        |    | Sequence 15, Appl |
| 53         |       |             |        |    | Sequence 14, Appl |
| 54         |       |             |        |    | Sequence 16, Appl |
| 55         |       |             |        |    | Sequence 14, Appl |
| 56         |       |             |        |    | Sequence 13, Appl |
| 57         |       |             |        |    | Sequence 13, Appl |
| 58         |       |             |        |    | Sequence 11, Appl |
| 59         |       |             |        |    | Sequence 8, Appl  |
| 60         |       |             |        |    | Sequence 33, Appl |
| 61         |       |             |        |    | Sequence 55, Appl |
| 62         |       |             |        |    | Sequence 7, Appl  |
| 63         |       |             |        |    | Sequence 7, Appl  |
| 64         |       |             |        |    | Sequence 19, Appl |
| 65         |       |             |        |    | Sequence 19, Appl |
| 66         |       |             |        |    | Sequence 51, Appl |
| 67         |       |             |        |    | Sequence 54, Appl |
| 68         |       |             |        |    | Sequence 13, Appl |
| 69         |       |             |        |    | Sequence 11, Appl |
| 70         |       |             |        |    | Sequence 8, Appl  |
| 71         |       |             |        |    | Sequence 33, Appl |
| 72         |       |             |        |    | Sequence 33, Appl |
| 73         |       |             |        |    | Sequence 55, Appl |
| 74         |       |             |        |    | Sequence 7, Appl  |
| 75         |       |             |        |    | Sequence 7, Appl  |
| 76         |       |             |        |    | Sequence 19, Appl |
| 77         |       |             |        |    | Sequence 19, Appl |
| 78         |       |             |        |    | Sequence 51, Appl |
| 79         |       |             |        |    | Sequence 54, Appl |
| 80         |       |             |        |    | Sequence 19, Appl |
| 81         |       |             |        |    | Sequence 8, Appl  |
| 82         |       |             |        |    | Sequence 9, Appl  |
| 83         |       |             |        |    | Sequence 5, Appl  |
| 84         |       |             |        |    | Sequence 2, Appl  |
| 85         |       |             |        |    | Sequence 2, Appl  |
| 86         |       |             |        |    | Sequence 2, Appl  |
| 87         |       |             |        |    | Sequence 2, Appl  |
| 88         |       |             |        |    | Sequence 2, Appl  |
| 89         |       |             |        |    | Sequence 2, Appl  |
| 90         |       |             |        |    | Sequence 2, Appl  |
| 91         |       |             |        |    | Sequence 2, Appl  |
| 92         |       |             |        |    | Sequence 2, Appl  |
| 93         |       |             |        |    | Sequence 2, Appl  |
| 94         |       |             |        |    | Sequence 2, Appl  |
| 95         |       |             |        |    | Sequence 2, Appl  |
| 96         |       |             |        |    | Sequence 2, Appl  |
| 97         |       |             |        |    | Sequence 2, Appl  |
| 98         |       |             |        |    | Sequence 2, Appl  |
| 99         |       |             |        |    | Sequence 2, Appl  |
| 100        |       |             |        |    | Sequence 2, Appl  |

Sequence 63, Appl  
Sequence 11, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 53, Appl  
Sequence 31, Appl  
Sequence 6, Appl  
Sequence 14, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 45, Appl  
Sequence 6, Appl  
Sequence 20, Appl  
Sequence 10, Appl  
Sequence 19, Appl  
Sequence 1, Appl  
Sequence 6, Appl  
Sequence 45, Appl  
Sequence 140, Appl  
Sequence 10, Appl  
Sequence 26, Appl  
Sequence 19, Appl  
Sequence 12, Appl  
Sequence 3, Appl  
Sequence 140, Appl  
Sequence 1, Appl  
Sequence 110, Appl  
Sequence 12, Appl  
Sequence 1, Appl  
Sequence 17, Appl  
Sequence 16, Appl  
Sequence 1, Appl  
Sequence 140, Appl  
Sequence 19, Appl  
Sequence 54, Appl  
Sequence 56, Appl  
Sequence 13, Appl  
Sequence 11, Appl  
Sequence 8, Appl  
Sequence 33, Appl  
Sequence 7, Appl  
Sequence 55, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 51, Appl  
Sequence 54, Appl  
Sequence 19, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
GENERAL INFORMA  
GENERAL INFORMA  
Sequence 5, Appl  
Sequence 2, Appl  
Sequence 90, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 38, Appl  
Sequence 30, Appl  
Sequence 38, Appl  
Sequence 15, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 10, Appl  
Sequence 14, Appl  
Sequence 15, Appl  
Sequence 16, Appl  
Sequence 38, Appl

CHOLESTEROL-OXIDASE-FROM  
CHOLESTEROL-OXIDASE-FROM

PCT-US92-08094-63  
US-08-488-015B-11  
US-07-862-831A-1  
US-07-862-831A-2  
US-08-126-564A-1  
US-08-126-564A-2  
US-08-126-564A-3  
US-09-153-242-31  
US-09-491-795-6  
US-10-055-732-14  
PCT-US94-09143-1  
PCT-US94-09143-2  
US-07-791-213D-45  
US-08-232-144-6  
US-08-242-402-20  
US-08-234-613-10  
US-08-370-180-19  
US-08-488-672-1  
US-08-533-912-6  
US-08-293-150A-45  
US-08-465-590-140  
US-08-237-973-10  
US-08-237-973-26  
US-08-682-423-19  
US-08-646-301A-12  
US-09-116-032-3  
US-08-711-417C-140  
US-09-220-794-10  
US-09-723-909-140  
US-08-708-354-1  
US-09-337-619-110  
US-09-686-631-12  
US-09-657-289A-1  
US-08-453-485B-17  
US-09-530-663B-16  
PCT-US93-05331-1  
PCT-US93-08743-140  
PCT-US95-05141-19  
PCT-US91-03680-54  
PCT-US91-03680-56  
US-08-646-301A-13  
US-09-632-538C-11  
US-09-263-692A-8  
PCT-US91-03680-33  
US-08-268-679B-7  
US-08-973-568-55  
US-07-630-288A-7  
US-08-468-049-7  
US-08-807-104-19  
US-08-480-068-19  
US-08-973-568-51  
US-08-973-568-54  
US-08-973-137-19  
US-09-498-608A-8  
US-09-498-608A-9  
CHOLESTEROL-OXIDASE-FROM  
CHOLESTEROL-OXIDASE-FROM  
US-09-248-093-5  
US-09-545-153-2  
PCT-US91-03680-90  
PCT-US92-10024-2  
PCT-US94-06456-9  
PCT-US94-06456-38  
PCT-US94-08023-30  
US-07-630-288A-38  
US-08-247-809A-15  
US-08-116-801C-1  
US-08-116-801C-2  
US-08-435-480-10  
US-08-381-097A-14  
US-08-381-097A-15  
US-08-381-097A-16  
US-08-468-049-38

ALIGNMENTS

RESULT 1  
US-08-533-912-7  
; Sequence 7, Application US/08533912  
; Patent No. 5744308  
; GENERAL INFORMATION:  
; APPLICANT: GUILLOU-BONNICI, Francoise  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: MALLET, Francois  
; APPLICANT: LEVASSEUR, Pierre  
; APPLICANT: MCALISTER, William  
; TITLE OF INVENTION: CHIMERA OLIGONUCLEOTIDE AND ITS  
; TITLE OF INVENTION: UTILIZATION FOR OBTAINING TRANSCRIPTS OF A NUCLEIC ACID  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Oliff & Berridge  
; STREET: 700 South Washington Street, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/533,912  
; FILING DATE: 26-SEP-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94011455  
; FILING DATE: 26-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 36613  
; TELEPHONE: 703-836-6400  
; TELEFAX: 703-836-2787  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-08-533-912-7

Query Match 83.3%; Score 5; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAGG 6  
DB 1 GAAGG 5

RESULT 2  
US-09-266-965-91  
; Sequence 91, Application US/09266965  
; Patent No. 6495348  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D  
; APPLICANT: Mao, Y  
; APPLICANT: Varoglu, M  
; APPLICANT: He, M  
; APPLICANT: Sheldon, P  
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS

; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
; FILE REFERENCE: 600.456US1  
; CURRENT APPLICATION NUMBER: US/09/266,965  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: US 08/624,447  
; EARLIER FILING DATE: 1996-08-19  
; EARLIER APPLICATION NUMBER: PCT/US94/11279  
; EARLIER FILING DATE: 1994-10-06  
; EARLIER APPLICATION NUMBER: US 08/133,963  
; EARLIER FILING DATE: 1993-10-07  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 91  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Streptomyces lavendulae  
US-09-266-965-91

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.4e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
DB 1 GGAAGG 6

RESULT 3  
US-09-266-965-93  
; Sequence 93, Application US/09266965  
; Patent No. 6495348  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D  
; APPLICANT: Mao, Y  
; APPLICANT: Varoglu, M  
; APPLICANT: He, M  
; APPLICANT: Sheldon, P  
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
; FILE REFERENCE: 600.456US1  
; CURRENT APPLICATION NUMBER: US/09/266,965  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: US 08/624,447  
; EARLIER FILING DATE: 1996-08-19  
; EARLIER APPLICATION NUMBER: PCT/US94/11279  
; EARLIER FILING DATE: 1994-10-06  
; EARLIER APPLICATION NUMBER: US 08/133,963  
; EARLIER FILING DATE: 1993-10-07  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 93  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Streptomyces lavendulae  
US-09-266-965-93

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.4e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
DB 1 GGAAGG 6

RESULT 4  
US-09-798-542-23  
; Sequence 23, Application US/09798542  
; Patent No. 6685948  
; GENERAL INFORMATION:  
; APPLICANT: Zeng, Lingling  
; APPLICANT: Markoff, Lewis  
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS



; TITLE OF INVENTION: VACCINES  
; FILE REFERENCE: NIH45-001C1  
; CURRENT APPLICATION NUMBER: US/09/798,542  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: PCT/US 99/02598  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 60/098,981  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 6  
; TYPE: RNA  
; ORGANISM: Flavivirus, Dengue Type 2  
US-09-798-542-23

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.4e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
| | | | |  
Db 1 GUAAGG 6

RESULT 5  
US-09-798-542-24/c  
; Sequence 24, Application US/09798542  
; Patent No. 6685948  
; GENERAL INFORMATION:  
; APPLICANT: Zeng, Lingling  
; APPLICANT: Markoff, Lewis  
; TITLE OF INVENTION: REPLICATION-DEFECTIVE DENGUE VIRUSES  
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS  
; FILE OF INVENTION: VACCINES  
; FILE REFERENCE: NIH45-001C1  
; CURRENT APPLICATION NUMBER: US/09/798,542  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: PCT/US 99/02598  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 60/098,981  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 6  
; TYPE: RNA  
; ORGANISM: Flavivirus, Dengue Type 2  
US-09-798-542-24

Query Match 73.3%; Score 4.4; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.4e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
| | | | |  
Db 6 GTAAGG 1

RESULT 6  
US-08-717-526-76/c  
; Sequence 76, Application US/08717526  
; Patent No. 5786147  
; GENERAL INFORMATION:  
; APPLICANT: MABILAT, CLAUDE  
; APPLICANT: RAULT, DIDIER  
; TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE  
; STREET: 700 SOUTH WASHINGTON STREET  
; CITY: ALEXANDRIA  
; STATE: VA

; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,526  
; FILING DATE: 17-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERRIDGE, WILLIAM P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38732  
; TELEPHONE: 703-836-6400  
; TELEFAX: 703-836-2787  
; INFORMATION FOR SEQ ID NO: 76:  
; LENGTH: 5 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-717-526-76

Query Match 66.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
| | | |  
Db 4 GGAA 1

RESULT 7  
US-08-873-709-8  
; Sequence 8, Application US/08873709  
; Patent No. 6037126  
; GENERAL INFORMATION:  
; APPLICANT: Grossman, Abraham  
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND  
; TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF  
; TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abraham Grossman  
; STREET: 666 Washington Avenue  
; CITY: Pleasantville  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10570  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/873,709  
; FILING DATE: 12-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: Q001/002  
; TELEPHONE: 914-747-9108  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: RNA

US-08-873-709-8

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
Db 2 GGAA 5

RESULT 8  
US-08-537-765-3/c  
Sequence 3, Application US/08537765  
Patent No. 6150169  
GENERAL INFORMATION:  
APPLICANT: SMITH, Austin Gerard  
APPLICANT: MOUNTFORD, Peter Scott  
APPLICANT: LATHE, Richard Frank  
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS GENES  
TITLE OF INVENTION: ACCORDING TO A TARGETED EXPRESSION PROFILE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Finnegan, Henderson, Farrahaw, Garrett &  
ADDRESSER: Dunner, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 02005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,765  
FILING DATE: 25-JAN-1996  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB94/00849  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9308271.7  
FILING DATE: 21-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9313323.9  
FILING DATE: 28-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9401011.3  
FILING DATE: 20-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, Leslie A  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 06999.0001  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-537-765-3

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
Db 2 GGAA 5

US-08-623-428D-62/c  
Sequence 62, Application US/08623428D  
Patent No. 6312890  
GENERAL INFORMATION:  
APPLICANT: W. MARSTON LINEHAN, MICHAEL  
LERMAN, FARIDA LATIF AND BERTON  
ZBAR  
TITLE OF INVENTION: PARTIAL INTRON SEQUENCE  
OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS  
OF DISEASE CARRIERS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/623,428D  
FILING DATE: 05-SEP-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/623,428  
FILING DATE: MARCH 28, 1996  
APPLICATION NUMBER: 08/061,889  
FILING DATE: May 14, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kathryn M. Brown  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4078US3  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 62  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 62

US-08-623-428D-62

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
Db 5 GGAA 2

US-09-869-875-5/c  
Sequence 5, Application US/09869875  
Patent No. 6521456  
GENERAL INFORMATION:  
APPLICANT: Siebenkotten, Gregor  
APPLICANT: Christline, Rainer  
TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACID  
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE  
FILE REFERENCE: 30430.IUSWO

QY 1 GGAA 4  
Db 5 GGAA 2

RESULT 9

US-08-623-428D-62/c  
Sequence 62, Application US/08623428D  
Patent No. 6312890  
GENERAL INFORMATION:  
APPLICANT: W. MARSTON LINEHAN, MICHAEL  
LERMAN, FARIDA LATIF AND BERTON  
ZBAR

TITLE OF INVENTION: PARTIAL INTRON SEQUENCE  
OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS  
OF DISEASE CARRIERS

NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/623,428D  
FILING DATE: 05-SEP-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/623,428  
FILING DATE: MARCH 28, 1996  
APPLICATION NUMBER: 08/061,889  
FILING DATE: May 14, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kathryn M. Brown  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4078US3  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 62  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 62

US-08-623-428D-62

Query Match 66.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
Db 5 GGAA 2

US-09-869-875-5/c  
Sequence 5, Application US/09869875  
Patent No. 6521456  
GENERAL INFORMATION:  
APPLICANT: Siebenkotten, Gregor  
APPLICANT: Christline, Rainer  
TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACID  
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE  
FILE REFERENCE: 30430.IUSWO

US-09-869-875-5/c

; CURRENT APPLICATION NUMBER: US/09/869,875  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: PCT/DE00/00061  
; PRIOR FILING DATE: 2000-01-03  
; PRIOR APPLICATION NUMBER: DE 199 00 513.3  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: DE 199 33 939.2  
; PRIOR FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA is PNA; mixed peptide/PNA sequence  
US-09-869-875-5

Query Match 66.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6  
DB 4 AAGG 1

RESULT 11  
US-09-869-875-11/c  
; Sequence 11, Application US/09869875  
; Patent No. 6521456  
; GENERAL INFORMATION:  
; APPLICANT: Siebenkotten, Gregor  
; TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACID  
; FILE REFERENCE: 30430.1USWO  
; CURRENT APPLICATION NUMBER: US/09/869,875  
; CURRENT FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: PCT/DE00/00061  
; PRIOR FILING DATE: 2000-01-03  
; PRIOR APPLICATION NUMBER: DE 199 00 513.3  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: DE 199 33 939.2  
; PRIOR FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA is PNA; mixed peptide/PNA sequence  
US-09-869-875-11

Query Match 66.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
DB 5 GGAA 2

RESULT 12  
PCT-US93-03027-8  
; Sequence 8, Application PC/TUS9303027  
; GENERAL INFORMATION:  
; APPLICANT: LEONARD, WARREN; TOLEDANO,  
; APPLICANT: MICHEL  
; TITLE OF INVENTION: CONTROL AND/OR  
; TITLE OF INVENTION: PREVENTION OF BINDING OF NF- B/REL/DORSAL

; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; OPERATING SYSTEM: IBM PC COMPATIBLE  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/03027  
; FILING DATE: 19930401  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/862,987  
; FILING DATE: 06-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOROTHY R. AUTH  
; REGISTRATION NUMBER: P-36,434  
; REFERENCE/DOCKET NUMBER: 2026-4010 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: oligonucleotide  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: "B" half of Ig- B binding  
; NAME/KEY: site  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
PCT-US93-03027-8

Query Match 66.7%; Score 4; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
DB 1 GGAA 4

RESULT 13  
US-08-211-682-7  
; Sequence 7, Application US/08211682  
; Patent No. 5670333  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN E. COLI UNDER  
; TITLE OF INVENTION: CONTROL OF THE E. COLI MDH-GENE PROMOTER  
; NUMBER OF SEQUENCES: 25  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211,682  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double

```
/
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-211-682-7

Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
Db 2 AAGG 5

RESULT 14
US-08-211-682-8
/ Sequence 8, Application US/08211682
/ Patent No. 5670333
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN E. COLI UNDER
/ TITLE OF INVENTION: CONTROL OF THE E. COLI MDH-GENE PROMOTER
/ NUMBER OF SEQUENCES: 25
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/211,682
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-211-682-8

Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
Db 2 GGAA 5

RESULT 15
US-08-553-185-5
/ Sequence 5, Application US/08553185
/ Patent No. 5922535
/ GENERAL INFORMATION:
/ APPLICANT: Huo Ph.D., Li
/ TITLE OF INVENTION: IDENTIFYING SEQUENCE DIFFERENCES IN
/ TITLE OF INVENTION: NUCLEIC ACID POPULATIONS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Choate, Hall & Stewart
/ STREET: 53 State Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: usa
/ ZIP: 01773
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553,185
/ FILING DATE: 07-NOV-1995
/ CLASSIFICATION: 435

/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jarrell Ph.D., Brenda H
/ REGISTRATION NUMBER: 39,223
/ REFERENCE/DOCKET NUMBER: 0379373-0001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 248-5175
/ TELEFAX: (617) 248-4000
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ IMMEDIATE SOURCE:
/ CLONE: sequence B
US-08-553-185-5

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
Db 1 GAAG 4

RESULT 16
US-08-442-809A-2/c
/ Sequence 2, Application US/08442809A
/ Patent No. 5976873
/ GENERAL INFORMATION:
/ APPLICANT: Bohinski, Robert J.,
/ APPLICANT: Whitsett, Jeffrey A.,
/ TITLE OF INVENTION: Nucleic Acid Sequences
/ TITLE OF INVENTION: Controlling Lung Cell -
/ TITLE OF INVENTION: Specific Gene Expression
/ NUMBER OF SEQUENCES: 76
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Carelia, Byrne, Bain, Gilfillan,
/ ADDRESSEE: Cecchi, Stewart & Olstein
/ STREET: 6 Becker Farm Road
/ CITY: Roseland
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch diskette
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/442,809A
/ FILING DATE: 17-MAY-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,356
/ FILING DATE: 18-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Olstein, Elliot M.
/ REGISTRATION NUMBER: 24,025
/ REFERENCE/DOCKET NUMBER: 271010-360
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: oligonucleotide
```

## US-08-442-809A-2

Query Match 66.7%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
Db 4 GAAG 1

## RESULT 17

US-08-442-809A-10  
; Sequence 10, Application US/08442809A  
; Patent No. 5976873  
; GENERAL INFORMATION:  
; APPLICANT: Bohinski, Robert J.,  
; APPLICANT: Whitsett, Jeffrey A.  
; TITLE OF INVENTION: Nucleic Acid Sequences  
; TITLE OF INVENTION: Controlling Lung Cell -  
; TITLE OF INVENTION: Specific Gene Expression  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
; ADDRESSEE: Cecchi, Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,809A  
; FILING DATE: 17-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/245,356  
; FILING DATE: 18-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olstein, Elliot M.  
; REGISTRATION NUMBER: 24,025  
; REFERENCE/DOCKET NUMBER: 271010-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: oligonucleotide

## US-08-442-809A-10

Query Match 66.7%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
Db 3 GAAG 6

## RESULT 18

US-09-056-868B-14/c  
; Sequence 14, Application US/09056868B  
; Patent No. 6316218  
; GENERAL INFORMATION:  
; APPLICANT: Podolsky, Daniel K.

## ; TITLE OF INVENTION: INTESTINAL TREFOIL PROTEINS

; FILE REFERENCE: 00786-066005  
; CURRENT APPLICATION NUMBER: US/09/056,868B  
; CURRENT FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: US 08/476,705  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/191,352  
; PRIOR FILING DATE: 1994-02-02  
; PRIOR APPLICATION NUMBER: US 08/037,741  
; PRIOR FILING DATE: 1993-03-25  
; PRIOR APPLICATION NUMBER: US 07/837,192  
; PRIOR FILING DATE: 1992-02-13  
; PRIOR APPLICATION NUMBER: US 07/655,965  
; PRIOR FILING DATE: 1991-02-14  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically generated primer  
US-09-056-868B-14

Query Match 66.7%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
Db 5 GGAA 2

## RESULT 19

US-09-632-538C-10/c  
; Sequence 10, Application US/09632538C  
; Patent No. 6440674  
; GENERAL INFORMATION:  
; APPLICANT: Misra, Santosh et al.  
; TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH  
; TITLE OF INVENTION: ITS USE  
; FILE REFERENCE: 54359  
; CURRENT APPLICATION NUMBER: US/09/632,538C  
; CURRENT FILING DATE: 2000-08-04  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (3)  
; OTHER INFORMATION: W = a, t, or u  
; OTHER INFORMATION: Description of Artificial Sequence: PROMOTER  
; OTHER INFORMATION: ELEMENT  
US-09-632-538C-10

Query Match 66.7%; Score 4; DB 3; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.4e+08;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
Db 6 GGTWGG 1

## RESULT 20

US-09-608-958-50  
; Sequence 50, Application US/09608958  
; Patent No. 6518066  
; GENERAL INFORMATION:  
; APPLICANT: McBride, K.

/ APPLICANT: Oulmassov, T.  
 / APPLICANT: Miller, P.  
 / APPLICANT: Anderson, J.C.  
 / APPLICANT: Crossland, L.  
 / APPLICANT: Adams, T.  
 / APPLICANT: Gavrias, V.  
 / TITLE OF INVENTION: Control of Gene Expression in Eukaryotic Cells  
 / FILE REFERENCE: 15376/03/US  
 / CURRENT APPLICATION NUMBER: US/09/608,958  
 / CURRENT FILING DATE: 2000-06-30  
 / PRIOR APPLICATION NUMBER: 60/148,441  
 / PRIOR FILING DATE: 1999-07-01  
 / PRIOR APPLICATION NUMBER: 60/177,578  
 / PRIOR FILING DATE: 2000-01-22  
 / PRIOR APPLICATION NUMBER: 60/195,690  
 / PRIOR FILING DATE: 2000-04-07  
 / NUMBER OF SEQ ID NOS: 57  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 50  
 / LENGTH: 6  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic Oligonucleotide  
 US-09-608-958-50

Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6  
 Db 1 AAGG 4

RESULT 21  
 US-09-608-958-51/c  
 / Sequence 51, Application US/09608958  
 / Patent No. 6518066  
 / GENERAL INFORMATION:  
 / APPLICANT: McBride, K.  
 / APPLICANT: Oulmassov, T.  
 / APPLICANT: Miller, P.  
 / APPLICANT: Anderson, J.C.  
 / APPLICANT: Crossland, L.  
 / APPLICANT: Adams, T.  
 / APPLICANT: Gavrias, V.  
 / TITLE OF INVENTION: Control of Gene Expression in Eukaryotic Cells  
 / FILE REFERENCE: 15376/03/US  
 / CURRENT APPLICATION NUMBER: US/09/608,958  
 / CURRENT FILING DATE: 2000-06-30  
 / PRIOR APPLICATION NUMBER: 60/148,441  
 / PRIOR FILING DATE: 1999-07-01  
 / PRIOR APPLICATION NUMBER: 60/177,578  
 / PRIOR FILING DATE: 2000-01-22  
 / PRIOR APPLICATION NUMBER: 60/195,690  
 / PRIOR FILING DATE: 2000-04-07  
 / NUMBER OF SEQ ID NOS: 57  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 51  
 / LENGTH: 6  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic Oligonucleotide  
 US-09-608-958-51

Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
 Db 4 GGAA 1  
 RESULT 22  
 US-09-435-327A-1  
 / Sequence 1, Application US/09435327A  
 / Patent No. 6537766  
 / GENERAL INFORMATION:  
 / APPLICANT: Uckun, Fatih M.  
 / APPLICANT: Crotty, Mya L.  
 / TITLE OF INVENTION: IKAROS ISOFORMS AND MUTANTS  
 / FILE REFERENCE: 12152.35USU1  
 / CURRENT APPLICATION NUMBER: US/09/435,327A  
 / CURRENT FILING DATE: 1999-11-05  
 / PRIOR APPLICATION NUMBER: 60/107,229  
 / PRIOR FILING DATE: 1998-11-05  
 / NUMBER OF SEQ ID NOS: 27  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 1  
 / LENGTH: 6  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-09-435-327A-1

Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
 Db 2 GGAA 5

RESULT 23  
 US-09-585-599A-7/c  
 / Sequence 7, Application US/09585599A  
 / Patent No. 6544780  
 / GENERAL INFORMATION:  
 / APPLICANT: Wang, Danher  
 / TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES LC  
 / FILE REFERENCE: 22488-706  
 / CURRENT APPLICATION NUMBER: US/09/585,599A  
 / CURRENT FILING DATE: 2000-06-02  
 / NUMBER OF SEQ ID NOS: 8  
 / SOFTWARE: PatentIn version 3.1  
 / SEQ ID NO 7  
 / LENGTH: 6  
 / TYPE: RNA  
 / ORGANISM: Artificial sequence  
 / FEATURE:  
 / OTHER INFORMATION: Modified RNA editing site.  
 US-09-585-599A-7

Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
 Db 6 GAAG 3

RESULT 24  
 US-09-585-599A-8/c  
 / Sequence 8, Application US/09585599A  
 / Patent No. 6544780  
 / GENERAL INFORMATION:  
 / APPLICANT: Wang, Danher  
 / TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES LC  
 / FILE REFERENCE: 22488-706  
 / CURRENT APPLICATION NUMBER: US/09/585,599A  
 / CURRENT FILING DATE: 2000-06-02  
 / NUMBER OF SEQ ID NOS: 8  
 / SOFTWARE: PatentIn version 3.1  
 / SEQ ID NO 7  
 / LENGTH: 6  
 / TYPE: RNA  
 / ORGANISM: Artificial sequence  
 / FEATURE:  
 / OTHER INFORMATION: Modified RNA editing site.  
 US-09-585-599A-7

Query Match 66.7%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: 22488-706  
CURRENT APPLICATION NUMBER: US/09/585,599A  
CURRENT FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 8  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: DNA of modified RNA editing site.  
US-09-585-599A-8

Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
Db 6 GAAG 3

RESULT 25  
US-10-014-973A-16  
Sequence 16, Application US/10014973A  
Patent No. 6706481  
GENERAL INFORMATION:  
APPLICANT: Ellington, Andrew  
APPLICANT: Jhaveri, Sulay  
APPLICANT: Rajendran, Manjula  
TITLE OF INVENTION: In Vitro Selection of Signaling Aptamers  
FILE REFERENCE: D6297  
CURRENT APPLICATION NUMBER: US/10/014,973A  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: US 60/244,010  
PRIOR FILING DATE: 2000-10-27  
NUMBER OF SEQ ID NOS: 19  
SEQ ID NO 16  
LENGTH: 6  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Sequence of the 6 nucleotide motif shared by  
Patent No. 6706481  
OTHER INFORMATION: Families 1 and 2  
US-10-014-973A-16

Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
Db 3 GAAG 6

RESULT 26  
US-09-851-271A-14  
Sequence 14, Application US/09851271A  
Patent No. 6733970  
GENERAL INFORMATION:  
APPLICANT: Gendaq Limited  
TITLE OF INVENTION: Screening System  
FILE REFERENCE: 674538-2003  
CURRENT APPLICATION NUMBER: US/09/851,271A  
CURRENT FILING DATE: 2001-05-08  
PRIOR APPLICATION NUMBER: PCT/GB99/03730  
PRIOR FILING DATE: 1999-11-09  
PRIOR APPLICATION NUMBER: GB9824544.2  
PRIOR FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 14

LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: RBS  
LOCATION: (1)..(6)  
OTHER INFORMATION: bacteriophage T7, gene 10 ribosome binding site  
US-09-851-271A-14

Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6  
Db 1 AAGG 4

RESULT 27  
US-10-134-188-13  
Sequence 13, Application US/10134188  
Patent No. 6803230  
GENERAL INFORMATION:  
APPLICANT: Bowdiah, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Wild, Martha  
TITLE OF INVENTION: PHAGEMID VECTORS  
FILE REFERENCE: 1087-22 (70)  
CURRENT APPLICATION NUMBER: US/10/134,188  
CURRENT FILING DATE: 2002-04-26  
PRIOR APPLICATION NUMBER: US 60/287,355  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 13  
LENGTH: 6  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: RBS  
US-10-134-188-13

Query Match 66.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6  
Db 1 AAGG 4

RESULT 28  
PCT-US92-08094-63  
Sequence 63, Application PC/TUS9208094  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: Amanto, Edward P.  
TITLE OF INVENTION: DIAGNOSING AND TREATING AUTOIMMUNE  
DISORDERS  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080-4990  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: PCT/US92/08094  
/ FILING DATE: 19920923  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 07/765222  
/ FILING DATE: 23-SEP-1991  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 07/779445  
/ FILING DATE: 18-OCT-1991  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 07/853362  
/ FILING DATE: 18-MAR-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Hensley, Max D.  
/ REGISTRATION NUMBER: 27,043  
/ REFERENCE/DOCKET NUMBER: 734P3  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415/225-1994  
/ TELEFAX: 415/952-9881  
/ TELEX: 910/371-7168  
/ INFORMATION FOR SEQ ID NO: 63:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6 bases  
/ TYPE: NUCLEIC ACID  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ PCT-US92-08094-63

Query Match 66.7%; Score 4; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.4e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 4  
DB 2 GGAA 5

RESULT 29  
US-08-488-015B-11/c  
/ Sequence 11, Application US/08488015B  
/ Patent No. 5780272  
/ GENERAL INFORMATION:  
/ APPLICANT: Jarrell, Kevin A.  
/ TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES  
/ TITLE OF INVENTION: AND REAGENTS  
/ NUMBER OF SEQUENCES: 29  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Foley, Hoag & Eliot  
/ STREET: One Post Office Square  
/ CITY: Boston  
/ STATE: MA  
/ COUNTRY: USA  
/ ZIP: 02109  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: ASCII (text)  
/ CURRENT APPLICATION DATA:  
/ FILING DATE: 07-JUN-1995  
/ APPLICATION NUMBER: US/08/488,015B  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Vincent, Matthew P.  
/ REGISTRATION NUMBER: 36,709  
/ REFERENCE/DOCKET NUMBER: HUV-008.02  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617) 832-1000  
/ TELEFAX: (617) 832-7000  
/ INFORMATION FOR SEQ ID NO: 11:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 5 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single

/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA  
/ US-08-488-015B-11

Query Match 60.0%; Score 3.6; DB 1; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.9e+08;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
DB 5 GGAG 2

RESULT 30  
US-07-862-831A-1  
/ Sequence 1, Application US/07862831A  
/ Patent No. 5356802  
/ GENERAL INFORMATION:  
/ APPLICANT: Chandrasegaran, Srinivasan  
/ TITLE OF INVENTION: Functional Domains in FokI Restriction  
/ TITLE OF INVENTION: Endonuclease  
/ NUMBER OF SEQUENCES: 20  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Cushman, Darby & Cushman  
/ STREET: 1615 L St., N.W.  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20036-5601  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/862,831A  
/ FILING DATE: 19920403  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Kokulis, Paul N.  
/ REGISTRATION NUMBER: 16,773  
/ REFERENCE/DOCKET NUMBER: PNK/4130/93738/SLO  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-861-3000  
/ TELEFAX: 202-822-0944  
/ TELEX: 6714627 CUSH  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 5 base pairs  
/ TYPE: NUCLEIC ACID  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-07-862-831A-1

Query Match 56.7%; Score 3.4; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 2.9e+08;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAG 5  
DB 1 GGATG 5

Search completed: July 21, 2005, 04:29:23  
Job time : 61 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds

(without alignments)  
169.325 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 5     | 83.3        | 5      | 9     | CL658581           |
| 2          | 5     | 83.3        | 6      | 9     | CL683697           |
| 3          | 4     | 66.7        | 4      | 7     | CF307853           |
| 4          | 4     | 66.7        | 4      | 7     | CF307853 ABF--01-G |
| 5          | 4     | 66.7        | 4      | 7     | CN755098           |
| 6          | 4     | 66.7        | 4      | 9     | CN755098 ID0AAA14D |
| 7          | 4     | 66.7        | 5      | 9     | CL677539           |
| 8          | 4     | 66.7        | 5      | 9     | CL677539 PRI0120C  |
| 9          | 4     | 66.7        | 6      | 1     | AL039368           |
| 10         | 4     | 66.7        | 6      | 1     | AL039947           |
| 11         | 4     | 66.7        | 6      | 1     | AL042484           |
| 12         | 3.4   | 56.7        | 5      | 9     | CL684862           |
| 13         | 3.4   | 56.7        | 6      | 9     | CL689395           |
| 14         | 3     | 50.0        | 3      | 7     | CF282217           |
| 15         | 3     | 50.0        | 3      | 7     | CF282217 14ETL--09 |
| 16         | 3     | 50.0        | 3      | 7     | CF300120           |
| 17         | 3     | 50.0        | 3      | 7     | CF309377           |
| 18         | 3     | 50.0        | 3      | 7     | CF311041           |
| 19         | 3     | 50.0        | 3      | 7     | CF315183           |
| 20         | 3     | 50.0        | 3      | 7     | CF340104           |
| 21         | 3     | 50.0        | 3      | 9     | CO790264           |
| 22         | 3     | 50.0        | 3      | 9     | CL654446           |
| 23         | 3     | 50.0        | 3      | 9     | CL674562           |
| 24         | 3     | 50.0        | 3      | 9     | CL679821           |
|            |       |             |        |       | CL694726           |

AL045617 DKFZp4340  
CF300913 7LEAF--05  
CF317789 HD--07-J1  
CF317847 HD--07-L0  
CF318240 HD--08-E1  
CF338536 RCL1--01-  
CF338536 RCL1--01-  
CK582549 IST WI5 4  
CL651736 PRI0112D  
CL679140 PRI0125B  
CL682759 PRI0134D  
AL042460 DKFZp434E  
AL046203 DKFZp434D  
CF300878 7LEAF--05  
CF327578 NACL--02-  
CF332399 NACL--08-  
CK584110 IST WI5 1  
CO779181 BL005D E0  
CL423471 01S0557-0  
CL61701 PRI013C C  
CL65291 PRI0140D  
CL696246 PRI018C C  
CA850767 D06C11 C1  
CA850861 D07D05 G1  
CA850904 D07H10 O2  
CF302557 7LEAF--08  
CF312755 ABF--08-K  
CF314367 HD--02-N2  
CF338772 RCL1--02-  
CL665420 PRI0149C  
CL65420 PRI0149C  
CL672294 PRI016C B  
CL679615 PRI0126C  
CL687157 PRI0146A  
CL687789 PRI0147D  
CA850974 D08G08 N2  
CL655267 PRI0122D  
CL670570 PRI0162C  
CL889653 abf96d10.  
CA853329 B07A01.se  
CF314074 HD--02-H0  
CF323326 HDN--03-I  
CO789717 NT007C G0  
CL688637 PRI014A B  
AL043164 DKFZp434F  
CF310635 ABF--05-G  
CF338261 RCL1--01-  
CL680271 PRI0128C  
CL694328 PRI0163D  
AL039341 DKFZp434F  
AL042337 DKFZp434O  
AL043859 DKFZp434B  
AL047069 DKFZp586P  
BX266185 BX266185  
BX266563 BX266563  
BX267118 BX267118  
CA850842 D07B06 C1  
CA850952 D08E09 J2  
CF280384 14ETL--07  
CF280511 14ETL--07  
CF281505 14ETL--08  
CF282353 14ETL--09  
CF291112 14ROOF--0  
CF292081 14ROOF--0  
CF295832 30DGS--05  
CF296698 30DGS--07  
CF299103 7LEAF--02  
CF299571 7LEAF--03  
CF299820 7LEAF--03  
CF300639 7LEAF--05  
CF301112 7LEAF--05  
CF302235 7LEAF--07  
CF302259 7LEAF--07  
CF307123 HD01--05-

98 2 33.3 2 7 CF307878 CF307878 ABF--01-H  
 99 2 33.3 2 7 CF311389 CF311389 ABF--06-J  
 100 2 33.3 2 7 CF311851 CF311851 ABF--07-E

## ALIGNMENTS

RESULT 1  
 LOCUS  
 DEFINITION  
 CL658581  
 PRI0131d\_E08 - PRI0131d.B21 (5) Mixed stage fosmid library of P.  
 pacificus var. California Pristionchus pacificus genomic, genomic  
 survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 CL658581.1 GI:50141502  
 GSS.  
 Pristionchus pacificus  
 Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 AppADB: an AcedB database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

FEATURES  
 source  
 1..5  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pEpifos-5 Fosmid vector"

Query Match 83.3%; Score 5; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GAAGG 6  
 |||||  
 Db 1 GAAGG 5

RESULT 2  
 CL683697/c  
 LOCUS  
 DEFINITION  
 CL683697  
 PRI0137c\_D12.2 - PRI0137c.BR (6) Mixed stage fosmid library of P.  
 pacificus var. California Pristionchus pacificus genomic, genomic  
 survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 CL683697.1 GI:50191457  
 GSS.  
 Pristionchus pacificus  
 Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.

REFERENCE  
 AUTHORS  
 TITLE  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 AppADB: an AcedB database for the nematode satellite organism

JOURNAL  
 COMMENT  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

FEATURES  
 source  
 1..6  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN  
 Query Match 83.3%; Score 5; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+09;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAAG 5  
 |||||  
 Db 5 GGAAG 1

RESULT 3  
 CF307853/c  
 LOCUS  
 DEFINITION  
 CF307853  
 ABF--01-G24.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--01-G24, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 CF307853.1 GI:33679614  
 EST.  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..4  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF--01-G24"  
 /tissue type="leaf"  
 /dev stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: pCK4-TOPO; Site\_1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

## ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

Db 4 AAGG 1

## RESULT 4

CN755098/c  
LOCUS  
DEFINITION CN755098 4 bp mRNA linear EST 19-MAY-2004  
ID0AAA14DE08M1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA14DE08  
5', mRNA sequence.

ACCESSION CN755098

VERSION 1 GI:47520134

SOURCE EST.

ACyrthosiphon pisum (pea aphid)

ORGANISM Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 4)

AUTHORS Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Winkler, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon pisum

JOURNAL Unpublished (2004)

COMMENT Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 14 row: E column: 8.

Location/Qualifiers

source

1. .4

/organism="Acyrthosiphon pisum"

/mol\_type="mRNA"

/cultivar="developmentstage"

/db\_xref="taxon:7029"

/clone="ID0AAA14DE08"

/tissue\_type="whole insect"

/dev\_stage="nymphs and adults (parthenogenetic females)"

/lab\_host="XLI-blue"

/clone\_lib="ApMS"

/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;  
Sample name: ID0AAA ; plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil, Sowing, date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

## ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

Db 4 AAGG 1

## RESULT 5

CN755098/c

LOCUS

DEFINITION

CN755098 4 bp DNA linear GSS 09-JUL-2004  
PRI0120c\_D05\_2 - PRI0120c.BR (4) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL677539

VERSION 1 GI:50183547

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 4)

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT Contact: Sommer RJ

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

source

1. .4

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

## ORIGIN

Query Match 66.7%; Score 4; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.5e+09;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5

Db 4 GAAG 1

## RESULT 6

CN755098/c

LOCUS

DEFINITION

CN755098 5 bp DNA linear GSS 09-JUL-2004  
PRI019a\_E01 - PRI019a.B21 (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL673276

VERSION 1 GI:50174761

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 5)

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT Contact: Sommer RJ

Evolutionary Biology

```

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends
Location/Qualifiers
 1..5
 /organism="Prioniochus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 66.7%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
 ||||
Db 4 AAGG 1

RESULT 7
AL039368
LOCUS
DEFINITION
 DKFZp434I0110_r1_434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION
 AL039368
VERSION
 AL039368.1 GI:49682284
KEYWORDS
 EST.
SOURCE
 Homo sapiens (human)
ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 6)
AUTHORS
 Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
 Wiemann,S.
TITLE
 EST (Duesterhoeft, et al.)
JOURNAL
 Unpublished (1999)
COMMENT
 Contact: MIPS
MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
 1..6
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp434J0112"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="434 (synonym: htes3)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
 ||||
Db 1 GGAA 4

RESULT 9
AL042484
LOCUS
DEFINITION
 DKFZp434F0321_r1_434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION
 AL042484
VERSION
 AL042484.1 GI:49682438
KEYWORDS
 EST.
SOURCE
 Homo sapiens (human)
ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 6)
AUTHORS
 Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE
 EST (Blum, et al.)
JOURNAL
 Unpublished (1999)
COMMENT
 Contact: MIPS
MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
 1..6
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp434F0321"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="434 (synonym: htes3)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 66.7%; Score 4; DB 1; Length 6;

```



```

Db
1 CGAGG 5

RESULT 13
LOCUS
DEFINITION
CL689395
PFI0151a.D04_2 - PFI0151a.BR (6) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL689395
CL689395.1 GI:50211303
GSS.
Pristionchus pacificus
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 6)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..6
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pPifos-5 Fosmid vector"

ORIGIN
Query Match 56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAAGG 6
|||
Db 6 GATGG 2

RESULT 14
CF282217
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K02,
mRNA sequence.
CF282217
CF282217.1 GI:33659604
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAAGG 6
|||
Db 6 GATGG 2

```

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-K02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGA 3
|||
Db 1 GGA 3

RESULT 15
CF300120/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G11, mRNA
sequence.
CF300120
CF300120.1 GI:33671881
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

```



```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3994.7"
/clone="HD--04-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCRA-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

## ORIGIN

```

Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGA 3

Db |||

Db 1 GGA 3

## RESULT 19

CF340104

LOCUS

```

DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-P10,
mRNA sequence.

```

ACCESSION CF340104.1 GI:33828568

VERSION

KEYWORDS

SOURCE

ORGANISM

```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

```

REFERENCE 1 (bases 1 to 3)

```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.

```

## FEATURES

source

1..3

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3994.7"
/clone="RCL1--06-P10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

```

## ORIGIN

```

Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 AAG 5

Db |||

Db 1 AAG 3

## RESULT 20

CF790264

LOCUS

```

DEFINITION
NT009A_H05 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5',
similar to hypothetical protein, mRNA sequence.

```

ACCESSION CF790264

VERSION

KEYWORDS

SOURCE

ORGANISM

```

Ambystoma mexicanum (axolotl)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.

```

REFERENCE 1 (bases 1 to 3)

```

AUTHORS Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
JOURNAL Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka

```

Tanaka lab

```

Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfotenhauserstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de

```

Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

Location/Qualifiers

1..3

/organism="Ambystoma mexicanum"

/mol\_type="mRNA"

/db\_xref="taxon:8296"

/tissue\_type="Neural Tube, Notochord, Somites"

/cell\_type="Includes Neural tube, notochord, somites"

/dev\_stage="Stage 18-22"

/clone\_lib="St18-22 Neural tube (NT)"

```

/notes="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydt primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 kb.
TAG_LTB=NT"

```

## ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 7; Length 3;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6

Db |||

Db 1 AGG 3

## RESULT 21

CL654446

LOCUS

```

DEFINITION
CL654446 P05 - PR10120C.B21 (3) Mixed stage foetid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.

```

ACCESSION CL654446

VERSION

KEYWORDS

SOURCE

ORGANISM

Pristionchus pacificus

Pristionchus pacificus



```

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 3)
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 3
Db |||
3 GGA 1

RESULT 23
LOCUS CL679821/c
DEFINITION CL679821
3 bp DNA linear GSS 09-JUL-2004
PRI0127a E01.2 - PRI0127a.BR (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL679821
CL679821.1 GI:50186536
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 3)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
Db |||
1 GAA 3

RESULT 22
LOCUS CL674562/c
DEFINITION CL674562
3 bp DNA linear GSS 09-JUL-2004
PRI0112c A06.2 - PRI0112c.BR (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL674562
CL674562.1 GI:50177804
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 3)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

FEATURES
source
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
Db |||
3 AGG 1

RESULT 24
LOCUS CL694726
DEFINITION CL694726
3 bp DNA linear GSS 10-JUL-2004
PRI0165a A06.2 - PRI0165a.BR (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL694726
CL694726.1 GI:50216634
VERSION
KEYWORDS
SOURCE
Pristionchus pacificus

```

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ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 3)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
 source 1..33
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
 |||
Db 1 GAA 3

RESULT 25
AL045617/c
LOCUS
DEFINITION
ACCESSION AL045617
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wienann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES Location/Qualifiers
 source 1..4
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp434O245"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="434 (synonym: htes3)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 50.0%; Score 3; DB 1; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
 |||
Db 1 GAA 3

RESULT 26
CF300913/c
LOCUS
DEFINITION
ACCESSION CF300913
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 4)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
 source 1..4
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--05-J02"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."
ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
 |||
Db 3 AGG 1

RESULT 27
CF317789/c
LOCUS
DEFINITION
ACCESSION CF317789
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

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REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .4
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="HD--07-L01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 3
 |||
Db 3 GGA 1

RESULT 28
LOCUS CF317847/c
DEFINITION HD--07-L01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-L01, mRNA sequence.
ACCESSION CF317847
VERSION CF317847.1 GI:33689608
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .4
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 3
 |||
Db 3 GGA 1

RESULT 28
LOCUS CF317847/c
DEFINITION HD--07-L01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-L01, mRNA sequence.
ACCESSION CF317847
VERSION CF317847.1 GI:33689608
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .4
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/clone="HD--07-L01"

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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAG 5
 |||
Db 4 AAG 2

RESULT 29
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DEFINITION HD--08-E17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-E17, mRNA sequence.
ACCESSION CF318240
VERSION CF318240.1 GI:33690001
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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Location/Qualifiers
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/db_xref="taxon:39947"
/clone="HD--08-E17"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAG 5
 |||
Db 2 AAG 4

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RESULT 30
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LOCUS
DEFINITION
CF338536
4 bp mRNA linear EST 18-AUG-2003
RCL1--01-P22.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P22,
mRNA sequence.
ACCESSION
CF338536
VERSION
CF338536.1 GI:33825460
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..4
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--01-P22"
/tissue_type="callus"
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5',
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induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"
ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGA 3
|||
Db 2 GGA 4
Search completed: July 21, 2005, 01:54:36
Job time : 1352.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds  
(without alignments)  
189.533 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description         |
|------------|-------|---------------|--------|----|---------------------|
| 1          | 5     | 83.3          | 6      | 13 | Adr32744 Human nic  |
| 2          | 5     | 83.3          | 6      | 13 | Adr32766 Human nic  |
| 3          | 5     | 83.3          | 6      | 13 | Adr32505 Human nic  |
| 4          | 4.4   | 73.3          | 6      | 10 | Adel0263 S. lavendu |
| 5          | 4.4   | 73.3          | 6      | 10 | Adel0336 S. lavendu |
| 6          | 4.4   | 73.3          | 6      | 10 | Adel10336           |
| 7          | 4.4   | 73.3          | 6      | 10 | ACA88957 Selection  |
| 8          | 4     | 66.7          | 6      | 12 | ADJ35621 Stabilisi  |
| 9          | 4     | 66.7          | 6      | 2  | AAQ38797 PCR prime  |
| 10         | 4     | 66.7          | 6      | 2  | AAQ70690 Triplex f  |
| 11         | 4     | 66.7          | 6      | 4  | AAF91829 Breast-ca  |
| 12         | 4     | 66.7          | 6      | 8  | ACC69109 Cucumbe    |
| 13         | 4     | 66.7          | 6      | 8  | ABZ23991 Nucleotid  |
| 14         | 4     | 66.7          | 6      | 9  | ACH50860 Hypotheti  |
| 15         | 4     | 66.7          | 6      | 9  | ACH50844 Hypotheti  |
| 16         | 4     | 66.7          | 6      | 10 | ADD66333 Ebola GP   |
| 17         | 4     | 66.7          | 6      | 10 | ADD66334 Ebola GP   |
| 18         | 4     | 66.7          | 6      | 10 | AD838305 Immune mo  |
| 19         | 4     | 66.7          | 6      | 10 | AD838325 Immune mo  |
| 20         | 4     | 66.7          | 6      | 10 | AD838297 Immune mo  |
|            |       |               |        |    | AD838301 Immune mo  |

|    |     |      |   |    |          |                    |
|----|-----|------|---|----|----------|--------------------|
| 21 | 4   | 66.7 | 6 | 12 | ADK14286 | Adk14286 Candida p |
| 22 | 4   | 66.7 | 6 | 12 | ADK14297 | Adk14297 Candida p |
| 23 | 4   | 66.7 | 6 | 12 | ADL09220 | Adl09220 T3 promot |
| 24 | 4   | 66.7 | 6 | 13 | ADR34774 | Adr34774 Human nic |
| 25 | 4   | 66.7 | 6 | 13 | ADR34775 | Adr34775 Human nic |
| 26 | 4   | 66.7 | 6 | 13 | ADR34773 | Adr34773 Human nic |
| 27 | 4   | 66.7 | 6 | 13 | ADR37260 | Adr37260 Human nic |
| 28 | 4   | 66.7 | 6 | 13 | ADR33235 | Adr33235 Human nic |
| 29 | 4   | 66.7 | 6 | 13 | ADR32580 | Adr32580 Human nic |
| 30 | 4   | 66.7 | 6 | 13 | ADR37262 | Adr37262 Human nic |
| 31 | 4   | 66.7 | 6 | 13 | ADR34776 | Adr34776 Human nic |
| 32 | 4   | 66.7 | 6 | 13 | ADR37261 | Adr37261 Human nic |
| 33 | 4   | 66.7 | 6 | 13 | ADR37263 | Adr37263 Human nic |
| 34 | 3.6 | 60.0 | 6 | 13 | ADR35732 | Adr35732 Human nic |
| 35 | 3.6 | 60.0 | 6 | 13 | ADR35725 | Adr35725 Human nic |
| 36 | 3.6 | 60.0 | 6 | 13 | ADR35729 | Adr35729 Human nic |
| 37 | 3.6 | 60.0 | 6 | 13 | ADR35730 | Adr35730 Human nic |
| 38 | 3.6 | 60.0 | 6 | 13 | ADR35731 | Adr35731 Human nic |
| 39 | 3.6 | 60.0 | 6 | 13 | ADR35728 | Adr35728 Human nic |
| 40 | 3.6 | 60.0 | 6 | 13 | ADR35727 | Adr35727 Human nic |
| 41 | 3.6 | 60.0 | 6 | 13 | ADR35726 | Adr35726 Human nic |
| 42 | 3.4 | 56.7 | 5 | 3  | AAA56981 | Aaa56981 Human col |
| 43 | 3.4 | 56.7 | 5 | 6  | ABT12403 | Abt12403 Orestes s |
| 44 | 3.4 | 56.7 | 5 | 8  | ACD56683 | Acd56683 HBV RT pr |
| 45 | 3.4 | 56.7 | 5 | 8  | ABZ75665 | Abz75665 Helicase- |
| 46 | 3.4 | 56.7 | 5 | 8  | ABZ75667 | Abz75667 Helicase- |
| 47 | 3.4 | 56.7 | 5 | 8  | ABZ75663 | Abz75663 Helicase- |
| 48 | 3.4 | 56.7 | 5 | 10 | ADH60372 | Adh60372 Myctophid |
| 49 | 3.4 | 56.7 | 5 | 10 | ACD91697 | Acd91697 Human col |
| 50 | 3.4 | 56.7 | 6 | 2  | AAQ61541 | Aaq61541 TDT promo |
| 51 | 3.4 | 56.7 | 6 | 2  | AAQ53911 | Aaq53911 Portion o |
| 52 | 3.4 | 56.7 | 6 | 2  | AAV45399 | Aav45399 TDT promo |
| 53 | 3.4 | 56.7 | 6 | 3  | AAA62709 | Aaa62709 FNA clamp |
| 54 | 3.4 | 56.7 | 6 | 6  | ABS78162 | Abs78162 Angiogene |
| 55 | 3.4 | 56.7 | 6 | 8  | ACD56688 | Acd56688 HBV RT pr |
| 56 | 3.4 | 56.7 | 6 | 8  | ACD56687 | Acd56687 HBV RT pr |
| 57 | 3.4 | 56.7 | 6 | 9  | ACD99934 | Acd99934 Immunoe   |
| 58 | 3.4 | 56.7 | 6 | 12 | ADJ35694 | Adj35694 Stabilisi |
| 59 | 3.4 | 56.7 | 6 | 12 | ADJ35808 | Adj35808 Stabilisi |
| 60 | 3.4 | 56.7 | 6 | 12 | ADJ35691 | Adj35691 Stabilisi |
| 61 | 3.4 | 56.7 | 6 | 12 | ADJ35355 | Adj35355 Stabilisi |
| 62 | 3.4 | 56.7 | 6 | 12 | ADO04837 | Ado04837 Cpg oligo |
| 63 | 3.4 | 56.7 | 6 | 13 | ADR33236 | Adr33236 Human nic |
| 64 | 3.2 | 53.3 | 6 | 3  | AAA28440 | Aaa28440 Synthetic |
| 65 | 3.2 | 53.3 | 6 | 4  | AAF91843 | Aaf91843 Breast-ca |
| 66 | 3.3 | 50.0 | 3 | 10 | AD858066 | Ad858066 Human gen |
| 67 | 3.3 | 50.0 | 4 | 4  | AAL24357 | Aal24357 Human bre |
| 68 | 3.3 | 50.0 | 4 | 4  | AAF61450 | Aaf61450 Cyclin bi |
| 69 | 3.3 | 50.0 | 4 | 8  | ACD56767 | Acd56767 Synthetic |
| 70 | 3.3 | 50.0 | 4 | 8  | ACD56782 | Acd56782 Synthetic |
| 71 | 3.3 | 50.0 | 4 | 8  | ACD56773 | Acd56773 Synthetic |
| 72 | 3.3 | 50.0 | 4 | 8  | ACD56681 | Acd56681 HBV RT pr |
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| 76 | 3.3 | 50.0 | 4 | 8  | ACD56678 | Acd56678 HBV RT pr |
| 77 | 3.3 | 50.0 | 4 | 8  | ACD56758 | Acd56758 Synthetic |
| 78 | 3.3 | 50.0 | 4 | 8  | ACD56759 | Acd56759 Synthetic |
| 79 | 3.3 | 50.0 | 4 | 12 | ADG43024 | Adg43024 Human rib |
| 80 | 3.3 | 50.0 | 4 | 12 | ADO40990 | Ado40990 Human cdn |
| 81 | 3.3 | 50.0 | 5 | 1  | AAV93676 | Aav93676 Synthetic |
| 82 | 3.3 | 50.0 | 5 | 2  | AAV72348 | Aav72348 US908745  |
| 83 | 3.3 | 50.0 | 5 | 4  | AAL19176 | Aal19176 Human bre |
| 84 | 3.3 | 50.0 | 5 | 4  | AAH56407 | Aah56407 Escherich |
| 85 | 3.3 | 50.0 | 5 | 6  | ABS78153 | Abs78153 Angiogene |
| 86 | 3.3 | 50.0 | 5 | 6  | ABN73147 | Abn73147 Bovine em |
| 87 | 3.3 | 50.0 | 5 | 6  | ABN73154 | Abn73154 Bovine em |
| 88 | 3.3 | 50.0 | 5 | 8  | ACD56685 | Acd56685 HBV RT pr |
| 89 | 3.3 | 50.0 | 5 | 8  | ACD56682 | Acd56682 HBV RT pr |
| 90 | 3.3 | 50.0 | 5 | 9  | ACD99926 | Acd99926 Immunoe   |
| 91 | 3.3 | 50.0 | 5 | 12 | ADF90315 | Adf90315 NEO ribos |
| 92 | 3.3 | 50.0 | 5 | 12 | AD161783 | Adi61783 NEO ribos |
| 93 | 3.3 | 50.0 | 5 | 12 | ADM32647 | Adm32647 Fragment  |

94 3 50.0 5 12 ADM88491 Adm88491 Gene expr  
c 95 3 50.0 5 12 ADO05794 ADO05794 Telomere-  
96 3 50.0 6 1 AAN81733 AAN81733 Gcein I r  
c 97 3 50.0 6 1 AAN81733 AAN81733 Gcein I r  
c 98 3 50.0 6 1 AAN93284 AAN93284 Promoter  
99 3 50.0 6 2 AAQ50333 AAQ50333 Ribozyme  
100 3 50.0 6 2 AAQ47786 AAQ47786 Mammalian

# ALIGNMENTS

RESULT 1  
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ID ADR32744 standard; DNA; 6 BP.  
XX  
AC ADR32744;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Human nicking agent target DNA #285.  
XX  
KW ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
XX  
OS Homo sapiens.  
XX  
PN WO2004067765-A2.  
XX  
PD 12-AUG-2004.  
XX  
PF 29-JAN-2004; 2004WO-US002720.  
XX  
PR 29-JAN-2003; 2003US-0443811P.  
XX  
PA (KECK-) KECK GRADUATE INST.  
XX  
PI Van Ness J, Galas DJ, Van Ness LK;  
XX  
DR WPI; 2004-581010/56.  
XX  
PT Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
PS Example 1; Page 76; 238pp; English.

The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a nicking agent, and the conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating oligonucleotide fragments, and subjecting one or more members of the family of initiating oligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA molecules e.g., cDNA, and for characterizing cDNA expression patterns. The method, kit or composition is useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, non-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species, and is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for bacterial content and/or contamination in the environment, monitoring food for bacterial contamination, monitoring manufacturing processes for bacterial contamination, monitoring quality assurance/quality control of laboratory tests involving microbiological assays, tracing bacterial contamination and/or outbreaks of bacterial infections, genome mapping, monitoring bioremediation sites, and for monitoring agricultural sites

CC for test crops, bacteria and recombinant molecules. This sequence  
CC corresponds to nucleic acid used in the method of the invention.  
XX  
SQ Sequence 6 BP; 2 A; 0 C; 4 G; 0 T; 0 U; 0 Other;  
Query Match 83.3%; Score 5; DB 13; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GAAGG 6  
Db 1 GAAGG 5  
RESULT 2  
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ID ADR32766 standard; DNA; 6 BP.  
XX  
AC ADR32766;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Human nicking agent target DNA #307.  
XX  
KW ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
XX  
OS Homo sapiens.  
XX  
PN WO2004067765-A2.  
XX  
PD 12-AUG-2004.  
XX  
PF 29-JAN-2004; 2004WO-US002720.  
XX  
PR 29-JAN-2003; 2003US-0443811P.  
XX  
PA (KECK-) KECK GRADUATE INST.  
XX  
PI Van Ness J, Galas DJ, Van Ness LK;  
XX  
DR WPI; 2004-581010/56.  
XX  
PT Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
PS Example 1; Page 76; 238pp; English.  
XX  
CC The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a nicking agent, and the conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating oligonucleotide fragments, and subjecting one or more members of the family of initiating oligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA molecules e.g., cDNA, and for characterizing cDNA expression patterns. The method, kit or composition is useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, non-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species, and is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for bacterial content and/or contamination in the environment, monitoring food for bacterial contamination, monitoring manufacturing processes for bacterial contamination, monitoring quality assurance/quality control of laboratory tests involving microbiological assays, tracing bacterial

CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. This sequence  
 CC corresponds to nucleic acid used in the method of the invention.

XX  
 SQ Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5  
 |||||  
 Db 1 GGAAG 5

RESULT 3  
 ADR32505/c  
 ID ADR32505 standard; DNA; 6 BP.  
 XX AC ADR32505;  
 XX DT 04-NOV-2004 (first entry)  
 XX DE Human nicking agent target DNA #46.  
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2004067765-A2.  
 PN  
 XX  
 XX 12-AUG-2004.  
 PD  
 XX  
 XX 29-JAN-2004; 2004WO-US002720.  
 PF  
 XX  
 XX 29-JAN-2003; 2003US-0443811P.  
 PR  
 XX (KECK-) KECK GRADUATE INST.  
 XX  
 XX Van Ness J, Galas DJ, Van Ness LK;  
 PI WPI; 2004-581010/56.  
 DR  
 XX  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.

XX  
 XX Example 1; Page 72; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for

CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC for test crops, bacteria and recombinant molecules. This sequence  
 CC corresponds to nucleic acid used in the method of the invention.

XX  
 SQ Sequence 6 BP; 0 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAGG 6  
 |||||  
 Db 6 GAAGG 2

RESULT 4  
 ADEL0263  
 ID ADEL0263 standard; DNA; 6 BP.  
 XX AC ADEL0263;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE S.lavendulae MitB potential ribosome binding site.  
 XX Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis;  
 KW tumour hypoxia; cytostatic; anti-tumour agent; cancer; ds;  
 KW ribozyme binding site; RBS.  
 XX  
 XX Streptomyces lavendulae.  
 OS  
 XX US2003134398-A1.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX  
 XX 12-SEP-2001; 2001US-00953348.  
 PF  
 XX  
 XX 12-SEP-2001; 2001US-00953348.  
 PR  
 XX (SHER/) SHERMAN D H.  
 PA (MAOY/) MAO Y.  
 PA (VARO/) VAROGLU M.  
 PA (HEMM/) HE M.  
 PA (SHEL/) SHELTON P.  
 XX  
 XX Sherman DH, Mao Y, Varoglu M, He M, Sheldon P;  
 PI WPI; 2003-863498/80.  
 DR  
 XX  
 XX New nucleic acid molecule comprising a sequence having mitomycin  
 PT biosynthetic gene cluster, useful for enhancing production of  
 PT antibiotics.

XX  
 XX Disclosure; SEQ ID NO 93; 308pp; English.

XX The invention relates to an isolated and purified nucleic acid molecule  
 CC comprising a sequence having mitomycin biosynthetic gene cluster, or its  
 CC variant or fragment. Also included are an expression cassette comprising  
 CC the novel nucleic acid molecule (operably linked to a promoter functional  
 CC in a host cell), a recombinant bacterial host cell in which at least a  
 CC portion of a nucleic acid molecule comprising mitomycin biosynthetic gene  
 CC cluster is disrupted (resulting in a recombinant host cell that produces  
 CC altered levels of mitomycin relative to a corresponding nonrecombinant  
 CC bacterial host cell), introducing exogenous DNA into a refractory  
 CC Streptomyces strain, identifying a nucleic acid molecule that is related  
 CC to at least a portion of a nucleic acid molecule comprising a mitomycin  
 CC gene cluster, preparing a compound or its salt from the recombinant host  
 CC cell and a product produced by the recombinant host cell. The nucleic  
 CC acid encodes a MitT, MitS, MitR, MitQ, MitP, MitO, MitN, MitM, MitL, or  
 CC MitK, MitJ, MitI, MitH, MitG, MitF, MitE, MitD, MitC, MitB, MitA and/or

CC MmcA-MmcY. The nucleic acid is useful for enhancing production of  
CC mitomycin antibiotics, which induce apoptosis and hence are useful as  
CC anti-tumour (via tumour hypoxia) agents and are useful in treating  
CC cancer. The gene cluster was isolated from Streptomyces lavendulae. The  
CC present sequence is a ribosome binding site from a gene encoding a  
CC mitomycin biosynthetic protein of the invention.  
XX  
SQ Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
| | | | |  
Db 1 GGAAGG 6

RESULT 5  
ADE10336  
ID ADE10336 standard; DNA; 6 BP.  
XX  
AC ADE10336;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE S. lavendulae MitA potential ribosome binding site.  
XX  
KW Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis;  
KW tumour hypoxia; cytostatic; anti-tumour agent; cancer; ds;  
KW ribosome binding site; RBS.  
XX  
OS Streptomyces lavendulae.  
XX  
PN US2003134398-A1.  
XX  
PD 17-JUL-2003.  
XX  
PF 12-SEP-2001; 2001US-00953348.  
XX  
PR 12-SEP-2001; 2001US-00953348.  
XX  
PA (SHER/) SHERMAN D H.  
PA (MAOY/) MAO Y.  
PA (VARO/) VAROGLU M.  
PA (HEMM/) HE M.  
PA (SHEL/) SHELTON P.  
XX  
PI Sherman DH, Mao Y, Varoglu M, He M, Sheldon P;  
XX  
DR WPI; 2003-863498/80.  
XX  
PT New nucleic acid molecule comprising a sequence having mitomycin  
PT biosynthetic gene cluster, useful for enhancing production of  
PT antibiotics.  
XX  
PS Disclosure; SEQ ID NO 91; 308pp; English.

CC The invention relates to an isolated and purified nucleic acid molecule  
CC comprising a sequence having mitomycin biosynthetic gene cluster, or its  
CC variant or fragment. Also included are an expression cassette comprising  
CC the novel nucleic acid molecule (operably linked to a promoter functional  
CC in a host cell), a recombinant bacterial host cell in which at least a  
CC portion of a nucleic acid molecule comprising mitomycin biosynthetic gene  
CC cluster is disrupted (resulting in a recombinant host cell that produces  
CC altered levels of mitomycin relative to a corresponding nonrecombinant  
CC bacterial host cell), introducing exogenous DNA into a refractory  
CC Streptomycin strain, identifying a nucleic acid molecule that is related  
CC to at least a portion of a nucleic acid molecule comprising a mitomycin  
CC gene cluster, preparing a compound or its salt from the recombinant host  
CC cell and a product produced by the recombinant host cell. The nucleic  
CC acid encodes a MitR, MitS, MitR, MitQ, MitP, MitN, MitM, MitL,  
CC MitK, MitJ, MitI, MitH, MitG, MitF, MitE, MitD, MitC, MitA and/or

CC MmcA-MmcY. The nucleic acid is useful for enhancing production of  
CC mitomycin antibiotics, which induce apoptosis and hence are useful as  
CC anti-tumour (via tumour hypoxia) agents and are useful in treating  
CC cancer. The gene cluster was isolated from Streptomyces lavendulae. The  
CC present sequence is a ribosome binding site from a gene encoding a  
CC mitomycin biosynthetic protein of the invention.  
XX  
SQ Sequence 6 BP; 3 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
| | | | |  
Db 1 GGAAGG 6

RESULT 6  
ACA88957  
ID ACA88957 standard; DNA; 6 BP.  
XX  
AC ACA88957;  
XX  
DT 08-JUL-2003 (first entry)  
XX  
DE Selection and amplification of genetic markers PCR related primer #68.  
XX  
KW Genetic marker selection; multiplex PCR amplification;  
KW prenatal diagnostic testing; foetal sex determination;  
KW genetic identification; DNA profiling; DNA fingerprinting;  
KW forensic analysis; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003031646-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 14-OCT-2002; 2002WO-AU001388.  
XX  
PR 12-OCT-2001; 2001AU-00008234.  
XX  
PR 12-OCT-2001; 2001AU-00008235.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Findlay I, Matthews PL, Mulcahy BK;  
XX  
DR WPI; 2003-381725/36.  
XX  
PT Selecting genetic markers as targets for nucleic acid sequence  
PT amplification, useful for improving genetic testing, e.g. fetal sex  
PT determination, comprises selecting each of the genetic markers according  
PT to a heterozygosity index.  
XX  
PS Claim 36; Page 40; 64pp; English.

CC The invention describes a method of selecting genetic markers as targets  
CC for nucleic acid sequence amplification comprising selecting each of the  
CC genetic markers according to a heterozygosity index of 0.5 or greater.  
CC Selecting and amplification of genetic markers are useful as targets for  
CC nucleic acid sequence amplification, for genetic testing or facilitating  
CC multiplex PCR amplification from limiting amounts of target nucleic acid.  
CC The methods are also useful for improving genetic diagnostic and  
CC screening methods, such as prenatal diagnostic testing, foetal sex  
CC determination or genetic identification, e.g. DNA profiling or DNA  
CC fingerprinting. The nucleic acid sequence amplification is also useful in  
CC forensic analysis of degraded, old, ancient and difficult samples that  
CC are difficult to amplify and identify. This sequence represents a PCR  
CC primer used in the selection and amplification of genetic markers  
XX  
SQ Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;



Query Match 73.3%; Score 4.4; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
||| ||  
Db 1 GGATGG 6

RESULT 7  
ADJ35621/c  
ID ADJ35621 standard; DNA; 6 BP.  
XX  
AC ADJ35621;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Stabilising anti-repression, STAR, element dyad sequence #287.  
XX  
KW STAR affiliated proteinaceous molecule; post translational modification;  
KW stabilising anti-repression; STAR; STAR element; ds; dyad.  
XX  
OS Unidentified.  
XX  
PN WO2003106674-A2.  
XX  
PD 24-DEC-2003.  
XX  
PF 30-MAY-2003; 2003WO-NL000410.  
XX  
PR 14-JUN-2002; 2002EP-00077344.  
XX  
PA (CHRO-) CHROMAGENICS BV.  
XX  
PI Otte AP, Kruckeberg AL, Satijn DPE;  
XX  
DR WPI; 2004-082195/08.  
XX

Producing proteinaceous molecules in cells by selecting a cell, providing  
a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti  
-Repression sequence and expressing proteinaceous molecule.  
XX  
PS Disclosure; Page 101; 177pp; English.  
XX

The invention relates to a method of producing a proteinaceous molecule  
(I) in a cell comprising selecting a cell for its suitability for  
producing (I), providing a nucleic acid encoding (I) with a nucleic acid  
comprising a Stabilising Anti-Repression (STAR) sequence, expressing the  
resulting nucleic acid in the cell and collecting (I). The method is  
useful for producing (I). A cell line (II) provided with a nucleic acid  
comprising a STAR sequence is useful for producing (I). (II) Enables  
production of affiliated proteinaceous molecule, as cell carries out  
proper post-translational modifications of produced proteins. The present  
sequence represents a stabilising anti-repression, STAR, element primer  
dyad sequence.  
XX  
SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 12; Length 6;  
Best Local Similarity 83.3%; Pred. No. 9.7e+08;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6  
||| ||  
Db 6 GGAGGG 1

RESULT 8  
AAQ38797  
ID AAQ38797 standard; DNA; 6 BP.  
XX  
AC AAQ38797;  
XX

DT 25-MAR-2003 (revised)  
DT 26-JUL-1993 (first entry)  
DE PCR primer #11 for analysis of lower TCR Vbeta gene usage in RA SILs.  
KW TCR; T cell receptor; autoimmune disease; rheumatoid arthritis; RA;  
KW J beta domain; V beta domain; T-cell mediated autoimmune disease;  
KW antagonists.  
XX  
OS Homo sapiens.  
XX  
PN WO9306135-A1.  
XX  
PD 01-APR-1993.  
XX  
PF 23-SEP-1992; 92WO-US008094.  
XX  
PR 23-SEP-1991; 91US-00765222.  
PR 18-OCT-1991; 91US-00779445.  
PR 18-MAR-1992; 92US-00853362.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Amento EP;  
XX  
DR WPI; 1993-117475/14.  
XX  
PT T-cell receptor antagonising polypeptide(s) - used in the diagnosis and  
treatment of auto-immune disorders, partic. rheumatoid arthritis.  
XX  
PS Example 1; Page 22; 51pp; English.  
XX  
CC This 5' PCR primer was used with a 3' primer designated a constant region  
sequence common to all TCR beta transcripts. It was used for the PCR  
analysis of lower TCR usage in synovial Vbetas. This primer was used for  
Vbeta family 2, subfamily 4.1, Jbeta 2.7, Cbeta 2 and corresponds to D &  
CC J translation MAR34165. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
||| |  
Db 2 GGAA 5

RESULT 9  
AAQ70690/c  
ID AAQ70690 standard; DNA; 6 BP.  
XX  
AC AAQ70690;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1995 (first entry)  
XX  
DE Triplex forming oligonucleotide directed against IL-2 gene.  
XX  
KW IL-2; upstream region; regulatory element; gene expression; triplex;  
KW antisense; inhibition; screening; identification; cancer; breast cancer;  
KW carcinoma; autoimmunity; transplantation; HIV;  
KW human immunodeficiency virus; ss.  
XX  
OS Synthetic.  
XX  
PN WO9417086-A1.  
XX  
PD 04-AUG-1994.  
XX  
PF 10-JAN-1994; 94WO-US000348.  
XX

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PR 25-JAN-1993; 93US-00008897.
XX (APOL-) APOLLON INC.
XX Yoon K, Lu M;
XX WPI; 1994-264018/32.
XX Composition for decreasing gene transcription - comprises
PT oligo:nucleotide or deriv. complementary to target gene region.
XX Claim 18; Page 45; 71pp; English.
XX The IL-2 gene has a purine rich segment with substantial mirror symmetry.
CC The purine rich region is characteristic of a nuclear factor activating T
CC -cell binding site. This triplex forming oligonucleotide directed against
CC the IL-2 region may be used in the treatment of HIV infection, diseases
CC requiring transplantation and, more generally, any disease involving the
CC expression of IL-2. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 6 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
Db 5 GGAA 2

RESULT 10
AAF91829/c
ID AAF91829 standard; DNA; 6 BP.
XX AC AAF91829;
XX DT 10-MAY-2001 (first entry)
XX DE Breast-cancer associated protein isoform BPI-56 preferred probe #1.
XX KW Human; breast cancer; breast cancer associated protein isoform; BPI;
XX KW breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.
XX OS Homo sapiens.
XX PN WO200113117-A2.
XX PD 22-FEB-2001.
XX PF 14-AUG-2000; 2000WO-GB003143.
XX PR 13-AUG-1999; 99GB-00019258.
XX PR 30-MAR-2000; 2000GB-00007754.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMCAC;
XX WPI; 2001-211252/21.
XX Screening, diagnosis or prognosis of breast cancer, by analyzing a sample
PT of serum or plasma by two dimensional electrophoresis to detect the
PT presence or level of a breast cancer-associated feature.
XX Claim 201; Page 45; 146pp; English.
XX The present invention describes a method for the screening, diagnosis or
CC prognosis of breast cancer (BC), determining the stage or severity of BC,
CC and monitoring the effect of therapy administered to a subject having BC,
CC comprising analysing a sample of body fluid by two dimensional
CC electrophoresis to generate a two-dimensional array of features,
CC comprising a chosen feature whose abundance correlates with BC or

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CC predicts the onset or course of BC. The method (I) involves: (a)
CC analysing a sample of body fluid from the subject by two-dimensional
CC electrophoresis to generate a two-dimensional array of features,
CC comprising a chosen feature whose relative abundance correlates with BC
CC or predicts the onset of BC; and (b) comparing the abundance of each
CC chosen feature in the sample with the abundance of that chosen feature in
CC the body fluid from one or more persons free from BC, or with a
CC previously determined reference range for that feature in subjects free
CC from BC, or with the abundance of an expression reference feature (ERF)
CC in the test sample. The method is useful for screening, diagnosis or
CC prognosis of breast cancer, determining the stage or severity of BC,
CC monitoring the effect of therapy administered to a subject having BC, and
CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340
CC represents breast cancer associated protein isoform (BPI) peptide
CC sequences, and AAF91543 to AAF91848 represent BPI probes used in the
CC exemplification of the present invention
XX Sequence 6 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
Db 6 GAAG 3

RESULT 11
ACC69109
ID ACC69109 standard; DNA; 6 BP.
XX AC ACC69109;
XX DT 10-JUL-2003 (first entry)
XX DE Cucumber BGL related target sequence SEQ ID NO:16.
XX KW Cucumber; expression profiling; DNA sequencing; plant; developmental;
XX KW physiological; horticultural; agricultural; target; ss.
XX OS Cucumis sp.
XX OS Synthetic.
XX PN EP1295950-A1.
XX PD 26-MAR-2003.
XX PF 25-SEP-2001; 2001EP-00203617.
XX PR 25-SEP-2001; 2001EP-00203617.
XX PA (GTDI-) GT DIAGNOSTICS BV.
XX PI Langeveld SA, Van Der Kop DAM, De Boer AD;
XX WPI; 2003-383798/37.
XX Determining developmental/physiological stage of organism (especially in
PT plants), comprises determining expression of first and second genes by
PT hybridizing nucleic acid templates derived from the genes with specific
PT primers.
XX Example; Fig 1A; 27pp; English.
XX The present invention describes a method (M) for determining a
CC developmental or physiological stage of an organism by determining
CC expression of a first and second gene (I)-(II), respectively, or gene
CC fragment. (M) comprises: (a) providing first and second nucleic acid
CC templates (T1)-(T2) derived from (I) and (II), respectively; (b)
CC hybridising first and second primers (P1)-(P2) to (T1) and (T2),
CC respectively; and (c) determining binding of the primers to the templates
CC in one reaction vessel. (M) is useful for determining a developmental or

```

CC physiological stage of an organism (especially a plant). (M) is  
CC particularly useful for expression profiling for use in testing plant  
CC quality of horticultural and agricultural products. With quality loss,  
CC e.g. stress-induced senescence, oxidative damage or desiccation, the  
CC plant tissues will go through various physiological stages, in which  
CC different genes are switched on or off. The level of expression of these  
CC marker genes reflects the physiological stage and therefore the condition  
CC and quality of the plant and/or product. Quality of fresh products is  
CC generally judged on subjective criteria that usually involves visual  
CC examination. The present invention provides a way of taking objective  
CC quantitative measurements using biotechnology: there is a direct relation  
CC between the pattern of gene expression at the RNA and protein level, and  
CC the physiological status of a cell. The present sequence represents a  
CC cucumber BGL target sequence, which is used in an example from the  
CC present invention.  
XX  
SQ Sequence 6 BP; 2 A; 2 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 66.7%; Score 4; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 AAGG 6  
Db 1 AAGG 4  
  
RESULT 12  
ABZ23991/c  
ID ABZ23991 standard; DNA; 6 BP.  
XX AC ABZ23991;  
DT 18-MAR-2003 (first entry)  
XX DE Nucleotide sequence of seq Id No. 5.  
XX  
KW Ligation; topoisomerase; nucleic acid generation; molecular cloning;  
KW topoisomerase I; topo65; ds.  
XX  
OS Synthetic.  
XX  
PN WO200290522-A2.  
XX  
PD 14-NOV-2002.  
XX  
PF 10-MAY-2002; 2002WO-US015072.  
XX  
PR 10-MAY-2001; 2001US-0290313P.  
PR 15-JUN-2001; 2001US-00882274.  
XX  
PA (UYSA-) UNIV SAN DIEGO STATE FOUND.  
PA (EMER-) EMERALD BIOSTRUCTURES INC.  
XX  
PI Burgin Alex B, Stewart LJ;  
XX  
DR WPI; 2003-120543/11.  
XX  
PT Ligating nucleic acid for generating RNA, by contacting polynucleotide-3'  
PT phosphorothiolate with acceptor polynucleotide, or polynucleotide-  
PT 5'phosphorothiolate with non-sequence specific topoisomerase and  
PT acceptor.  
XX  
PS Disclosure; Page 101; 105pp; English.  
XX  
CC The invention relates to ligating a nucleic acid. The method involves:  
CC (a) non-enzymatic ligation by contacting a polynucleotide-3'  
CC phosphorothiolate with an acceptor polynucleotide under conditions that  
CC allow formation of a phosphodiester bond between the polynucleotide-3'  
CC phosphorothiolate and the acceptor polynucleotide; or (b) contacting a  
CC polynucleotide-5'phosphorothiolate with a non-sequence specific  
CC topoisomerase, or its fragment or modification, and an acceptor  
CC polynucleotide under conditions that allow formation of a phosphodiester

CC bond between the polynucleotide-5' phosphorothiolate and the acceptor  
CC polynucleotide, with the proviso that the polynucleotide-5'  
CC phosphorothiolate does not contain the nucleotide sequence shown in  
CC ABZ23991. The method is useful for ligating a nucleic acid, for  
CC generating RNA or DNA molecules, RNA-DNA hybrids, vectors and inserts  
CC useful for molecular cloning and complex polynucleotide structures.  
CC Sequences ABZ23991-993 represent nucleotide sequences that are  
CC particularly excluded from the term polynucleotide-5' phosphorothiolate  
XX  
SQ Sequence 6 BP; 0 A; 2 C; 1 G; 2 T; 0 U; 1 Other;  
  
Query Match 66.7%; Score 4; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 AAGG 6  
Db 6 AAGG 3  
  
RESULT 13  
ACH50860  
ID ACH50860 standard; DNA; 6 BP.  
XX AC ACH50860;  
DT 13-OCT-2003 (first entry)  
XX DE Hypothetical positively hybridised probe #3 extension probe #4.  
XX  
KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;  
KW biodiversity; genetic disorder.  
XX  
OS Synthetic.  
XX  
PN US2003073623-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 30-JUL-2001; 2001US-00918995.  
XX  
PR 30-JUL-2001; 2001US-00918995.  
XX  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
XX  
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX  
DR WPI; 2003-615964/59.  
XX  
PT New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.  
XX  
PS Example 19; Page 36; 44pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence

CC is a hypothetical probe used to illustrate a method of  
 CC detecting/determining mutations and polymorphisms  
 XX  
 SQ Sequence 6 BP; 3 A; 1 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6  
 DB 3 AAGG 6  
 RESULT 14  
 ACH50844/c  
 ID ACH50844 standard; DNA; 6 BP.  
 XX  
 AC ACH50844;  
 DT 13-OCT-2003 (first entry)  
 XX  
 DE Hypothetical positively hybridised probe #2.  
 XX  
 KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;  
 KW biodiversity; genetic disorder.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003073623-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 30-JUL-2001; 2001US-00918995.  
 XX  
 PR 30-JUL-2001; 2001US-00918995.  
 XX  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX  
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 XX  
 DR WPI; 2003-615964/58.  
 XX  
 PT New polynucleotide sequences obtained from various cDNA libraries, useful  
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
 PT mapping, in the recombinant production of protein, or in generating  
 PT antisense DNA or RNA.  
 XX  
 PS Example 19; Page 36; 44pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide comprising any one of  
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 CC determined by the technique of SBH (sequencing by hybridisation). Also  
 CC included is a purified polypeptide comprising a sequence corresponding to  
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
 CC are useful in diagnostics as expressed sequence tags (EST) for  
 CC identifying expressed genes or for physical mapping of the human genome,  
 CC in forensics, in assessing biodiversity, or in identifying mutations  
 CC responsible for genetic disorders and other traits. The nucleotide  
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
 CC for chromosome and gene mapping, in the recombinant production of  
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
 CC is useful for generating antibodies specific for it. The present sequence  
 CC is a hypothetical probe used to illustrate a method of  
 CC detecting/determining mutations and polymorphisms  
 XX  
 SQ Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4  
 DB 6 GGAA 3  
 RESULT 15  
 ADD66333/c  
 ID ADD66333 standard; DNA; 6 BP.  
 XX  
 AC ADD66333;  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Ebola GP gene modified DNA.  
 XX  
 KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;  
 KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;  
 KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;  
 KW HIV infection; ds.  
 XX  
 OS Ebola virus.  
 XX  
 PN US2003138459-A1.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PF 17-MAR-2003; 2003US-00286332.  
 XX  
 PR 02-JUN-2000; 2000US-00585599.  
 PR 04-JUN-2001; 2001WO-US018238.  
 PR 01-NOV-2001; 2001US-00003035.  
 XX  
 PA (WANG/) WANG D.  
 XX  
 PI Wang D;  
 XX  
 DR WPI; 2003-851718/79.  
 XX  
 PT Enhancing the immunity of a host to infection of a first and second  
 PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or  
 PT HIV infections comprises administering to the host a first and a second  
 PT recombinant adenovirus.  
 XX  
 PS Example; SEQ ID NO 7; 185pp; English.  
 XX  
 CC The invention relates to a method of enhancing the immunity of a host to  
 CC infection of a first and second pathogenic virus comprising administering  
 CC to the host a first and a second recombinant adenovirus. The method is  
 CC useful for enhancing immunity of the host to infections, e.g. influenza,  
 CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes  
 CC simplex or human papilloma virus or HIV infections. The present sequence  
 CC is used in the exemplification of the invention.  
 XX  
 SQ Sequence 6 BP; 0 A; 2 C; 0 G; 0 T; 4 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5  
 DB 6 GAAG 3  
 RESULT 16  
 ADD66334/c  
 ID ADD66334 standard; mRNA; 6 BP.  
 XX  
 AC ADD66334;  
 XX

DT 15-JAN-2004 (first entry)  
XX DE Ebola GP gene mRNA.  
XX KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;  
KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;  
KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;  
KW HIV infection; ss.  
XX OS Ebola virus.  
XX PN US2003138459-A1.  
XX PD 24-JUL-2003.  
XX PF 17-MAR-2003; 2003US-00286332.  
XX PR 02-JUN-2000; 2000US-00585599.  
XX PR 04-JUN-2001; 2001WO-US018238.  
XX PR 01-NOV-2001; 2001US-00003035.  
XX PA (WANG/) WANG D.  
XX PI Wang D;  
XX WPI; 2003-851718/79.  
XX Enhancing the immunity of a host to infection of a first and second  
PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or  
PT HIV infections comprises administering to the host a first and a second  
PT recombinant adenovirus.  
XX Disclosure; SEQ ID NO 8; 185pp; English.  
XX The invention relates to a method of enhancing the immunity of a host to  
CC infection of a first and second pathogenic virus comprising administering  
CC to the host a first and a second recombinant adenovirus. The method is  
CC useful for enhancing immunity of the host to infections, e.g. influenza,  
CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes  
CC simplex or human papilloma virus or HIV infections. The present sequence  
CC is used in the exemplification of the invention.  
XX  
SQ Sequence 6 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 66.7%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GAAG 5  
DB 6 GAAG 3  
RESULT 17  
ADE38305  
ID ADE38305 standard; DNA; 6 BP.  
XX AC ADE38305;  
XX 29-JAN-2004 (first entry)  
XX Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:44.  
DE autoimmune disease; statin; antigen-specific immunomodulatory agent;  
XX non-antigen-specific immunomodulatory agent; immunomodulatory;  
KW antidiabetic; antiarthritic; vasotropic; gene therapy;  
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;  
KW rheumatoid arthritis; autoimmune uveitis; ss.  
XX OS Synthetic.  
XX WO2003082269-A1.  
XX PN Treating an autoimmune disease by co-administering to a patient a statin  
PT and an antigen-specific non-antigen-specific immunomodulatory agent.

PD 09-OCT-2003.  
XX 31-MAR-2003; 2003WO-US009807.  
XX PF 29-MAR-2002; 2002US-0368803P.  
XX PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX PA (BAYH-) BAYHILL THERAPEUTICS INC.  
XX PI Garren H, Steinman L;  
XX WPI; 2003-803953/75.  
XX Treating an autoimmune disease by co-administering to a patient a statin  
PT and an antigen-specific non-antigen-specific immunomodulatory agent.  
XX Disclosure; SEQ ID NO 44; 90pp; English.  
XX The present invention describes a method for treating an autoimmune  
CC disease comprising co-administering to a patient a statin and an antigen-  
CC specific/non-antigen-specific immunomodulatory agent. The  
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic  
CC activities, and can be used in gene therapy. The method is useful for  
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent  
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 6 BP; 2 A; 1 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 66.7%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AAGG 6  
DB 1 AAGG 4  
RESULT 18  
ADE38325  
ID ADE38325 standard; DNA; 6 BP.  
XX AC ADE38325;  
XX 29-JAN-2004 (first entry)  
XX Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:48.  
DE autoimmune disease; statin; antigen-specific immunomodulatory agent;  
XX non-antigen-specific immunomodulatory agent; immunomodulatory;  
KW antidiabetic; antiarthritic; vasotropic; gene therapy;  
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;  
KW rheumatoid arthritis; autoimmune uveitis; ss.  
XX OS Synthetic.  
XX WO2003082269-A1.  
XX PN 09-OCT-2003.  
XX 31-MAR-2003; 2003WO-US009807.  
XX PF 29-MAR-2002; 2002US-0368803P.  
XX PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX PA (BAYH-) BAYHILL THERAPEUTICS INC.  
XX PI Garren H, Steinman L;  
XX WPI; 2003-803953/75.  
XX Treating an autoimmune disease by co-administering to a patient a statin  
PT and an antigen-specific non-antigen-specific immunomodulatory agent.

|                       |                                                                           |
|-----------------------|---------------------------------------------------------------------------|
| XX                    | Disclosure; SEQ ID NO 48; 90pp; English.                                  |
| XX                    |                                                                           |
| XX                    | The present invention describes a method for treating an autoimmune       |
| CC                    | disease comprising co-administering to a patient a statin and an antigen- |
| CC                    | specific/non-antigen-specific immunomodulatory agent. The                 |
| CC                    | immunomodulatory agent has antidiabetic, antiarthritic and vasotropic     |
| CC                    | activities, and can be used in gene therapy. The method is useful for     |
| CC                    | treating autoimmune disease e.g., multiple sclerosis, insulin dependent   |
| CC                    | diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The |
| CC                    | present sequence is used in the exemplification of the present invention. |
| XX                    |                                                                           |
| XX                    | Sequence 6 BP; 2 A; 1 C; 2 G; 1 T; 0 U; 0 Other;                          |
| QQ                    |                                                                           |
| Query Match           | 66.7%; Score 4; DB 10; Length 6;                                          |
| Best Local Similarity | 100.0%; Pred. No. 9.7e+08;                                                |
| Matches               | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0                         |
| QY                    | 3 AAGG 6                                                                  |
|                       |                                                                           |
| DB                    | 1 AAGG 4                                                                  |
| RESULT 19             |                                                                           |
| ADE38297              |                                                                           |
| ID                    | ADE38297 standard; DNA; 6 BP.                                             |
| XX                    |                                                                           |
| AC                    | ADE38297;                                                                 |
| XX                    |                                                                           |
| DT                    | 29-JAN-2004 (first entry)                                                 |
| XX                    |                                                                           |
| DE                    | Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:36.    |
| XX                    |                                                                           |
| KW                    | autoimmune disease; statin; antigen-specific immunomodulatory agent;      |
| KW                    | non-antigen-specific immunomodulatory agent; immunomodulatory;            |
| KW                    | antidiabetic; antiarthritic; vasotropic; gene therapy;                    |
| KW                    | multiple sclerosis; insulin dependent diabetes mellitus; IDDM;            |
| KW                    | rheumatoid arthritis; autoimmune uveitis; ss.                             |
| XX                    |                                                                           |
| OS                    | Synthetic.                                                                |
| XX                    |                                                                           |
| PN                    | WO2003082269-A1.                                                          |
| XX                    |                                                                           |
| PD                    | 09-OCT-2003.                                                              |
| XX                    |                                                                           |
| PF                    | 31-MAR-2003; 2003WO-US009807.                                             |
| XX                    |                                                                           |
| PR                    | 29-MAR-2002; 2002US-0368803P.                                             |
| XX                    |                                                                           |
| PA                    | (STRD ) UNIV LEIAND STANFORD JUNIOR.                                      |
| PA                    | (BAYH-) BAYHILL THERAPEUTICS INC.                                         |
| XX                    |                                                                           |
| PI                    | Garren H, Steinman L;                                                     |
| XX                    |                                                                           |
| DR                    | WPI; 2003-803953/75.                                                      |
| XX                    |                                                                           |
| PT                    | Treating an autoimmune disease by co-administering to a patient a statin  |
| PT                    | and an antigen-specific non-antigen-specific immunomodulatory agent.      |
| XX                    |                                                                           |
| XX                    | Disclosure; SEQ ID NO 36; 90pp; English.                                  |
| XX                    |                                                                           |
| CC                    | The present invention describes a method for treating an autoimmune       |
| CC                    | disease comprising co-administering to a patient a statin and an antigen- |
| CC                    | specific/non-antigen-specific immunomodulatory agent. The                 |
| CC                    | immunomodulatory agent has antidiabetic, antiarthritic and vasotropic     |
| CC                    | activities, and can be used in gene therapy. The method is useful for     |
| CC                    | treating autoimmune disease e.g., multiple sclerosis, insulin dependent   |
| CC                    | diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The |
| CC                    | present sequence is used in the exemplification of the present invention. |
| XX                    |                                                                           |
| XX                    | Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 0 Other;                          |
| QQ                    |                                                                           |
| Query Match           | 66.7%; Score 4; DB 10; Length 6;                                          |

XX Candida promoter motif URS1-like sequence SEQ ID NO:15.  
 DE  
 XX  
 KW Candida tropicalis; CYP gene promoter; modified CYP gene promoter;  
 KW yeast host cell; URS1; URS2; URS1-like; URS2-like;  
 KW beta oxidation pathway; omega oxidation pathway; gene; ds.  
 XX  
 OS Candida sp.  
 XX  
 PN WO2004016756-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 15-AUG-2003; 2003WO-US025545.  
 XX  
 PR 16-AUG-2002; 2002US-0403979P.  
 PR 14-AUG-2003; 2003US-00640962.  
 XX  
 PA (COGN-) COGNIS CORP.  
 XX  
 PI Wilson RC, Craft DL, Zhang Y, Stavenhagen JB;  
 PI WPI; 2004-203787/19.  
 DR  
 XX  
 PF New modified Candida tropicalis CYP gene promoters comprising nucleotide  
 XX sequence for a CYP gene promoter, useful for modulating expression of a  
 PT protein of the beta or omega oxidation pathway in a yeast cell.  
 PR  
 XX  
 PS Claim 4; SEQ ID NO 15; 99pp; English.  
 XX  
 CC The present invention describes modified Candida tropicalis CYP gene  
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also  
 CC described: (1) a yeast host cell comprising the modified Candida  
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression  
 CC of a protein of the beta or omega oxidation pathway in a yeast cell  
 CC comprising: (a) isolating a CYP gene promoter from C. tropicalis; (b)  
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like  
 CC or URS2-like sequences; (c) operably linking the modified promoter with a  
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)  
 CC transforming a yeast cell with the modified promoter operably linked to  
 CC the coding sequence; and (e) growing the yeast under conditions  
 CC favourable for expression of the coding sequence under the control of the  
 CC modified promoter. The promoters are useful for modulating expression of  
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 BP; 4 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AAGG 6  
 Db |||||  
 2 AAGG 5  
 RESULT 22  
 ADK14297  
 ID ADK14297 standard; DNA; 6 BP.  
 XX  
 AC ADK14297;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Candida promoter motif URS1-like sequence SEQ ID NO:26.  
 XX  
 KW Candida tropicalis; CYP gene promoter; modified CYP gene promoter;  
 KW yeast host cell; URS1; URS2; URS1-like; URS2-like;  
 KW beta oxidation pathway; omega oxidation pathway; gene; ds.  
 XX  
 OS Candida sp.  
 XX  
 PN WO2004016756-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 15-AUG-2003; 2003WO-US025545.  
 XX  
 PR 16-AUG-2002; 2002US-0403979P.  
 PR 14-AUG-2003; 2003US-00640962.  
 XX  
 PA (COGN-) COGNIS CORP.  
 XX  
 PI Wilson RC, Craft DL, Zhang Y, Stavenhagen JB;  
 PI WPI; 2004-203787/19.  
 DR  
 XX  
 PF New modified Candida tropicalis CYP gene promoters comprising nucleotide  
 XX sequence for a CYP gene promoter, useful for modulating expression of a  
 PT protein of the beta or omega oxidation pathway in a yeast cell.  
 PR  
 XX  
 PS Claim 4; SEQ ID NO 15; 99pp; English.  
 XX  
 CC The present invention describes modified Candida tropicalis CYP gene  
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also  
 CC described: (1) a yeast host cell comprising the modified Candida  
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression  
 CC of a protein of the beta or omega oxidation pathway in a yeast cell  
 CC comprising: (a) isolating a CYP gene promoter from C. tropicalis; (b)  
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like  
 CC or URS2-like sequences; (c) operably linking the modified promoter with a  
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)  
 CC transforming a yeast cell with the modified promoter operably linked to  
 CC the coding sequence; and (e) growing the yeast under conditions  
 CC favourable for expression of the coding sequence under the control of the  
 CC modified promoter. The promoters are useful for modulating expression of  
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 BP; 4 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 4; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AAGG 6  
 Db |||||  
 2 AAGG 5  
 RESULT 23  
 ADL09220  
 ID ADL09220 standard; DNA; 6 BP.  
 XX  
 AC ADL09220;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE T3 promoter DNA fragment #15.  
 XX  
 KW amplification; primer; promoter; RNA polymerase; ds.  
 XX  
 OS Bacteriophage T3.  
 XX  
 PN WO2004016757-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 15-AUG-2003; 2003WO-US025564.  
 XX  
 PR 16-AUG-2002; 2002US-0404075P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Karin M, Park JM;





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XX 12-AUG-2004.
PD 29-JAN-2004; 2004WO-US002720.
PF 29-JAN-2003; 2003US-0443811P.
XX (KECK-) KECK GRADUATE INST.
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX Example 3; Page 105-219; 238pp; English.
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial contamination, monitoring quality assurance/quality control of
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring microbiological assays, tracing bacterial
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX Sequence 6 BP; 2 A; 0 C; 2 G; 1 T; 0 U; 1 Other;
SQ Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAAGG 6
Db :|||
1 SGAATG 6
RESULT 26
ADR34773
ID ADR34773 standard; DNA; 6 BP.
XX ADR34773;
AC ADR34773;
XX 04-NOV-2004 (first entry)
DE Human nicking agent DNA containing BstNBI restriction site #1193.
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX

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OS Homo sapiens.
XX WO2004067765-A2.
PD 12-AUG-2004.
XX 29-JAN-2004; 2004WO-US002720.
XX 29-JAN-2003; 2003US-0443811P.
XX (KECK-) KECK GRADUATE INST.
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX Example 3; Page 105-219; 238pp; English.
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial contamination, monitoring quality assurance/quality control of
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring microbiological assays, tracing bacterial
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX Sequence 6 BP; 2 A; 0 C; 2 G; 1 T; 0 U; 1 Other;
SQ Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAAGG 6
Db :|||
1 SGAATG 6
RESULT 27
ADR37260
ID ADR37260 standard; DNA; 6 BP.
XX ADR37260;
AC ADR37260;
XX 04-NOV-2004 (first entry)
DE Human nicking agent DNA containing BstNBI restriction site #3680.
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW

```

KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 OS Homo sapiens.  
 XX WO2004067765-A2.  
 XX 12-AUG-2004.  
 XX 29-JAN-2004; 2004WO-US002720.  
 XX 29-JAN-2003; 2003US-0443811P.  
 XX (KECK-) KECK GRADUATE INST.  
 XX Van Ness J, Galas DJ, Van Ness LK;  
 XX WPI; 2004-581010/56.  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT straining involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX Example 3; Page 105-219; 238pp; English.  
 XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
 CC ADR37496 correspond to target nucleic acids containing an NbscNBI  
 CC restriction site and used in the method of the invention.  
 XX Sequence 6 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 1 Other;  
 SQ Query Match 66.7%; Score 4; DB 13; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGAAGG 6  
 Db 1 SGATGG 6  
 RESULT 28  
 ADR33235  
 ID ADR33235 standard; DNA; 6 BP.  
 XX ADR33235;  
 AC ADR33235;  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX

DE Human nicking agent target DNA #776.  
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 XX Homo sapiens.  
 XX WO2004067765-A2.  
 XX 12-AUG-2004.  
 XX 29-JAN-2004; 2004WO-US002720.  
 XX 29-JAN-2003; 2003US-0443811P.  
 XX (KECK-) KECK GRADUATE INST.  
 XX Van Ness J, Galas DJ, Van Ness LK;  
 XX WPI; 2004-581010/56.  
 XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT straining involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX Example 1; Page 84; 238pp; English.  
 XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring manufacturing processes for  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. This sequence  
 CC corresponds to nucleic acid used in the method of the invention.  
 XX Sequence 6 BP; 4 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 66.7%; Score 4; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GAAG 5  
 Db 2 GAAG 5  
 RESULT 29  
 ADR32580/C  
 ID ADR32580 standard; DNA; 6 BP.  
 XX ADR32580;  
 AC ADR32580;  
 XX

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DT 04-NOV-2004 (first entry)
DE Human nicking agent target DNA #121.
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 73; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAAG 5
Db 5 GAAG 2
RESULT 30
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ID ADR37262 standard; DNA; 6 BP.
XX
AC ADR37262;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #3682.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 1 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAAGG 6
Db 1 SGATGG 6
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Job time : 192.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds  
(without alignments)  
393.838 Million cell updates/sec

Title: US-09-735-363A-42  
Perfect score: 6  
Sequence: 1 ggaagg 6

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
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| 1          | 6     | 100.0       | 6      | AX175278 | Sequence           |
| 2          | 5     | 83.3        | 5      | CQ868961 | Sequence           |
| C 3        | 5     | 83.3        | 5      | CQ868981 | Sequence           |
| 4          | 5     | 83.3        | 5      | CQ869110 | Sequence           |
| C 5        | 5     | 83.3        | 5      | CQ869130 | Sequence           |
| 6          | 5     | 83.3        | 5      | AX207361 | Sequence           |
| 7          | 5     | 83.3        | 6      | AX236985 | Sequence           |
| 8          | 5     | 83.3        | 6      | AX557112 | Sequence           |
| 9          | 5     | 83.3        | 6      | AX805872 | Sequence           |
| C 10       | 5     | 83.3        | 6      | S85691   | S85691 p53 [human, |
| 11         | 4.4   | 73.3        | 6      | BD269460 | BD269460 Mitomycin |
| 12         | 4.4   | 73.3        | 6      | BD269461 | BD269461 Mitomycin |
| C 13       | 4.4   | 73.3        | 6      | CQ755704 | Sequence           |
| C 14       | 4.4   | 73.3        | 6      | CQ755751 | Sequence           |
| C 15       | 4.4   | 73.3        | 6      | CQ756128 | Sequence           |
| C 16       | 4.4   | 73.3        | 6      | CQ757942 | Sequence           |
| C 17       | 4.4   | 73.3        | 6      | CQ757989 | Sequence           |
| C 18       | 4.4   | 73.3        | 6      | CQ758366 | Sequence           |
| C 19       | 4.4   | 73.3        | 6      | AX175264 | Sequence           |

|                       |                                                          |                                        |               |           |          |                 |          |          |
|-----------------------|----------------------------------------------------------|----------------------------------------|---------------|-----------|----------|-----------------|----------|----------|
| c 93                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755705 | Sequence        | CQ755705 | Sequence |
| c 94                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755709 | Sequence        | CQ755709 | Sequence |
| c 95                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755716 | Sequence        | CQ755716 | Sequence |
| c 96                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755718 | Sequence        | CQ755718 | Sequence |
| c 97                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755739 | Sequence        | CQ755739 | Sequence |
| c 98                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755755 | Sequence        | CQ755755 | Sequence |
| c 99                  | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755766 | Sequence        | CQ755766 | Sequence |
| c 100                 | 3.4                                                      | 56.7                                   | 6             | 6         | CQ755779 | Sequence        | CQ755779 | Sequence |
| ALIGNMENTS            |                                                          |                                        |               |           |          |                 |          |          |
| RESULT 1              |                                                          |                                        |               |           |          |                 |          |          |
| AX175278              | AX175278                                                 | Sequence 42 from Patent WO0144465.     | 6 bp          | DNA       | linear   | PAT 03-JUL-2001 |          |          |
| LOCUS                 | AX175278                                                 | Sequence 42 from Patent WO0144465.     |               |           |          |                 |          |          |
| DEFINITION            | AX175278                                                 | Sequence 42 from Patent WO0144465.     |               |           |          |                 |          |          |
| ACCESSION             | AX175278                                                 | Sequence 42 from Patent WO0144465.     |               |           |          |                 |          |          |
| VERSION               | AX175278.1                                               | GI:14598646                            |               |           |          |                 |          |          |
| KEYWORDS              |                                                          |                                        |               |           |          |                 |          |          |
| SOURCE                |                                                          | synthetic construct                    |               |           |          |                 |          |          |
| ORGANISM              |                                                          | other sequences; artificial sequences. |               |           |          |                 |          |          |
| REFERENCE             | 1                                                        | (bases 1 to 6)                         |               |           |          |                 |          |          |
| AUTHORS               | Phillips,N.C. and Filion,M.C.                            |                                        |               |           |          |                 |          |          |
| TITLE                 | Therapeutically useful synthetic oligonucleotides        |                                        |               |           |          |                 |          |          |
| JOURNAL               | Patent: WO 0144465-A 42 21-JUN-2001;                     |                                        |               |           |          |                 |          |          |
| FEATURES              | Bioniche Life Sciences Inc. (CA)                         |                                        |               |           |          |                 |          |          |
| source                | Location/Qualifiers                                      |                                        |               |           |          |                 |          |          |
|                       | 1..6                                                     |                                        |               |           |          |                 |          |          |
|                       | /organism="synthetic construct"                          |                                        |               |           |          |                 |          |          |
|                       | /mol_type="genomic DNA"                                  |                                        |               |           |          |                 |          |          |
|                       | /db_xref="taxon:32630"                                   |                                        |               |           |          |                 |          |          |
| ORIGIN                |                                                          |                                        |               |           |          |                 |          |          |
| Query Match           | 100.0%;                                                  | Score 6;                               | DB 6;         | Length 6; |          |                 |          |          |
| Best Local Similarity | 100.0%;                                                  | Pred. No. 8.1e+09;                     |               |           |          |                 |          |          |
| Matches               | 6;                                                       | Conservative 0;                        | Mismatches 0; | Indels 0; | Gaps 0;  |                 |          |          |
| QY                    | 1 GGAAGG 6                                               |                                        |               |           |          |                 |          |          |
|                       |                                                          |                                        |               |           |          |                 |          |          |
| DB                    | 1 GGAAGG 6                                               |                                        |               |           |          |                 |          |          |
| RESULT 2              |                                                          |                                        |               |           |          |                 |          |          |
| CQ868961              | CQ868961                                                 | Sequence 115 from Patent WO2004074429. | 5 bp          | DNA       | linear   | PAT 13-SEP-2004 |          |          |
| LOCUS                 | CQ868961                                                 | Sequence 115 from Patent WO2004074429. |               |           |          |                 |          |          |
| DEFINITION            | CQ868961                                                 | Sequence 115 from Patent WO2004074429. |               |           |          |                 |          |          |
| ACCESSION             | CQ868961                                                 | Sequence 115 from Patent WO2004074429. |               |           |          |                 |          |          |
| VERSION               | CQ868961.1                                               | GI:51998888                            |               |           |          |                 |          |          |
| KEYWORDS              |                                                          |                                        |               |           |          |                 |          |          |
| SOURCE                |                                                          | synthetic construct                    |               |           |          |                 |          |          |
| ORGANISM              |                                                          | other sequences; artificial sequences. |               |           |          |                 |          |          |
| REFERENCE             | 1                                                        |                                        |               |           |          |                 |          |          |
| AUTHORS               | freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K. |                                        |               |           |          |                 |          |          |
| TITLE                 | Method for producing second-generation library           |                                        |               |           |          |                 |          |          |
| JOURNAL               | Patent: WO 2004074429-A 115 02-SEP-2004;                 |                                        |               |           |          |                 |          |          |
| FEATURES              | Nuevolution A/S (DK)                                     |                                        |               |           |          |                 |          |          |
| source                | Location/Qualifiers                                      |                                        |               |           |          |                 |          |          |
|                       | 1..5                                                     |                                        |               |           |          |                 |          |          |
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|                       | /mol_type="unassigned DNA"                               |                                        |               |           |          |                 |          |          |
|                       | /db_xref="taxon:32630"                                   |                                        |               |           |          |                 |          |          |
|                       | /note="synthetic construct"                              |                                        |               |           |          |                 |          |          |
| ORIGIN                |                                                          |                                        |               |           |          |                 |          |          |
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| Best Local Similarity | 100.0%;                                                  | Pred. No. 9.7e+09;                     |               |           |          |                 |          |          |
| Matches               | 5;                                                       | Conservative 0;                        | Mismatches 0; | Indels 0; | Gaps 0;  |                 |          |          |
| QY                    | 1 GGAAG 5                                                |                                        |               |           |          |                 |          |          |
|                       |                                                          |                                        |               |           |          |                 |          |          |
| DB                    | 1 GGAAG 5                                                |                                        |               |           |          |                 |          |          |
| RESULT 3              |                                                          |                                        |               |           |          |                 |          |          |
| CQ868981              | CQ868981                                                 | Sequence 135 from Patent WO2004074429. | 5 bp          | DNA       | linear   | PAT 13-SEP-2004 |          |          |
| LOCUS                 | CQ868981                                                 | Sequence 135 from Patent WO2004074429. |               |           |          |                 |          |          |
| DEFINITION            | CQ868981                                                 | Sequence 135 from Patent WO2004074429. |               |           |          |                 |          |          |
| ACCESSION             | CQ868981                                                 | Sequence 135 from Patent WO2004074429. |               |           |          |                 |          |          |
| VERSION               | CQ868981.1                                               | GI:51998908                            |               |           |          |                 |          |          |
| KEYWORDS              |                                                          |                                        |               |           |          |                 |          |          |
| SOURCE                |                                                          | synthetic construct                    |               |           |          |                 |          |          |
| ORGANISM              |                                                          | other sequences; artificial sequences. |               |           |          |                 |          |          |
| REFERENCE             | 1                                                        |                                        |               |           |          |                 |          |          |
| AUTHORS               | freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K. |                                        |               |           |          |                 |          |          |
| TITLE                 | Method for producing second-generation library           |                                        |               |           |          |                 |          |          |
| JOURNAL               | Patent: WO 2004074429-A 135 02-SEP-2004;                 |                                        |               |           |          |                 |          |          |
| FEATURES              | Nuevolution A/S (DK)                                     |                                        |               |           |          |                 |          |          |
| source                | Location/Qualifiers                                      |                                        |               |           |          |                 |          |          |
|                       | 1..5                                                     |                                        |               |           |          |                 |          |          |
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|                       | /mol_type="unassigned DNA"                               |                                        |               |           |          |                 |          |          |
|                       | /db_xref="taxon:32630"                                   |                                        |               |           |          |                 |          |          |
|                       | /note="synthetic construct"                              |                                        |               |           |          |                 |          |          |
| ORIGIN                |                                                          |                                        |               |           |          |                 |          |          |
| Query Match           | 83.3%;                                                   | Score 5;                               | DB 6;         | Length 5; |          |                 |          |          |
| Best Local Similarity | 100.0%;                                                  | Pred. No. 9.7e+09;                     |               |           |          |                 |          |          |
| Matches               | 5;                                                       | Conservative 0;                        | Mismatches 0; | Indels 0; | Gaps 0;  |                 |          |          |
| QY                    | 1 GGAAG 5                                                |                                        |               |           |          |                 |          |          |
|                       |                                                          |                                        |               |           |          |                 |          |          |
| DB                    | 1 GGAAG 5                                                |                                        |               |           |          |                 |          |          |
| RESULT 5              |                                                          |                                        |               |           |          |                 |          |          |
| CQ869130              | CQ869130                                                 | Sequence 284 from Patent WO2004074429. | 5 bp          | DNA       | linear   | PAT 13-SEP-2004 |          |          |
| LOCUS                 | CQ869130                                                 | Sequence 284 from Patent WO2004074429. |               |           |          |                 |          |          |
| DEFINITION            | CQ869130                                                 | Sequence 284 from Patent WO2004074429. |               |           |          |                 |          |          |
| ACCESSION             | CQ869130                                                 | Sequence 284 from Patent WO2004074429. |               |           |          |                 |          |          |
| VERSION               | CQ869130.1                                               | GI:51999057                            |               |           |          |                 |          |          |

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
freakg Rd.P.O., Goulliaev,A.H., Thisted,T. and Olsen,B.K.  
Method for producing second-generation library  
TITLE Patent: WO 2004074429-A 284 02-SEP-2004;  
JOURNAL Nuevolution A/S (DK)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic construct"

ORIGIN  
Query Match 83.3%; Score 5; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.7e+09; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 2 GAAGG 6  
|||||  
Db 5 GAAGG 1

RESULT 6  
AX207361  
LOCUS AX207361  
DEFINITION Sequence 86 from Patent WO015571.  
ACCESSION AX207361  
VERSION AX207361.1 GI:15395161  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 (bases 1 to 5)  
AUTHORS Mauro,V.P., Edelman,G.M., Chappell,G.M., Jones,P.S., Owens,G. and Meech,R.  
TITLE Methods of identifying synthetic transcriptional and translational regulatory elements, and compositions relating to same  
JOURNAL Patent: WO 0155371-A 86 02-AUG-2001;  
The Scripps Research Institute (US)  
FEATURES  
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/mol\_type="genomic DNA"  
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/note="core motif"

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Query Match 83.3%; Score 5; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.7e+09; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 2 GAAGG 6  
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Db 1 GAAGG 5

RESULT 7  
AX236985  
LOCUS AX236985  
DEFINITION Sequence 4 from Patent WO0164959.  
ACCESSION AX236985  
VERSION AX236985.1 GI:15796558  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 (bases 1 to 6)  
AUTHORS Goudemir,J., Yates,S.C., Penning,M.T. and weijer van De,L.H.  
TITLE Detection of hepatitis b virus rna

JOURNAL Patent: WO 0164959-A 4 07-SEP-2001;  
Akzo Nobel N.V. (NL)  
FEATURES  
source Location/Qualifiers  
1..6  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotides"

ORIGIN  
Query Match 83.3%; Score 5; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.1e+09; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 2 GAAGG 6  
|||||  
Db 2 GAAGG 6

RESULT 8  
AX557112  
LOCUS AX557112  
DEFINITION Sequence 10 from Patent WO0244353.  
ACCESSION AX557112  
VERSION AX557112.1 GI:25900165  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
AUTHORS Wolffe,A.P.  
TITLE Human heparanase gene regulatory sequences  
JOURNAL Patent: WO 0244353-A 10 06-JUN-2002;  
Sangamo Biosciences Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..6  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="EST1 binding site"

ORIGIN  
Query Match 83.3%; Score 5; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.1e+09; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GGAAG 5  
|||||  
Db 2 GGAAG 6

RESULT 9  
AX805872  
LOCUS AX805872  
DEFINITION Sequence 18 from Patent WO03060163.  
ACCESSION AX805872  
VERSION AX805872.1 GI:38522783  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
AUTHORS van Eijk,M.J. and van Schaik,C.  
TITLE Discrimination and detection of target nucleotide sequences using mass spectrometry  
JOURNAL Patent: WO 03060163-A 18 24-JUL-2003;  
Keygene N.V. (NL)  
FEATURES  
source Location/Qualifiers  
1..6  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="stuffer sequence"

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ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAAGG 6
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Db 1 GAAGG 5

RESULT 10
S85691/c
LOCUS S85691.1 GI:246481
DEFINITION p53 [human, endometrial adenocarcinoma T152, mRNA Partial Mutant, 6
nt].
ACCESSION S85691
VERSION S85691.1
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6)
AUTHORS Kohler,M.F., Berchuck,A., Davidoff,A.M., Humphrey,P.A., Dodge,R.K.,
Iglehart,J.D., Soper,J.T., Clarke-Pearson,D.L., Bast,R.C. Jr. and
Marks,J.R.
TITLE Overexpression and mutation of p53 in endometrial carcinoma
JOURNAL Cancer Res. 52 (6), 1622-1627 (1992)
MEDLINE 92174188
PUBMED 1540970
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 85691] from the original journal article.
COMMENT TGC to TTC change at codon 242 (Cys to Phe).
FEATURES
source 1..6
/mol_type="mRNA"
/db_xref="taxon:9606"
gene 1..6
/gene="p53"

ORIGIN
Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAAGG 6
 |||||
Db 6 GAAGG 2

RESULT 11
BD269460
LOCUS BD269460
DEFINITION Mitomycin biosynthetic gene cluster.
ACCESSION BD269460
VERSION BD269460.1 GI:33079228
KEYWORDS JP 2002537833-A/74.
SOURCE Streptomyces lavendulae
ORGANISM Streptomyces lavendulae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 6)
AUTHORS Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P.C.
TITLE Mitomycin biosynthetic gene cluster
JOURNAL Patent: JP 2002537833-A 74 12-NOV-2002;
REGENTS OF THE UNIVERSITY OF MINNESOTA
COMMENT OS Streptomyces lavendulae
PN JP 2002537833-A/74
PD 12-NOV-2002
PF 10-MAR-2000 JP 2000603359
PR 12-MAR-1999 US 09/266965

ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
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Db 1 GGAAGG 6

RESULT 13
CQ755704/c

```

```

PI DAVID H SHERMAN, YINGQING MAO, MUSTAFA VAROGLU, MIN HE, PAUL C PI
SHELDON
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P17/10 PC
,C12Q1/68, G01N33/53,
PC G01N33/566//C12N9/00, (C12P17/10, C12R1:465), C12N15/00, C12N5/00
CC Mitomycin biosynthetic gene cluster
FH Key Location/Qualifiers
FT source 1..6
 /organism='Streptomyces lavendulae'.
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source 1..6
/mol_type="genomic DNA"
/db_xref="taxon:1914"
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Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
 |||||
Db 1 GGAAGG 6

RESULT 12
BD269461
LOCUS BD269461
DEFINITION Mitomycin biosynthetic gene cluster.
ACCESSION BD269461
VERSION BD269461.1 GI:33079229
KEYWORDS JP 2002537833-A/75.
SOURCE Streptomyces lavendulae
ORGANISM Streptomyces lavendulae
Bacteria; Actinobacteria; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 6)
AUTHORS Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P.C.
TITLE Mitomycin biosynthetic gene cluster
JOURNAL Patent: JP 2002537833-A 75 12-NOV-2002;
REGENTS OF THE UNIVERSITY OF MINNESOTA
COMMENT OS Streptomyces lavendulae
PN JP 2002537833-A/75
PD 12-NOV-2002
PF 10-MAR-2000 JP 2000603359
PR 12-MAR-1999 US 09/266965
PI DAVID H SHERMAN, YINGQING MAO, MUSTAFA VAROGLU, MIN HE, PAUL C PI
SHELDON
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P17/10 PC
,C12Q1/68, G01N33/53,
PC G01N33/566//C12N9/00, (C12P17/10, C12R1:465), C12N15/00, C12N5/00
CC Mitomycin biosynthetic gene cluster
FH Key Location/Qualifiers
FT source 1..6
 /organism='Streptomyces lavendulae'.
FEATURES
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Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
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Db 1 GGAAGG 6

RESULT 13
CQ755704/c

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LOCUS CQ755704 6 bp DNA linear PAT 01-MAR-2004  
 DEFINITION Sequence 205 from Patent WO2003106674.  
 ACCESSION CQ755704  
 VERSION CQ755704.1 GI:44846509  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
 TITLE Means and methods for regulating gene expression  
 JOURNAL Patent: WO 2003106674-A 205 24-DEC-2003;  
 Chromagenics B.V. (NL)  
 FEATURES  
 source 1..6  
 Location/Qualifiers  
 /organism="synthetic construct"  
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 ORIGIN  
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 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GGAAGG 6  
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 Db 6 GGAGGG 1  
 RESULT 14  
 CQ755751/c  
 LOCUS CQ755751 6 bp DNA linear PAT 01-MAR-2004  
 DEFINITION Sequence 252 from Patent WO2003106674.  
 ACCESSION CQ755751  
 VERSION CQ755751.1 GI:44846556  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
 TITLE Means and methods for regulating gene expression  
 JOURNAL Patent: WO 2003106674-A 252 24-DEC-2003;  
 Chromagenics B.V. (NL)  
 FEATURES  
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 /organism="synthetic construct"  
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 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GGAAGG 6  
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 Db 6 GGAACG 1  
 RESULT 15  
 CQ756128/c  
 LOCUS CQ756128 6 bp DNA linear PAT 01-MAR-2004  
 DEFINITION Sequence 629 from Patent WO2003106674.  
 ACCESSION CQ756128  
 VERSION CQ756128.1 GI:44846933  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.  
 TITLE Means and methods for regulating gene expression  
 JOURNAL Patent: WO 2003106674-A 629 24-DEC-2003;  
 Chromagenics B.V. (NL)  
 FEATURES  
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 /db\_xref="taxon:32630"  
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 ORIGIN  
 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GGAAGG 6  
 |||||  
 Db 6 GGAGGG 1  
 RESULT 16  
 CQ757942/c  
 LOCUS CQ757942 6 bp DNA linear PAT 01-MAR-2004  
 DEFINITION Sequence 246 from Patent WO2003106684.  
 ACCESSION CQ757942  
 VERSION CQ757942.1 GI:44847963  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
 TITLE A method for the simultaneous production of multiple proteins;  
 vectors and cells for use therein  
 JOURNAL Patent: WO 2003106684-A 246 24-DEC-2003;  
 Chromagenics B.V. (NL)  
 FEATURES  
 source 1..6  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="oligonucleotide patterns over-represented in STAR elements"  
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 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GGAAGG 6  
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 Db 6 GGAGGG 1  
 RESULT 17  
 CQ757989/c  
 LOCUS CQ757989 6 bp DNA linear PAT 01-MAR-2004  
 DEFINITION Sequence 293 from Patent WO2003106684.  
 ACCESSION CQ757989  
 VERSION CQ757989.1 GI:44848010  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.  
 TITLE A method for the simultaneous production of multiple proteins;  
 vectors and cells for use therein  
 JOURNAL Patent: WO 2003106684-A 293 24-DEC-2003;  
 Chromagenics B.V. (NL)

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FEATURES
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Location/Qualifiers
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/note="oligonucleotide patterns over-represented in STAR
elements"

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Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 6 GGACGG 1

RESULT 18
AX1758366/c
LOCUS
DEFINITION
Sequence 670 from Patent WO2003106684.
ACCESSION
CQ758366
VERSION
CQ758366.1 GI:44848387
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE
A method for the simultaneous production of multiple proteins;
vectors and cells for use therein
JOURNAL
Patent: WO 2003106684-A 670 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
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ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 6 GGACGG 1

RESULT 19
AX175264/c
LOCUS
DEFINITION
Sequence 28 from Patent WO0144465.
ACCESSION
AX175264
VERSION
AX175264.1 GI:14598632
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 28 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGAGGG 6

RESULT 20
AX175281
LOCUS
DEFINITION
Sequence 45 from Patent WO0144465.
ACCESSION
AX175281
VERSION
AX175281.1 GI:14598649
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 45 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGAGGG 6

RESULT 21
AX175283
LOCUS
DEFINITION
Sequence 47 from Patent WO0144465.
ACCESSION
AX175283
VERSION
AX175283.1 GI:14598651
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 47 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Location/Qualifiers
1..6
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGAGGG 6

RESULT 22
AX552607

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LOCUS AX552607 6 bp RNA linear PAT 27-NOV-2002  
 DEFINITION Sequence 23 from Patent WO02074963.  
 ACCESSION AX552607  
 VERSION AX552607.1 GI:25896616  
 KEYWORDS Dengue virus type 2  
 SOURCE Dengue virus type 2  
 ORGANISM Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.  
 REFERENCE 1  
 AUTHORS Markoff, L. and Zeng, L.  
 TITLE Dengue viruses that are replication defective in mosquitoes for use as vaccines  
 JOURNAL Patent: WO 02074963-A 23 26-SEP-2002;  
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
 FEATURES  
 source 1. .6  
 /organism="Dengue virus type 2"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:11060"  
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 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGAAGG 6  
 |||||  
 Db 1 GTAAGG 6  
 RESULT 23  
 AX552608/c  
 LOCUS AX552608 6 bp RNA linear PAT 27-NOV-2002  
 DEFINITION Sequence 24 from Patent WO02074963.  
 ACCESSION AX552608  
 VERSION AX552608.1 GI:25896617  
 KEYWORDS Dengue virus type 2  
 SOURCE Dengue virus type 2  
 ORGANISM Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.  
 REFERENCE 1  
 AUTHORS Markoff, L. and Zeng, L.  
 TITLE Dengue viruses that are replication defective in mosquitoes for use as vaccines  
 JOURNAL Patent: WO 02074963-A 24 26-SEP-2002;  
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
 FEATURES  
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 /organism="Dengue virus type 2"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:11060"  
 ORIGIN  
 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGAAGG 6  
 |||||  
 Db 6 GTAAGG 1  
 RESULT 24  
 AX743310  
 LOCUS AX743310 6 bp DNA linear PAT 12-MAY-2003  
 DEFINITION Sequence 2 from Patent WO03028764.  
 ACCESSION AX743310  
 VERSION AX743310.1 GI:30577236  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM

other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Phillips, N.C., Filion, M.C. and Herrera-Gayol, A.C.  
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides  
 JOURNAL Patent: WO 03028764-A 2 10-APR-2003;  
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)  
 FEATURES  
 source 1. .6  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic Oligonucleotide"  
 ORIGIN  
 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGAAGG 6  
 |||||  
 Db 1 GGGAGG 6  
 RESULT 25  
 AX743314  
 LOCUS AX743314 6 bp DNA linear PAT 12-MAY-2003  
 DEFINITION Sequence 6 from Patent WO03028764.  
 ACCESSION AX743314  
 VERSION AX743314.1 GI:30577240  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Phillips, N.C., Filion, M.C. and Herrera-Gayol, A.C.  
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides  
 JOURNAL Patent: WO 03028764-A 6 10-APR-2003;  
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)  
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 /note="Synthetic Oligonucleotide"  
 (TEG) Cholesteryl Synthetic Oligonucleotide"  
 ORIGIN  
 Query Match 73.3%; Score 4.4; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGAAGG 6  
 |||||  
 Db 1 GGGAGG 6  
 RESULT 26  
 AX764742/c  
 LOCUS AX764742 6 bp DNA linear PAT 25-JUN-2003  
 DEFINITION Sequence 212 from Patent WO03004704.  
 ACCESSION AX764742  
 VERSION AX764742.1 GI:32258950  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte, A.P. and Kruckeberg, A.L.  
 TITLE Dna sequences comprising gene transcription regulatory qualities and methods for detecting and using such dna sequences  
 JOURNAL Patent: WO 03004704-A 212 16-JAN-2003;

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Chromagenics B.V. (NL)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN

Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
 |||||
Db 6 GGAGGG 1

RESULT 29
LOCUS AX805866/c
DEFINITION Sequence 12 from Patent WO03060163.
ACCESSION AX805866
VERSION AX805866.1 GI:38522777
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS van Eijk,M.J. and van Schaik,C.
TITLE Discrimination and detection of target nucleotide sequences using
 mass spectrometry
JOURNAL Patent: WO 03060163-A 12 24-JUL-2003;
 Keygene N.V. (NL)
FEATURES Location/Qualifiers
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 1..6
 /organism="synthetic construct"
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 /note="stuffer sequence"

ORIGIN

Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
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Db 6 GGAGGG 1

RESULT 30
LOCUS AX816715
DEFINITION Sequence 3 from Patent WO02085340.
ACCESSION AX816715
VERSION AX816715.1 GI:39647044
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Filon,M.C. and Phillips,N.C.
TITLE Oligonucleotide compositions and their use to induce
 differentiation of cells
JOURNAL Patent: WO 02085340-A 3 31-OCT-2002;
 Bioniche Life Sciences Inc. (CA)
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VERSION AX764789.1 GI:32258997
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P. and Kruckeberg,A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
JOURNAL Patent: WO 03004704-A 259 16-JAN-2003;
 Chromagenics B.V. (NL)
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ACCESSION AX765166
VERSION AX765166.1 GI:32259374
KEYWORDS .
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REFERENCE 1
AUTHORS Otte,A.P. and Kruckeberg,A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
JOURNAL Patent: WO 03004704-A 636 16-JAN-2003;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

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| Sequence 74, Appl |       |             |        |    |                   |
| Sequence 79, Appl |       |             |        |    |                   |
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| Sequence 4, Appl  |       |             |        |    |                   |

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| 6 | 9  | US-09-735-363A-24    | Sequence 24, Appl |
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US-09-735-363A-25
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; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
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US-09-735-363A-25

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; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
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US-09-735-363A-25

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; APPLICANT: Fillion, Mario
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; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
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; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
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; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
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US-09-735-363A-79

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; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
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; PRIOR FILING DATE: 1999-12-13  
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; SEQ ID NO 5  
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; TYPE: DNA  
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; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-09-879-668-5

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; Publication No. US20030045493A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiat

; FILE REFERENCE: 02811-0261 (42368-273010)  
; CURRENT APPLICATION NUMBER: US/10/127,645  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US 60/286,158  
; PRIOR FILING DATE: 2001-04-24  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
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US-10-127-645-2

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; Publication No. US20030045493A1  
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; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiat

; FILE REFERENCE: 02811-0261 (42368-273010)  
; CURRENT APPLICATION NUMBER: US/10/127,645  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US 60/286,158  
; PRIOR FILING DATE: 2001-04-24  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
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US-10-127-645-2

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Query Match 100.0%; Score 6; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030119776A1  
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; TITLE OF INVENTION: Modulation of Fas and FasL Expression

; FILE REFERENCE: 02811-0242 (42368-279803)  
; CURRENT APPLICATION NUMBER: US/10/280,274  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 09/879,668  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-5

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 1 GGGTGG 6

RESULT 8  
US-10-264-280-1  
; Sequence 1, Application US/10264280  
; Publication No. US20030125290A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; APPLICANT: Phillips, Nigel C.

; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleot  
; FILE REFERENCE: 02811-0271 (42368-277492)  
; CURRENT APPLICATION NUMBER: US/10/264,280  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 60/326,884  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-10-264-280-1

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-264-280-1

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 1 GGGTGG 6

## RESULT 9

US-10-264-280-3/c  
; Sequence 3, Application US/10264280  
; Publication No. US20030125290A1

; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.  
; APPLICANT: Phillips, Nigel C.

; APPLICANT: Herrera-Gayol, Andrea C.

; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide

; FILE REFERENCE: 02811-0271 42368-277492

; CURRENT APPLICATION NUMBER: US/10/264,280

; CURRENT FILING DATE: 2002-10-03

; PRIOR APPLICATION NUMBER: US 60/326,884

; PRIOR FILING DATE: 2001-10-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-264-280-3

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 6 GGGTGG 1

## RESULT 10

US-10-264-280-5  
; Sequence 5, Application US/10264280  
; Publication No. US20030125290A1

; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.

; APPLICANT: Phillips, Nigel C.

; APPLICANT: Herrera-Gayol, Andrea C.

; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide

; FILE REFERENCE: 02811-0271 42368-277492

; CURRENT APPLICATION NUMBER: US/10/264,280

; CURRENT FILING DATE: 2002-10-03

; PRIOR APPLICATION NUMBER: US 60/326,884

; PRIOR FILING DATE: 2001-10-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide

US-10-264-280-5

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 1 GGGTGG 6

## RESULT 11

US-10-264-280-7/c

; Sequence 7, Application US/10264280

; Publication No. US20030125290A1

; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario C.

; APPLICANT: Phillips, Nigel C.

; APPLICANT: Herrera-Gayol, Andrea C.

; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide

; FILE REFERENCE: 02811-0271 42368-277492

; CURRENT APPLICATION NUMBER: US/10/264,280

; CURRENT FILING DATE: 2002-10-03

; PRIOR APPLICATION NUMBER: US 60/326,884

; PRIOR FILING DATE: 2001-10-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide

US-10-264-280-7

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 6 GGGTGG 1

## RESULT 12

US-10-168-327-1

; Sequence 1, Application US/10168327

; Publication No. US20030176381A1

; GENERAL INFORMATION:  
; APPLICANT: Fillion, Nigel C.

; APPLICANT: Phillips, Nigel C.

; APPLICANT: Herrera-Gayol, Andrea C.

; TITLE OF INVENTION: Hyaluronic Acid in the Treatment of Cancer

; FILE REFERENCE: 02811-0211 (42368-274915)

; CURRENT APPLICATION NUMBER: US/10/168,327

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: PCT/CA00/01562

; PRIOR FILING DATE: 2000-12-28

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide

US-10-168-327-1

Query Match 100.0%; Score 6; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 1 GGGTGG 6

## RESULT 13

US-10-190-312A-252/c

; Sequence 252, Application US/10190312A

; Publication No. US20030199469A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; PRIOR FILING DATE: 2002-07-05

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 252

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-252

Query Match 100.0%; Score 6; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 6 GGGTGG 1

## RESULT 14

US-10-190-312A-1009/c

; Sequence 1009, Application US/10190312A

; Publication No. US20030199469A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; PRIOR FILING DATE: 2002-07-05

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1009

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Dyad patterns over-represented in STAR elements

US-10-190-312A-1009

Query Match 100.0%; Score 6; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 6 GGGTGG 1

## RESULT 15

US-10-420-513A-3

; Sequence 3, Application US/10420513A

; Publication No. US2004005883A1

; GENERAL INFORMATION:

; APPLICANT: Phillips, Nigel C.

; APPLICANT: Fillion, Mario C.

; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of

; FILE REFERENCE: 02811-0301 (42368-283135)

; CURRENT APPLICATION NUMBER: US/10/420,513A

; CURRENT FILING DATE: 2003-04-22

; PRIOR APPLICATION NUMBER: US 60/374,540

; PRIOR FILING DATE: 2002-04-22

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-420-513A-3

Query Match 100.0%; Score 6; DB 18; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6  
|||||  
Db 1 GGGTGG 6

## RESULT 16

US-09-735-363A-60

; Sequence 60, Application US/09735363A

; Patent No. US20010041681A1

; GENERAL INFORMATION:

; APPLICANT: Fillion, Mario

; APPLICANT: Phillip, Nigel

; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

; FILE REFERENCE: 02811-0181

; CURRENT APPLICATION NUMBER: US/09/735,363A

; CURRENT FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: 60/170,325

; PRIOR FILING DATE: 1999-12-13

; PRIOR APPLICATION NUMBER: 60/228,925

; NUMBER OF SEQ ID NOS: 87

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 60

; LENGTH: 5

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-09-735-363A-60

Query Match 83.3%; Score 5; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGTGG 6  
|||||  
Db 1 GGGTGG 5

## RESULT 17

US-09-735-363A-61

; Sequence 61, Application US/09735363A

; Patent No. US20010041681A1

; GENERAL INFORMATION:

; APPLICANT: Fillion, Mario

```
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-61

Query Match 83.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 1 GGGTG 5

RESULT 18
US-10-185-369-2/c
; Sequence 2, Application US/10185369
; Publication No. US2003008256A1
; GENERAL INFORMATION:
; APPLICANT: Androphy, Elliot
; APPLICANT: Doshi, Nishita
; APPLICANT: Belayew, Alexandra
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer
; FILE REFERENCE: 18475-041
; CURRENT APPLICATION NUMBER: US/10/185,369
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,384
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-185-369-2

Query Match 83.3%; Score 5; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 5 GGGTG 1

RESULT 19
US-10-628-432-8/c
; Sequence 8, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Modified ADAMTS4 molecules
; FILE REFERENCE: AM101378
; CURRENT APPLICATION NUMBER: US/10/628,432
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
```

```
; SEQ ID NO 8
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-10-628-432-8

Query Match 83.3%; Score 5; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
Db 5 GGTGG 1

RESULT 20
US-08-463-404-52
; Sequence 52, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,404
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-404-52

Query Match 83.3%; Score 5; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5  
|||||  
Db 2 GGTGG 6

## RESULT 21

US-09-735-363A-24  
; Sequence 24, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-24

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6  
|||||  
Db 1 GGTGG 5

## RESULT 22

US-09-735-363A-73  
; Sequence 73, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 73  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-73

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6  
|||||  
Db 1 GGTGG 5

## RESULT 23

US-09-879-668-4  
; Sequence 4, Application US/09879668  
; Patent No. US20020091095A1  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0241 42368-256931  
; CURRENT APPLICATION NUMBER: US/09/879,668  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-09-879-668-4

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6  
|||||  
Db 1 GGTGG 5

## RESULT 24

US-10-280-274-4  
; Sequence 4, Application US/10280274  
; Publication No. US20030119776A1  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Nigel C.  
; APPLICANT: Fillion, Mario C.  
; TITLE OF INVENTION: Modulation of Fas and FasL Expression  
; FILE REFERENCE: 02811-0242 42368-279803  
; CURRENT APPLICATION NUMBER: US/10/280,274  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/CA00/01467  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 09/879,668  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: US 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: US 60/266,229  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/735,363  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide  
US-10-280-274-4

Query Match 83.3%; Score 5; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-280-274-4

Query Match 83.3%; Score 5; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 GGTGG 6  
Db 1 GGTGG 5

RESULT 25

US-10-232-927A-70  
; Sequence 70, Application US/10232927A  
; Publication No. US20030190638A1

GENERAL INFORMATION:

APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. McEachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,927A

FILING DATE: 29-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,535

FILING DATE: 20-Aug-1999

APPLICATION NUMBER: 08/819,867

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Chambers, Daniel M.

REGISTRATION NUMBER: 34,561

REFERENCE/DOCKET NUMBER: 224/232

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Query Match

Best Local Similarity 83.3%; Score 5; DB 16; Length 6;  
100.0%; Pred. No. 1e+09; 0; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GGTGG 5  
Db 6 GGTGG 2

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGG 5  
Db 2 GGTGG 6

RESULT 26

US-10-190-312A-214/c

; Sequence 214, Application US/10190312A

; Publication No. US20030199468A1

GENERAL INFORMATION:

APPLICANT: Chromagenics B.V.

APPLICANT: Otte, Arie P.

APPLICANT: Kruckeberg, Arthur L.

TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities &  
METHODS FOR DETECTING AND USING SUCH DNA SEQUENCES

FILE REFERENCE: 2183-4993.1

CURRENT APPLICATION NUMBER: US/10/190,312A

PRIOR FILING DATE: 2002-07-05

PRIOR APPLICATION NUMBER: 60/303,199

PRIOR FILING DATE: 2001-07-05

NUMBER OF SEQ ID NOS: 1079

SOFTWARE: PatentIn version 3.1

SEQ ID NO 214

LENGTH: 6

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-214

Query Match

Best Local Similarity 83.3%; Score 5; DB 16; Length 6;

100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGG 5  
Db 5 GGTGG 1

RESULT 27

US-10-190-312A-234/c

; Sequence 234, Application US/10190312A

; Publication No. US20030199468A1

GENERAL INFORMATION:

APPLICANT: Chromagenics B.V.

APPLICANT: Otte, Arie P.

APPLICANT: Kruckeberg, Arthur L.

TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities &  
METHODS FOR DETECTING AND USING SUCH DNA SEQUENCES

FILE REFERENCE: 2183-4993.1

CURRENT APPLICATION NUMBER: US/10/190,312A

PRIOR FILING DATE: 2002-07-05

PRIOR APPLICATION NUMBER: 60/303,199

PRIOR FILING DATE: 2001-07-05

NUMBER OF SEQ ID NOS: 1079

SOFTWARE: PatentIn version 3.1

SEQ ID NO 234

LENGTH: 6

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-234

Query Match

Best Local Similarity 83.3%; Score 5; DB 16; Length 6;

100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGG 5  
Db 6 GGTGG 2

RESULT 28  
US-10-190-312A-242/c  
; Sequence 242, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 242  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-242

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6  
|||||  
DB 6 GGTGG 2

RESULT 29  
US-10-190-312A-280/c  
; Sequence 280, Application US/10190312A  
; Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 280  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-280

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
DB 5 GGGTG 1

RESULT 30  
US-10-190-312A-334/c  
; Sequence 334, Application US/10190312A

Publication No. US20030199468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chromagenics B.V.  
; APPLICANT: Otte, Arie P.  
; APPLICANT: Kruckeberg, Arthur L.  
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities  
; TITLE OF INVENTION: methods for detecting and using such DNA sequences  
; FILE REFERENCE: 2183-4993.1  
; CURRENT APPLICATION NUMBER: US/10/190,312A  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: 60/303,199  
; PRIOR FILING DATE: 2001-07-05  
; NUMBER OF SEQ ID NOS: 1079  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 334  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements  
US-10-190-312A-334

Query Match 83.3%; Score 5; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6  
|||||  
DB 5 GGTGG 1

Search completed: July 21, 2005, 07:13:15  
Job time : 712.6 secs

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